



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 12:35 PM GMT

PDB ID : 2ADF
Title : Crystal Structure and Paratope Determination of 82D6A3, an Antithrombotic Antibody Directed Against the von Willebrand factor A3-Domain
Authors : Staelens, S.; Hadders, M.A.; Vauterin, S.; Platteau, C.; Vanhoorelbeke, K.; Huizinga, E.G.; Deckmyn, H.
Deposited on : 2005-07-20
Resolution : 1.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

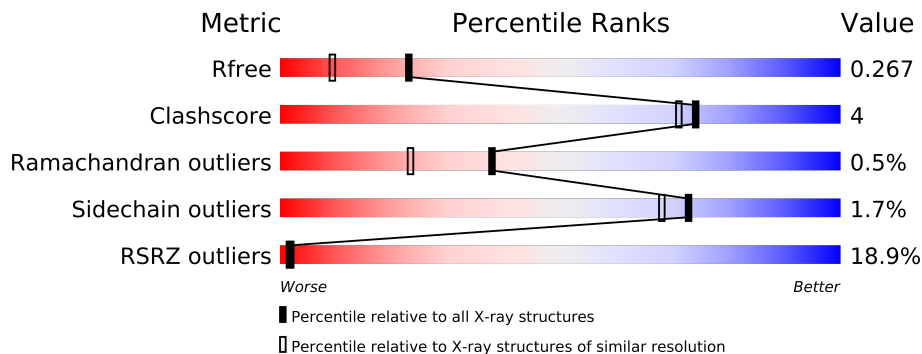
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	196	
2	H	218	
3	L	209	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	SO4	L	1003	-	X
6	GOL	H	1004	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5165 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Von Willebrand factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	189	Total	C	N	O	S	0	0	0
			1414	894	242	272	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	916	GLY	-	EXPRESSION TAG	UNP P04275
A	917	SER	-	EXPRESSION TAG	UNP P04275
A	918	HIS	-	EXPRESSION TAG	UNP P04275
A	919	MET	-	EXPRESSION TAG	UNP P04275

- Molecule 2 is a protein called 82D6A3 IgG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	218	Total	C	N	O	S	0	0	0
			1665	1056	272	330	7			

- Molecule 3 is a protein called 82D6A3 IgG.

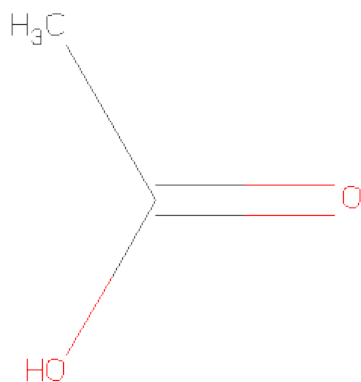
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	209	Total	C	N	O	S	0	0	0
			1624	1015	274	329	6			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			6	3	3		

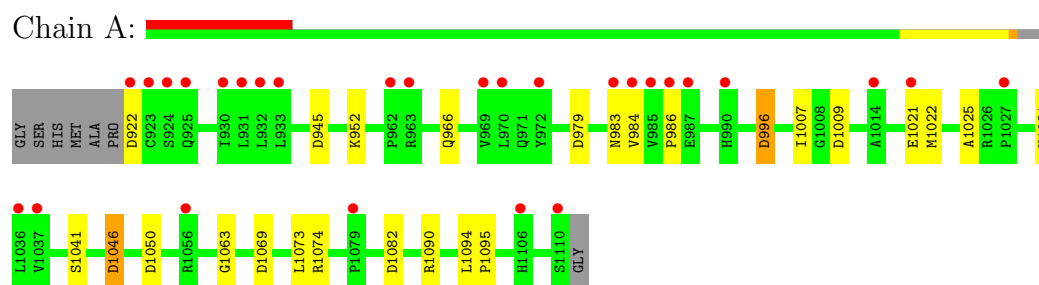
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	136	Total	O	0	0
			136	136		
7	H	155	Total	O	0	0
			155	155		
7	L	151	Total	O	0	0
			151	151		

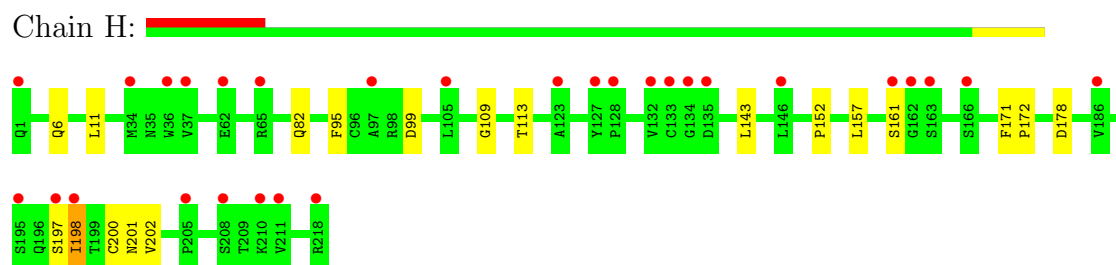
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

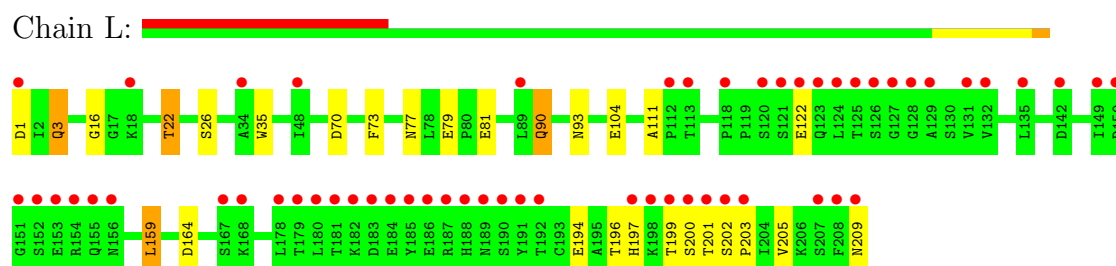
- Molecule 1: Von Willebrand factor



- Molecule 2: 82D6A3 IgG



- Molecule 3: 82D6A3 IgG



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.18Å 89.08Å 123.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.35 – 1.90 27.34 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (27.35-1.90) 99.8 (27.34-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.25 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.191 , 0.220 0.246 , 0.267	Depositor DCC
R_{free} test set	3240 reflections (5.12%)	DCC
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 30.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63303 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5165	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.48	0/1439	0.86	10/1957 (0.5%)
2	H	0.46	0/1709	0.74	2/2333 (0.1%)
3	L	0.60	2/1662 (0.1%)	0.81	3/2253 (0.1%)
All	All	0.52	2/4810 (0.0%)	0.80	15/6543 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	209	ASN	C-OXT	13.29	1.48	1.23
3	L	122	GLU	CD-OE1	5.28	1.31	1.25

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	979	ASP	CB-CG-OD2	7.34	124.91	118.30
3	L	159	LEU	CA-CB-CG	6.80	130.94	115.30
2	H	99	ASP	CB-CG-OD2	5.67	123.41	118.30
1	A	1009	ASP	CB-CG-OD2	5.66	123.40	118.30
1	A	1082	ASP	CB-CG-OD2	5.63	123.36	118.30
1	A	1050	ASP	CB-CG-OD2	5.54	123.28	118.30
1	A	1090	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	A	922	ASP	CB-CG-OD2	5.28	123.06	118.30
3	L	70	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	1046	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	996	ASP	CB-CG-OD2	5.20	122.98	118.30
3	L	164	ASP	CB-CG-OD2	5.08	122.88	118.30
1	A	1069	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	945	ASP	CB-CG-OD2	5.03	122.83	118.30
2	H	178	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1414	0	1425	10	0
2	H	1665	0	1621	13	0
3	L	1624	0	1567	14	0
4	H	5	0	0	0	0
4	L	5	0	0	0	0
5	A	4	0	3	0	0
6	H	6	0	8	1	0
7	A	136	0	0	2	0
7	H	155	0	0	4	0
7	L	151	0	0	2	0
All	All	5165	0	4624	38	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (38) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:L:200:SER:HB3	3:L:202:SER:O	1.63	0.99
2:H:161:SER:H	2:H:201:ASN:HD21	1.24	0.84
1:A:1021:GLU:HG2	7:A:1227:HOH:O	1.78	0.83
1:A:984:VAL:O	1:A:986:PRO:HD3	1.87	0.74
2:H:6:GLN:HE21	2:H:109:GLY:HA3	1.53	0.73
3:L:200:SER:CB	3:L:202:SER:O	2.37	0.72
3:L:22:THR:HG22	7:L:1049:HOH:O	1.93	0.66
2:H:161:SER:H	2:H:201:ASN:ND2	1.95	0.63
6:H:1004:GOL:H32	7:H:1066:HOH:O	1.99	0.62
2:H:157:LEU:HD11	2:H:200:CYS:HB2	1.82	0.61
3:L:16:GLY:HA2	3:L:77:ASN:HD22	1.65	0.61
1:A:952:LYS:NZ	1:A:996:ASP:OD1	2.34	0.58
2:H:157:LEU:HD13	2:H:202:VAL:HG22	1.84	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:L:200:SER:HB2	7:L:1024:HOH:O	2.04	0.57
2:H:113:THR:HG22	7:H:1014:HOH:O	2.02	0.57
3:L:199:THR:O	3:L:200:SER:HB2	2.06	0.55
3:L:79:GLU:OE1	3:L:81:GLU:OE2	2.27	0.53
1:A:966:GLN:HE21	1:A:983:ASN:H	1.57	0.52
3:L:202:SER:HB3	3:L:203:PRO:HD2	1.92	0.52
3:L:90:GLN:HE22	3:L:93:ASN:H	1.58	0.51
2:H:143:LEU:HD12	2:H:198:ILE:HG21	1.97	0.47
1:A:1007:ILE:HD12	1:A:1041:SER:HB2	1.97	0.46
3:L:35:TRP:CE2	3:L:73:PHE:HB2	2.51	0.45
2:H:6:GLN:HE22	2:H:95:PHE:HA	1.81	0.45
1:A:1094:LEU:HB3	1:A:1095:PRO:HD3	1.99	0.45
1:A:952:LYS:CE	1:A:996:ASP:OD1	2.64	0.45
3:L:194:GLU:HG2	3:L:205:VAL:HG22	2.00	0.44
3:L:111:ALA:HA	3:L:199:THR:HB	1.99	0.44
2:H:6:GLN:HE21	2:H:109:GLY:CA	2.28	0.42
3:L:196:THR:CG2	3:L:203:PRO:HB3	2.49	0.42
1:A:1063:GLY:HA3	1:A:1073:LEU:HD11	2.00	0.42
2:H:11:LEU:HD22	2:H:152:PRO:HG3	2.01	0.41
3:L:3:GLN:HG2	3:L:26:SER:HB3	2.02	0.41
2:H:171:PHE:HA	2:H:172:PRO:HD3	1.96	0.41
1:A:1074:ARG:NH2	7:A:1242:HOH:O	2.50	0.40
2:H:82:GLN:NE2	7:H:1158:HOH:O	2.55	0.40
2:H:113:THR:HG21	7:H:1105:HOH:O	2.21	0.40
1:A:1025:ALA:HB1	1:A:1031:LYS:HZ2	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	187/196 (95%)	180 (96%)	7 (4%)	0	100	100
2	H	216/218 (99%)	210 (97%)	4 (2%)	2 (1%)	25	10
3	L	207/209 (99%)	200 (97%)	6 (3%)	1 (0%)	38	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	610/623 (98%)	590 (97%)	17 (3%)	3 (0%)	38	23

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	197	SER
3	L	197	HIS
2	H	198	ILE

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	156/160 (98%)	154 (99%)	2 (1%)	80	77
2	H	187/187 (100%)	187 (100%)	0	100	100
3	L	185/185 (100%)	178 (96%)	7 (4%)	44	31
All	All	528/532 (99%)	519 (98%)	9 (2%)	73	68

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1022	MET
1	A	1046	ASP
3	L	1	ASP
3	L	3	GLN
3	L	22	THR
3	L	90	GLN
3	L	104	GLU
3	L	159	LEU
3	L	201	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	959	ASN

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Mol	Chain	Res	Type
1	A	966	GLN
2	H	6	GLN
2	H	169	HIS
2	H	201	ASN
3	L	77	ASN
3	L	90	GLN
3	L	137	ASN
3	L	160	ASN
3	L	189	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

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	$\# Z > 2$
5	ACY	A	1112	-	3,3,3	0.63	0	3,3,3	0.63	0
4	SO4	H	1002	-	4,4,4	0.35	0	6,6,6	0.23	0
6	GOL	H	1004	-	5,5,5	0.34	0	5,5,5	0.36	0
4	SO4	L	1003	-	4,4,4	0.12	0	6,6,6	0.19	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
5	ACY	A	1112	-	-	0/0/0/0	0/0/0/0
4	SO4	H	1002	-	-	0/0/0/0	0/0/0/0
6	GOL	H	1004	-	-	0/4/4/4	0/0/0/0
4	SO4	L	1003	-	-	0/0/0/0	0/0/0/0

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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	189/196 (96%)	0.85	31 (16%)	2 2	10, 16, 30, 38	0
2	H	218/218 (100%)	0.96	29 (13%)	4 3	10, 22, 34, 35	0
3	L	209/209 (100%)	1.50	57 (27%)	1 1	13, 17, 25, 43	0
All	All	616/623 (98%)	1.11	117 (18%)	2 2	10, 17, 33, 43	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	201	THR	10.2
3	L	199	THR	8.2
1	A	985	VAL	7.9
3	L	128	GLY	6.6
3	L	181	THR	6.4
3	L	191	TYR	6.4
1	A	984	VAL	6.0
3	L	185	TYR	6.0
3	L	124	LEU	5.9
3	L	125	THR	5.7
3	L	198	LYS	5.4
3	L	190	SER	5.3
2	H	133	CYS	5.3
3	L	149	ILE	5.2
3	L	183	ASP	4.9
3	L	155	GLN	4.7
3	L	180	LEU	4.6
3	L	209	ASN	4.5
3	L	189	ASN	4.5
2	H	197	SER	4.4
3	L	129	ALA	4.4
3	L	118	PRO	4.3
3	L	156	ASN	4.3

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Mol	Chain	Res	Type	RSRZ
3	L	187	ARG	4.2
3	L	200	SER	4.1
3	L	152	SER	4.1
3	L	121	SER	4.0
2	H	210	LYS	4.0
2	H	208	SER	4.0
3	L	202	SER	3.9
1	A	922	ASP	3.9
3	L	123	GLN	3.8
3	L	1	ASP	3.8
3	L	168	LYS	3.8
1	A	1021	GLU	3.7
3	L	188	HIS	3.7
2	H	134	GLY	3.7
2	H	127	TYR	3.6
3	L	203	PRO	3.6
3	L	184	GLU	3.6
3	L	208	PHE	3.6
2	H	195	SER	3.4
1	A	932	LEU	3.4
3	L	182	LYS	3.4
1	A	986	PRO	3.4
3	L	135	LEU	3.4
2	H	198	ILE	3.3
3	L	122	GLU	3.3
2	H	146	LEU	3.3
2	H	128	PRO	3.3
3	L	154	ARG	3.2
1	A	931	LEU	3.2
2	H	162	GLY	3.2
2	H	163	SER	3.2
3	L	126	SER	3.2
1	A	925	GLN	3.1
1	A	1036	LEU	3.1
1	A	970	LEU	3.0
1	A	1034	VAL	3.0
1	A	1035	ILE	2.9
1	A	923	CYS	2.9
1	A	963	ARG	2.9
2	H	132	VAL	2.9
2	H	123	ALA	2.9
3	L	127	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
3	L	186	GLU	2.8
3	L	151	GLY	2.8
3	L	179	THR	2.7
2	H	36	TRP	2.7
1	A	969	VAL	2.7
3	L	207	SER	2.7
2	H	1	GLN	2.7
3	L	197	HIS	2.7
3	L	192	THR	2.6
1	A	1033	VAL	2.5
1	A	1056	ARG	2.5
2	H	62	GLU	2.5
2	H	166	SER	2.5
1	A	1079	PRO	2.5
3	L	89	LEU	2.5
1	A	1106	HIS	2.5
2	H	97	ALA	2.5
3	L	120	SER	2.4
2	H	135	ASP	2.4
2	H	211	VAL	2.4
1	A	930	ILE	2.4
3	L	153	GLU	2.3
3	L	18	LYS	2.3
1	A	933	LEU	2.3
2	H	161	SER	2.3
1	A	1037	VAL	2.3
3	L	48	ILE	2.3
1	A	983	ASN	2.2
2	H	218	ARG	2.2
2	H	37	VAL	2.2
3	L	131	VAL	2.2
3	L	150	ASP	2.2
2	H	65	ARG	2.2
2	H	186	VAL	2.2
3	L	34	ALA	2.2
3	L	178	LEU	2.2
1	A	1027	PRO	2.2
1	A	972	TYR	2.2
2	H	34	MET	2.2
3	L	132	VAL	2.2
3	L	112	PRO	2.2
1	A	1014	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	L	167	SER	2.1
1	A	1110	SER	2.1
1	A	987	GLU	2.1
1	A	990	HIS	2.1
3	L	142	ASP	2.1
2	H	205	PRO	2.1
3	L	113	THR	2.1
2	H	105	LEU	2.1
1	A	924	SER	2.0
1	A	962	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	GOL	H	1004	6/6	0.26	4.68	41,42,43,43	0
4	SO4	L	1003	5/5	0.17	3.27	38,39,40,40	0
4	SO4	H	1002	5/5	0.19	1.38	29,30,33,33	0
5	ACY	A	1112	4/4	0.12	-0.55	35,35,35,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.