



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 09:39 PM EDT

PDB ID : 1FC5  
Title : CRYSTAL STRUCTURE OF MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN  
Authors : Huang, W.; Cygler, M.; Montreal-Kingston Bacterial Structural Genomics Initiative (BSGI)  
Deposited on : 2000-07-17  
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

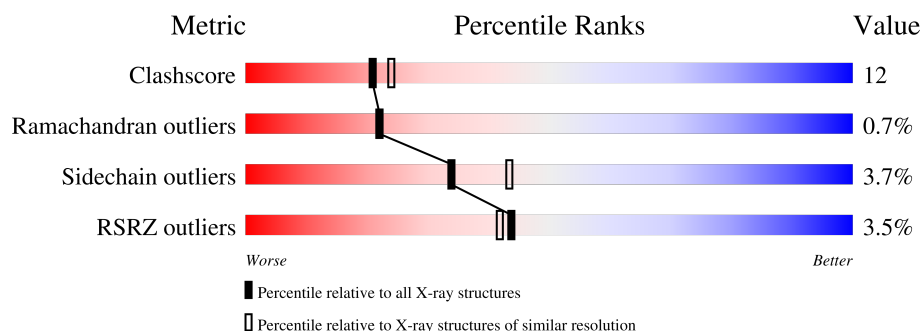
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	411	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div> </div>
1	B	411	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6589 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	Se	0	0	0
			3047	1922	532	580	6	7			
1	B	403	Total	C	N	O	S	Se	0	0	0
			3040	1918	531	578	6	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	8	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	17	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	58	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	99	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	113	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	120	MSE	MET	MODIFIED RESIDUE	UNP P12281
A	212	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	1	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	8	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	17	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	58	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	99	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	113	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	120	MSE	MET	MODIFIED RESIDUE	UNP P12281
B	212	MSE	MET	MODIFIED RESIDUE	UNP P12281

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

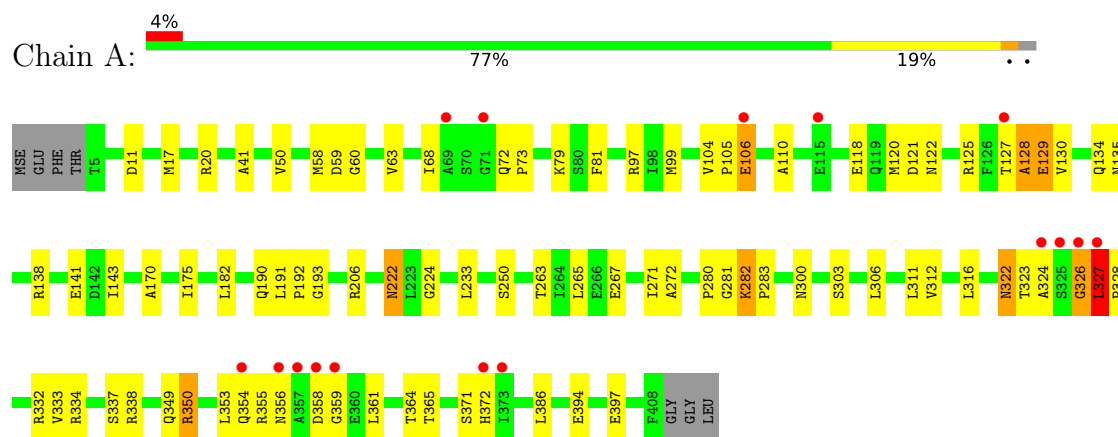
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	201	Total 201	O 201	0	0
3	B	299	Total 299	O 299	0	0

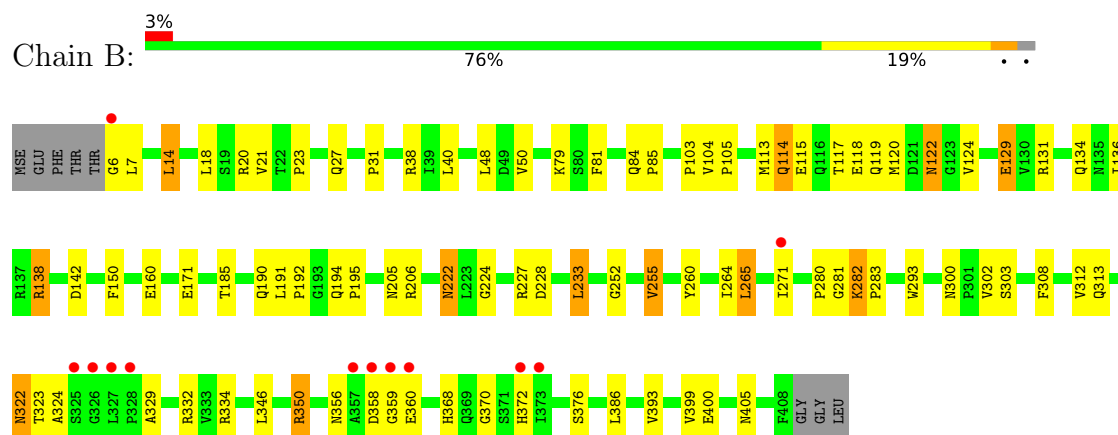
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN



#### • Molecule 1: MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.64Å 101.85Å 103.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 19.99 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 97.9 (19.99-2.20)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.19 (at 2.19Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.253 , 0.297 0.231 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.9	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 48.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6589	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.39	0/3099	0.64	0/4201
1	B	0.40	0/3092	0.65	0/4191
All	All	0.40	0/6191	0.65	0/8392

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3047	0	3044	78	1
1	B	3040	0	3037	78	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	201	0	0	2	0
3	B	299	0	0	8	0
All	All	6589	0	6081	149	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (149) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:ARG:HB3	1:A:338:ARG:NH1	1.72	1.04
1:A:338:ARG:HB3	1:A:338:ARG:HH11	1.17	1.02
1:A:300:ASN:HD21	1:A:371:SER:HB2	1.26	1.01
1:A:190:GLN:HE21	1:A:191:LEU:H	1.02	0.98
1:B:265:LEU:HD22	1:B:271:ILE:HG13	1.48	0.95
1:A:332:ARG:HE	1:B:360:GLU:HG3	1.31	0.94
1:B:81:PHE:HB2	1:B:84:GLN:HB2	1.58	0.84
1:A:327:LEU:HB3	1:A:328:PRO:HD2	1.61	0.83
1:A:300:ASN:ND2	1:A:371:SER:HB2	1.96	0.81
1:B:122:ASN:HD22	1:B:122:ASN:H	1.29	0.79
1:A:190:GLN:NE2	1:A:191:LEU:H	1.81	0.78
1:A:190:GLN:HE21	1:A:191:LEU:N	1.82	0.76
1:B:85:PRO:HB3	1:B:103:PRO:HG2	1.67	0.75
1:B:119:GLN:C	1:B:120:MSE:HE2	2.08	0.74
1:B:119:GLN:O	1:B:120:MSE:HE2	1.86	0.73
1:A:326:GLY:O	1:A:327:LEU:HB2	1.90	0.71
1:A:355:ARG:NH2	1:B:400:GLU:OE1	2.23	0.70
1:B:300:ASN:HD22	1:B:303:SER:H	1.39	0.70
1:A:79:LYS:HG3	1:A:97:ARG:HB3	1.73	0.69
1:A:322:ASN:HD22	1:A:323:THR:N	1.91	0.69
1:B:118:GLU:HB3	1:B:120:MSE:HE3	1.75	0.68
1:B:222:ASN:HD22	1:B:224:GLY:H	1.43	0.65
1:A:280:PRO:HD2	1:A:306:LEU:HD22	1.80	0.64
1:B:194:GLN:HE21	1:B:195:PRO:HD2	1.63	0.64
1:A:372:HIS:O	1:B:142:ASP:OD1	2.16	0.63
1:B:322:ASN:ND2	1:B:324:ALA:H	1.97	0.63
1:B:136:ILE:HG21	1:B:138:ARG:NH2	2.12	0.63
1:A:191:LEU:HB3	1:A:192:PRO:HD2	1.81	0.62
1:B:85:PRO:HB3	1:B:103:PRO:CG	2.29	0.61
1:A:127:THR:O	1:A:128:ALA:CB	2.47	0.61
1:A:170:ALA:HB2	1:B:192:PRO:HB2	1.82	0.61
1:A:73:PRO:HB3	1:A:120:MSE:HG3	1.83	0.61
1:B:194:GLN:HG3	1:B:195:PRO:HD2	1.84	0.60
1:B:228:ASP:HA	1:B:260:TYR:OH	2.01	0.60
1:A:79:LYS:HE3	1:A:97:ARG:HG3	1.83	0.60
1:A:338:ARG:HH11	1:A:338:ARG:CB	2.04	0.59
1:A:222:ASN:HD22	1:A:224:GLY:H	1.50	0.59
1:A:60:GLY:O	1:A:97:ARG:HD2	2.02	0.59
1:B:222:ASN:ND2	1:B:224:GLY:H	2.01	0.58
1:A:364:THR:HG22	1:A:365:THR:N	2.17	0.58
1:A:300:ASN:HD22	1:A:303:SER:H	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:MSE:HG3	1:B:115:GLU:HG2	1.86	0.58
1:B:79:LYS:HD3	1:B:81:PHE:CZ	2.40	0.57
1:A:63:VAL:HG21	1:A:68:ILE:HD11	1.87	0.56
1:A:327:LEU:HB3	1:A:328:PRO:CD	2.33	0.56
1:A:222:ASN:ND2	1:A:224:GLY:H	2.05	0.55
1:A:322:ASN:ND2	1:A:324:ALA:H	2.04	0.55
1:B:356:ASN:OD1	1:B:358:ASP:HB3	2.06	0.55
1:B:322:ASN:HD22	1:B:323:THR:N	2.05	0.55
1:A:263:THR:O	1:A:267:GLU:HG3	2.08	0.54
1:B:368:HIS:CD2	1:B:372:HIS:HE1	2.26	0.54
1:B:6:GLY:O	1:B:7:LEU:HD23	2.07	0.54
1:B:350:ARG:HD2	1:B:376:SER:CB	2.38	0.54
1:B:117:THR:HG23	1:B:124:VAL:HG13	1.90	0.54
1:A:327:LEU:CB	1:A:328:PRO:HD2	2.36	0.54
1:A:282:LYS:HB3	1:A:283:PRO:HD3	1.90	0.53
1:B:350:ARG:HD2	1:B:376:SER:OG	2.09	0.53
1:A:300:ASN:HB2	3:A:2198:HOH:O	2.09	0.53
3:A:2230:HOH:O	1:B:192:PRO:HB3	2.09	0.52
1:B:190:GLN:HE21	1:B:191:LEU:H	1.58	0.52
1:A:121:ASP:O	1:A:122:ASN:HB2	2.09	0.52
1:B:332:ARG:HA	1:B:399:VAL:O	2.09	0.52
1:A:206:ARG:HD2	1:A:222:ASN:HD21	1.75	0.52
1:A:353:LEU:HD22	1:A:361:LEU:HB3	1.92	0.52
1:A:358:ASP:HB3	1:B:332:ARG:HH12	1.75	0.51
1:B:150:PHE:CZ	1:B:160:GLU:HB3	2.45	0.51
1:B:281:GLY:O	1:B:282:LYS:CB	2.59	0.51
1:B:206:ARG:HH11	1:B:222:ASN:HD21	1.58	0.51
1:A:106:GLU:N	1:A:106:GLU:OE1	2.44	0.50
1:B:281:GLY:O	1:B:282:LYS:HB2	2.11	0.50
1:B:356:ASN:OD1	1:B:359:GLY:N	2.45	0.50
1:A:20:ARG:NH1	1:A:20:ARG:HB3	2.26	0.49
1:A:282:LYS:HB3	1:A:283:PRO:CD	2.42	0.49
1:A:125:ARG:NH1	1:A:125:ARG:HB3	2.27	0.49
1:B:368:HIS:CD2	1:B:370:GLY:H	2.30	0.49
1:A:138:ARG:O	1:A:141:GLU:HG2	2.13	0.49
1:A:17:MSE:SE	1:A:311:LEU:HD22	2.63	0.49
1:A:358:ASP:C	1:B:332:ARG:NH1	2.66	0.48
1:A:118:GLU:CD	1:A:125:ARG:HH12	2.16	0.48
1:B:350:ARG:HD2	1:B:376:SER:HB2	1.95	0.48
1:B:122:ASN:H	1:B:122:ASN:ND2	2.05	0.48
1:A:356:ASN:OD1	1:A:359:GLY:N	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:THR:O	1:A:128:ALA:HB3	2.14	0.48
1:A:222:ASN:HD22	1:A:222:ASN:C	2.16	0.47
1:A:337:SER:OG	1:A:364:THR:HG23	2.13	0.47
1:B:118:GLU:CB	1:B:120:MSE:HE3	2.43	0.47
1:B:300:ASN:HD21	1:B:302:VAL:HB	1.79	0.47
1:A:322:ASN:HD22	1:A:322:ASN:C	2.13	0.47
1:A:72:GLN:HB3	1:A:73:PRO:HD2	1.97	0.47
1:B:38:ARG:NH2	3:B:2025:HOH:O	2.48	0.47
1:B:20:ARG:NH2	3:B:2127:HOH:O	2.47	0.47
1:B:308:PHE:HA	1:B:312:VAL:HG23	1.95	0.47
1:B:31:PRO:HA	1:B:171:GLU:HG2	1.96	0.47
1:B:21:VAL:HG12	1:B:293:TRP:CE2	2.50	0.46
1:B:129:GLU:HG3	3:B:2244:HOH:O	2.14	0.46
1:B:329:ALA:HB3	3:B:2503:HOH:O	2.14	0.46
1:A:354:GLN:O	1:A:361:LEU:HA	2.15	0.46
1:B:50:VAL:O	1:B:142:ASP:HB2	2.16	0.46
1:B:233:LEU:HD12	1:B:264:ILE:HD12	1.97	0.46
1:B:48:LEU:HD22	3:B:2254:HOH:O	2.16	0.46
1:B:233:LEU:CD1	1:B:264:ILE:HD12	2.46	0.46
1:B:122:ASN:HD22	1:B:122:ASN:N	1.97	0.45
1:B:14:LEU:HD22	1:B:18:LEU:CD1	2.47	0.45
1:B:131:ARG:O	1:B:134:GLN:HG2	2.16	0.45
1:B:370:GLY:HA3	1:B:372:HIS:CE1	2.52	0.45
1:A:129:GLU:CD	1:A:130:VAL:H	2.21	0.44
1:A:333:VAL:HG13	1:A:361:LEU:O	2.18	0.44
1:A:58:MSE:HG3	1:A:135:ASN:CG	2.37	0.44
1:A:81:PHE:HD1	1:A:99:MSE:HG3	1.83	0.44
1:A:182:LEU:HD11	1:A:250:SER:HB3	2.00	0.44
1:A:106:GLU:H	1:A:106:GLU:CD	2.21	0.43
1:A:20:ARG:HB3	1:A:20:ARG:HH11	1.84	0.43
1:A:333:VAL:HG12	1:A:334:ARG:N	2.32	0.43
1:B:280:PRO:HG3	1:B:302:VAL:HG12	2.00	0.43
1:A:120:MSE:SE	1:A:125:ARG:NH1	3.01	0.43
1:A:281:GLY:O	1:A:282:LYS:HB2	2.19	0.43
1:A:355:ARG:HD3	1:A:359:GLY:HA2	2.01	0.43
1:A:338:ARG:NH2	1:A:394:GLU:OE2	2.46	0.42
1:B:346:LEU:HD12	1:B:386:LEU:O	2.18	0.42
1:B:14:LEU:HD22	1:B:18:LEU:HD11	2.01	0.42
1:B:205:ASN:HB2	3:B:2106:HOH:O	2.19	0.42
1:A:110:ALA:HB1	1:A:134:GLN:HG2	2.01	0.42
1:B:222:ASN:HD22	1:B:222:ASN:C	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:PRO:O	1:A:106:GLU:C	2.57	0.42
1:B:118:GLU:CD	1:B:120:MSE:HE1	2.39	0.42
1:B:122:ASN:ND2	1:B:122:ASN:N	2.65	0.42
1:B:104:VAL:HA	1:B:105:PRO:HD3	1.89	0.42
1:B:255:VAL:HB	1:B:283:PRO:HB2	2.02	0.41
1:B:356:ASN:C	1:B:358:ASP:N	2.73	0.41
1:A:79:LYS:HA	1:A:97:ARG:O	2.20	0.41
1:B:118:GLU:OE2	1:B:120:MSE:HE1	2.20	0.41
1:B:114:GLN:O	1:B:117:THR:HB	2.20	0.41
1:B:23:PRO:HG2	3:B:2336:HOH:O	2.21	0.41
1:A:50:VAL:HB	1:A:143:ILE:HB	2.03	0.41
1:A:358:ASP:O	1:B:332:ARG:NH1	2.53	0.41
1:A:41:ALA:HB2	1:A:175:ILE:HD13	2.02	0.41
1:A:312:VAL:O	1:A:316:LEU:HG	2.21	0.41
1:A:394:GLU:O	1:A:397:GLU:HG3	2.21	0.41
1:B:185:THR:O	1:B:252:GLY:HA3	2.21	0.41
1:A:338:ARG:HE	1:A:394:GLU:CD	2.24	0.41
1:A:353:LEU:C	1:A:354:GLN:HG3	2.41	0.41
1:B:368:HIS:CD2	1:B:372:HIS:CE1	3.08	0.41
1:A:271:ILE:HG22	1:A:272:ALA:N	2.36	0.40
1:A:104:VAL:HA	1:A:105:PRO:HD3	1.90	0.40
1:A:349:GLN:NE2	1:A:386:LEU:HD12	2.35	0.40
1:B:313:GLN:HE22	1:B:405:ASN:HD21	1.69	0.40
1:B:324:ALA:HB2	3:B:2050:HOH:O	2.22	0.40
1:A:350:ARG:HD3	1:A:350:ARG:N	2.37	0.40
1:B:233:LEU:HB3	1:B:264:ILE:HD13	2.02	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:GLY:O	1:B:227:ARG:NH1[3_645]	2.14	0.06

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	402/411 (98%)	385 (96%)	12 (3%)	5 (1%)	13	10
1	B	401/411 (98%)	388 (97%)	12 (3%)	1 (0%)	47	55
All	All	803/822 (98%)	773 (96%)	24 (3%)	6 (1%)	22	22

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	GLU
1	A	128	ALA
1	A	282	LYS
1	B	282	LYS
1	A	327	LEU
1	A	326	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	326/323 (101%)	317 (97%)	9 (3%)	43	56
1	B	325/323 (101%)	310 (95%)	15 (5%)	27	34
All	All	651/646 (101%)	627 (96%)	24 (4%)	34	43

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ASP
1	A	59	ASP
1	A	129	GLU
1	A	222	ASN
1	A	233	LEU
1	A	265	LEU
1	A	322	ASN

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Mol	Chain	Res	Type
1	A	327	LEU
1	A	350	ARG
1	B	14	LEU
1	B	27	GLN
1	B	40	LEU
1	B	114	GLN
1	B	122	ASN
1	B	129	GLU
1	B	138	ARG
1	B	222	ASN
1	B	233	LEU
1	B	255	VAL
1	B	265	LEU
1	B	322	ASN
1	B	334	ARG
1	B	350	ARG
1	B	393	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	84	GLN
1	A	190	GLN
1	A	205	ASN
1	A	210	HIS
1	A	222	ASN
1	A	300	ASN
1	A	310	GLN
1	A	313	GLN
1	A	322	ASN
1	B	34	GLN
1	B	122	ASN
1	B	190	GLN
1	B	194	GLN
1	B	205	ASN
1	B	210	HIS
1	B	222	ASN
1	B	300	ASN
1	B	310	GLN
1	B	313	GLN
1	B	322	ASN

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Mol	Chain	Res	Type
1	B	368	HIS
1	B	372	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	397/411 (96%)	-0.06	16 (4%)	38 36	10, 22, 36, 42	3 (0%)
1	B	396/411 (96%)	-0.11	12 (3%)	50 48	9, 20, 34, 42	3 (0%)
All	All	793/822 (96%)	-0.08	28 (3%)	44 42	9, 21, 36, 42	6 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	326	GLY	5.4
1	A	327	LEU	4.6
1	A	326	GLY	4.5
1	A	358	ASP	4.4
1	B	271	ILE	4.3
1	B	372	HIS	3.9
1	A	373	ILE	3.8
1	A	372	HIS	3.7
1	A	325	SER	3.5
1	A	69	ALA	3.5
1	B	357	ALA	3.3
1	A	127	THR	3.3
1	A	357	ALA	3.1
1	B	327	LEU	3.1
1	A	106	GLU	3.1
1	B	328	PRO	3.0
1	B	358	ASP	2.8
1	B	325	SER	2.8
1	B	359	GLY	2.8
1	A	354	GLN	2.7
1	B	6	GLY	2.7
1	A	71	GLY	2.5
1	A	115	GLU	2.4
1	A	324	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	373	ILE	2.3
1	B	360	GLU	2.3
1	A	359	GLY	2.0
1	A	356	ASN	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	B	4001	1/1	0.92	0.04	22,22,22,22	0
2	MG	A	4002	1/1	0.94	0.04	19,19,19,19	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.