



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 5, 2023 – 06:42 PM EDT

PDB ID : 4D9Q
Title : Inhibiting Alternative Pathway Complement Activation by Targeting the Exosite on Factor D
Authors : Murray, J.M.; Wiesmann, C.
Deposited on : 2012-01-11
Resolution : 2.28 Å(reported)

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

We welcome your comments at 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>.

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 : 2.35
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) : 2.35

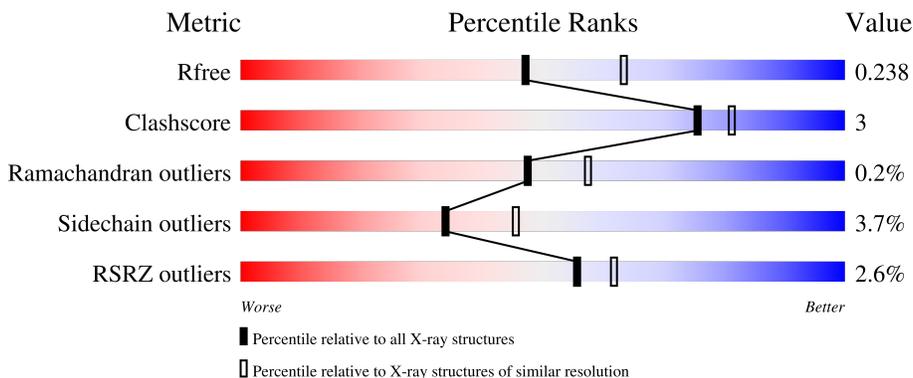
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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.



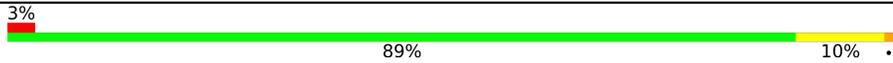
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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 ≥ 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	228	93% 7% .
1	B	228	87% 12% .
2	D	213	87% 13%
2	L	213	92% 8%
3	E	217	88% 8% ..

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Mol	Chain	Length	Quality of chain
3	H	217	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a small red segment on the left labeled '3%', a large green segment in the middle labeled '89%', and a small yellow segment on the right labeled '10%'. A small black dot is located at the far right end of the bar.</p>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 10620 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 Factor D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	228	1726	1063	330	322	11	0	2	0
1	B	228	1726	1063	330	322	11	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	VAL	LEU	conflict	UNP F6YBP7
B	47	VAL	LEU	conflict	UNP F6YBP7

- Molecule 2 is a protein called Anti-Factor D, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	213	1624	1011	270	338	5	0	0	0
2	L	213	1624	1011	270	338	5	0	0	0

- Molecule 3 is a protein called Anti-Factor D, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	212	1592	1009	260	317	6	0	0	0
3	H	216	1618	1024	265	323	6	0	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	H	1	Total C O 6 3 3	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

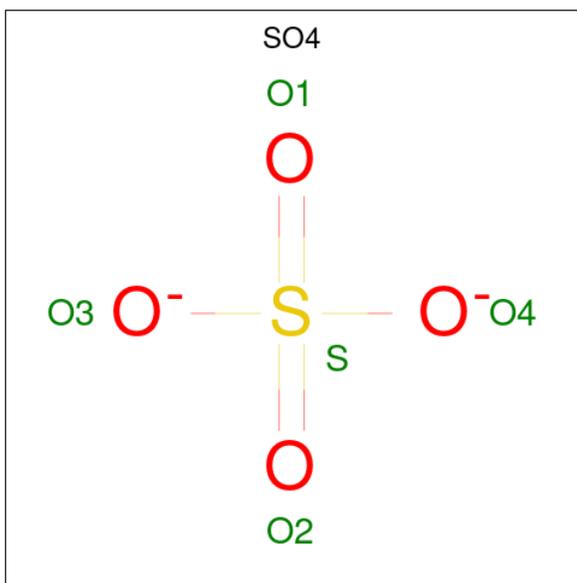
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0
5	B	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	2	Total	Zn	0	0
			2	2		
5	H	1	Total	Zn	0	0
			1	1		
5	L	2	Total	Zn	0	0
			2	2		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	124	Total	O	0	0
			124	124		
7	B	69	Total	O	0	0
			69	69		
7	D	133	Total	O	0	0
			133	133		

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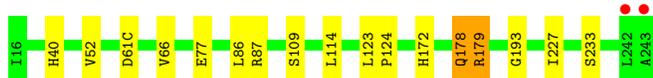
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	E	113	Total 113	O 113	0	0
7	H	66	Total 66	O 66	0	0
7	L	123	Total 123	O 123	0	0

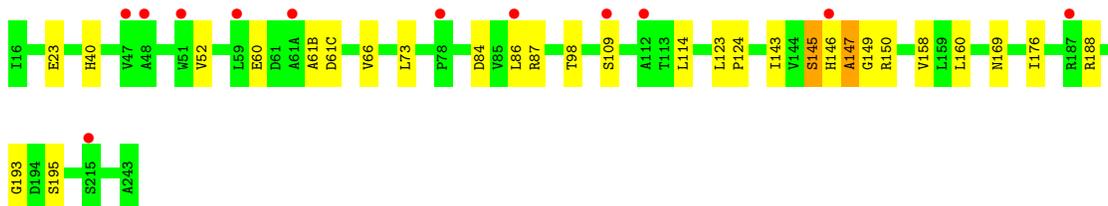
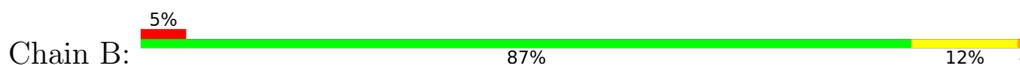
3 Residue-property plots [i](#)

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.

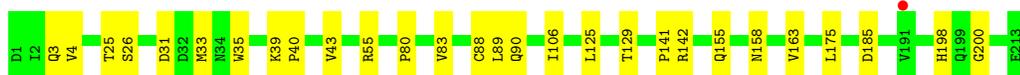
- Molecule 1: Factor D



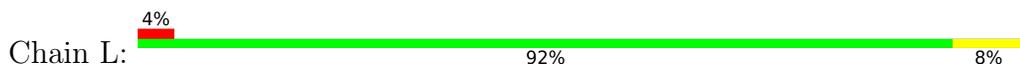
- Molecule 1: Factor D



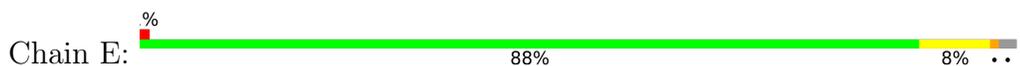
- Molecule 2: Anti-Factor D, light chain



- Molecule 2: Anti-Factor D, light chain

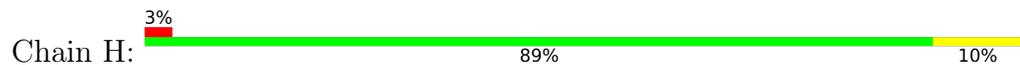


- Molecule 3: Anti-Factor D, heavy chain





- Molecule 3: Anti-Factor D, heavy chain



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.33Å 80.76Å 142.63Å 90.00° 107.19° 90.00°	Depositor
Resolution (Å)	33.38 – 2.28 73.27 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.6 (33.38-2.28) 99.8 (73.27-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.29Å)	Xtrriage
Refinement program	BUSTER-TNT BUSTER 2.11.2, BUSTER 2.11.2	Depositor
R, R_{free}	0.189 , 0.230 0.199 , 0.238	Depositor DCC
R_{free} test set	4589 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtrriage
Anisotropy	0.263	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10620	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ZN, GOL

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	0.58	0/1771	0.68	0/2406
1	B	0.57	0/1771	0.70	0/2406
2	D	0.54	0/1656	0.71	0/2252
2	L	0.53	0/1656	0.70	0/2252
3	E	0.50	0/1631	0.71	0/2224
3	H	0.47	0/1658	0.70	0/2261
All	All	0.53	0/10143	0.70	0/13801

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	147	ALA	Peptide

5.2 Too-close contacts [i](#)

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	1726	0	1709	8	0
1	B	1726	0	1709	10	0
2	D	1624	0	1582	16	0
2	L	1624	0	1582	10	0
3	E	1592	0	1550	10	0
3	H	1618	0	1579	12	0
4	A	12	0	16	0	0
4	B	18	0	24	0	0
4	D	12	0	16	1	0
4	E	12	0	16	0	0
4	H	6	0	8	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	D	2	0	0	0	0
5	H	1	0	0	0	0
5	L	2	0	0	0	0
6	A	10	0	0	0	0
6	B	5	0	0	0	0
7	A	124	0	0	1	0
7	B	69	0	0	0	0
7	D	133	0	0	2	0
7	E	113	0	0	1	0
7	H	66	0	0	0	0
7	L	123	0	0	0	0
All	All	10620	0	9791	62	0

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 3.

The worst 5 of 62 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)
2:D:155:GLN:HE21	2:D:158:ASN:HD21	1.31	0.75
1:B:169:ASN:HD21	1:B:176:ILE:H	1.36	0.73
1:A:77:GLU:HG3	7:A:522:HOH:O	1.90	0.71
3:E:109:ASN:HD21	3:E:111:TRP:HE1	1.41	0.69
1:A:123:LEU:HD12	1:A:124:PRO:HD2	1.76	0.68

There are no symmetry-related clashes.

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	228/228 (100%)	222 (97%)	6 (3%)	0	100	100
1	B	228/228 (100%)	217 (95%)	10 (4%)	1 (0%)	34	40
2	D	211/213 (99%)	204 (97%)	6 (3%)	1 (0%)	29	34
2	L	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
3	E	208/217 (96%)	201 (97%)	7 (3%)	0	100	100
3	H	214/217 (99%)	205 (96%)	9 (4%)	0	100	100
All	All	1300/1316 (99%)	1254 (96%)	44 (3%)	2 (0%)	47	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	61(B)	ALA
2	D	40	PRO

5.3.2 Protein sidechains [i](#)

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	186/184 (101%)	181 (97%)	5 (3%)	44	59
1	B	186/184 (101%)	173 (93%)	13 (7%)	15	18
2	D	190/190 (100%)	185 (97%)	5 (3%)	46	60
2	L	190/190 (100%)	186 (98%)	4 (2%)	53	68
3	E	179/183 (98%)	172 (96%)	7 (4%)	32	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	182/183 (100%)	175 (96%)	7 (4%)	33	44
All	All	1113/1114 (100%)	1072 (96%)	41 (4%)	34	45

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	214	LYS
3	H	187	SER
3	E	222	LYS
3	H	50	TRP
2	L	89	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	109	ASN
3	H	208	HIS
2	L	210	ASN
2	L	52	ASN
3	H	205	ASN

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 20 ligands modelled in this entry, 7 are monoatomic - leaving 13 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	D	301	-	5,5,5	0.24	0	5,5,5	0.86	0
4	GOL	A	302	-	5,5,5	0.08	0	5,5,5	0.37	0
4	GOL	H	301	-	5,5,5	0.15	0	5,5,5	0.45	0
4	GOL	B	302	-	5,5,5	0.16	0	5,5,5	0.29	0
4	GOL	E	302	-	5,5,5	0.12	0	5,5,5	0.26	0
4	GOL	A	301	-	5,5,5	0.25	0	5,5,5	0.48	0
6	SO4	A	305	-	4,4,4	0.17	0	6,6,6	0.12	0
4	GOL	B	301	-	5,5,5	0.11	0	5,5,5	0.25	0
4	GOL	E	301	-	5,5,5	0.17	0	5,5,5	0.54	0
6	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.23	0
4	GOL	B	303	-	5,5,5	0.12	0	5,5,5	0.49	0
6	SO4	B	305	-	4,4,4	0.14	0	6,6,6	0.23	0
4	GOL	D	302	-	5,5,5	0.23	0	5,5,5	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	D	301	-	-	4/4/4/4	-
4	GOL	A	302	-	-	1/4/4/4	-
4	GOL	H	301	-	-	2/4/4/4	-
4	GOL	B	302	-	-	0/4/4/4	-
4	GOL	E	302	-	-	1/4/4/4	-
4	GOL	A	301	-	-	1/4/4/4	-
4	GOL	B	301	-	-	0/4/4/4	-
4	GOL	E	301	-	-	4/4/4/4	-
4	GOL	B	303	-	-	1/4/4/4	-
4	GOL	D	302	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	301	GOL	C1-C2-C3-O3
4	H	301	GOL	C1-C2-C3-O3
4	B	303	GOL	O1-C1-C2-C3
4	E	301	GOL	C1-C2-C3-O3
4	D	301	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	301	GOL	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	228/228 (100%)	0.11	2 (0%) 84 87	28, 40, 73, 99	0
1	B	228/228 (100%)	0.59	12 (5%) 26 31	24, 53, 86, 98	0
2	D	213/213 (100%)	0.27	1 (0%) 91 93	22, 40, 71, 105	0
2	L	213/213 (100%)	0.37	9 (4%) 36 41	25, 42, 75, 114	0
3	E	212/217 (97%)	0.13	3 (1%) 75 79	24, 43, 74, 109	0
3	H	216/217 (99%)	0.32	7 (3%) 47 53	25, 51, 80, 114	0
All	All	1310/1316 (99%)	0.30	34 (2%) 56 62	22, 46, 79, 114	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	61(A)	ALA	8.9
3	H	138	SER	8.9
3	H	140	SER	6.7
3	H	137	LYS	6.1
1	B	78	PRO	5.7

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, 95th 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(Å ²)	Q<0.9
4	GOL	A	302	6/6	0.76	0.32	76,77,78,79	0
4	GOL	D	302	6/6	0.76	0.26	55,62,66,69	0
4	GOL	H	301	6/6	0.76	0.33	59,62,63,64	0
4	GOL	E	301	6/6	0.83	0.23	44,60,65,65	0
4	GOL	B	303	6/6	0.83	0.25	64,69,70,73	0
6	SO4	A	305	5/5	0.84	0.26	127,127,128,129	0
4	GOL	B	302	6/6	0.87	0.17	58,64,68,70	0
4	GOL	D	301	6/6	0.87	0.22	38,51,52,54	0
4	GOL	E	302	6/6	0.89	0.22	49,57,60,62	0
5	ZN	D	304	1/1	0.94	0.13	83,83,83,83	0
5	ZN	L	302	1/1	0.94	0.10	96,96,96,96	0
5	ZN	A	303	1/1	0.94	0.18	124,124,124,124	0
5	ZN	H	302	1/1	0.95	0.14	73,73,73,73	0
6	SO4	B	305	5/5	0.95	0.11	82,84,84,87	0
4	GOL	B	301	6/6	0.97	0.15	30,31,34,35	0
5	ZN	L	301	1/1	0.98	0.24	41,41,41,41	0
5	ZN	D	303	1/1	0.98	0.23	33,33,33,33	0
4	GOL	A	301	6/6	0.98	0.12	32,32,33,34	0
5	ZN	B	304	1/1	0.98	0.17	36,36,36,36	0
6	SO4	A	304	5/5	0.99	0.11	53,53,53,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.