



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 11:18 PM GMT

PDB ID : 2V4A
Title : CRYSTAL STRUCTURE OF THE SEMET-LABELED PROLYL-4 HYDROXYLASE (P4H) TYPE I FROM GREEN ALGAE CHLAMYDOMONAS REINHARDTII.
Authors : Koski, M.K.; Hieta, R.; Bollner, C.; Kivirikko, K.I.; Myllyharju, J.; Wierenga, R.K.
Deposited on : 2007-06-28
Resolution : 1.93 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>

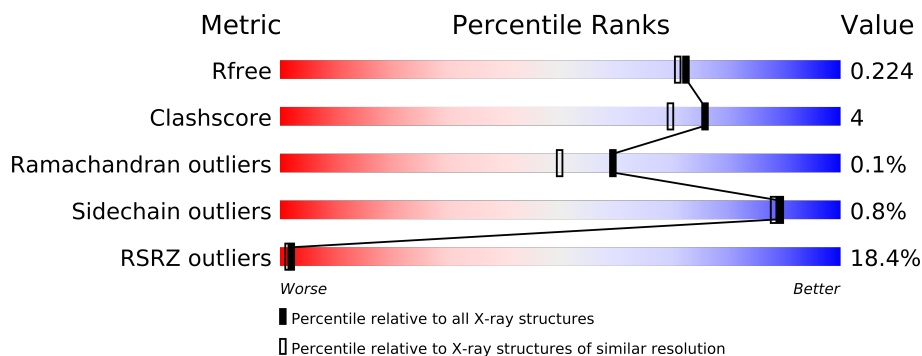
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.93 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	2024 (1.96-1.92)
Clashscore	79885	2281 (1.96-1.92)
Ramachandran outliers	78287	2255 (1.96-1.92)
Sidechain outliers	78261	2255 (1.96-1.92)
RSRZ outliers	66119	2024 (1.96-1.92)

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	233	
1	B	233	
1	C	233	
1	D	233	

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

Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	B	1251	-	X
3	GOL	D	1251	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6127 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 PROLYL-4 HYDROXYLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	Se	0	0	0
			1423	906	243	265	3	6			
1	B	174	Total	C	N	O	S	Se	0	0	0
			1359	868	232	250	3	6			
1	C	187	Total	C	N	O	S	Se	0	0	0
			1461	931	250	271	3	6			
1	D	194	Total	C	N	O	S	Se	0	0	0
			1530	976	259	286	3	6			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

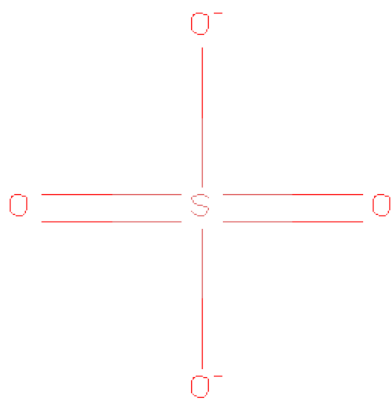
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



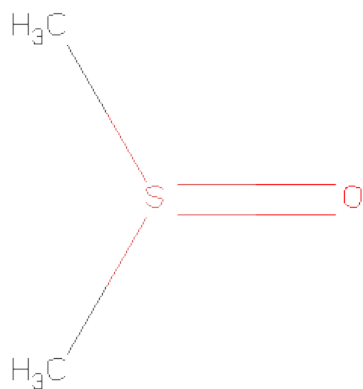
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

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



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

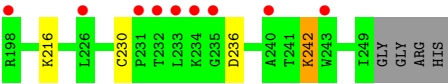
- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	99	Total	O	0	0
			99	99		
6	B	88	Total	O	0	0
			88	88		
6	C	67	Total	O	0	0
			67	67		
6	D	59	Total	O	0	0
			59	59		



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	137.49Å 137.49Å 88.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.87 – 1.93 19.86 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.87-1.93) 99.6 (19.86-1.93)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.3.0028	Depositor
R, R_{free}	0.188 , 0.223 0.191 , 0.224	Depositor DCC
R_{free} test set	3176 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	1 of 63507 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6127	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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, DMS, SO4, CL

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	0.83	0/1451	0.75	2/1951 (0.1%)
1	B	0.94	2/1386 (0.1%)	0.78	1/1864 (0.1%)
1	C	0.80	2/1490 (0.1%)	0.68	1/2004 (0.0%)
1	D	0.87	5/1566 (0.3%)	0.76	3/2110 (0.1%)
All	All	0.86	9/5893 (0.2%)	0.74	7/7929 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	32	GLY	C-O	19.94	1.55	1.23
1	C	194	GLU	CD-OE2	10.82	1.37	1.25
1	B	32	GLY	CA-C	10.28	1.68	1.51
1	C	194	GLU	CD-OE1	10.26	1.36	1.25
1	D	236	ASP	CG-OD2	9.36	1.46	1.25
1	D	174	GLU	C-N	9.01	1.49	1.33
1	D	72	PRO	C-N	7.93	1.52	1.34
1	D	197	LYS	C-N	5.87	1.47	1.34
1	D	135	HIS	C-O	5.73	1.34	1.23

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	32	GLY	CA-C-O	-11.46	99.98	120.60
1	D	236	ASP	CB-CG-OD1	-10.24	109.08	118.30
1	D	135	HIS	CA-CB-CG	-6.04	103.32	113.60
1	C	34	LEU	CA-CB-CG	5.59	128.15	115.30
1	D	236	ASP	CB-CG-OD2	5.33	123.10	118.30
1	A	185	GLN	CB-CA-C	-5.17	100.05	110.40
1	A	208	ASP	CB-CG-OD1	5.14	122.92	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	1423	0	1402	7	0
1	B	1359	0	1345	3	0
1	C	1461	0	1446	7	0
1	D	1530	0	1473	27	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	2	0
3	D	6	0	8	0	0
4	A	5	0	0	0	0
5	B	8	0	12	0	0
6	A	99	0	0	2	0
6	B	88	0	0	1	0
6	C	67	0	0	0	0
6	D	59	0	0	4	0
All	All	6127	0	5710	44	1

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

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:74:MSE:HE3	1:D:96:THR:HB	1.47	0.96
1:D:39:ARG:HH11	1:D:39:ARG:CG	1.85	0.89
1:C:50:ARG:HH11	3:C:1251:GOL:H11	1.39	0.87
1:D:195:CYS:HG	1:D:230:CYS:HG	0.89	0.83
1:D:39:ARG:HH11	1:D:39:ARG:HG2	1.48	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:156:GLU:HG2	1:A:157:HIS:H	1.60	0.67
1:D:39:ARG:HH11	1:D:39:ARG:HG3	1.61	0.64
1:D:175:GLY:HA2	1:D:177:GLU:OE1	1.99	0.63
1:A:156:GLU:HG2	1:A:157:HIS:N	2.13	0.61
1:C:48:SER:HB3	1:C:184:GLU:HB2	1.89	0.55
1:C:99:TRP:CZ3	1:C:130:GLN:HB2	2.42	0.54
1:D:177:GLU:CG	1:D:196:ALA:HB2	2.38	0.53
1:D:39:ARG:NH1	1:D:39:ARG:CG	2.54	0.53
1:D:149:ASP:HB3	1:D:152:ASN:HD22	1.74	0.53
1:C:38:TRP:CZ2	1:C:40:GLY:HA3	2.43	0.53
1:D:242:LYS:HE3	6:D:2024:HOH:O	2.11	0.51
1:D:216:LYS:NZ	6:D:2048:HOH:O	2.42	0.51
1:D:105:ASP:HB2	1:D:108:ILE:HG12	1.94	0.50
1:D:176:GLY:HA2	1:D:230:CYS:O	2.11	0.50
1:B:48:SER:HB3	1:B:184:GLU:HB3	1.94	0.50
1:C:50:ARG:NH1	3:C:1251:GOL:H11	2.19	0.49
1:D:74:MSE:HE3	1:D:96:THR:CB	2.31	0.48
1:D:39:ARG:NH1	1:D:39:ARG:HG2	2.21	0.47
1:D:62:GLU:HB3	1:D:111:ILE:HD11	1.95	0.47
1:B:55:LYS:NZ	6:B:2011:HOH:O	2.47	0.47
1:A:184:GLU:OE1	6:A:2067:HOH:O	2.20	0.47
1:D:74:MSE:HE1	1:D:133:HIS:HB3	1.97	0.47
1:D:38:TRP:CZ2	1:D:40:GLY:HA3	2.51	0.46
1:A:227:HIS:HD2	6:A:2089:HOH:O	1.99	0.45
1:D:74:MSE:CE	6:D:2028:HOH:O	2.64	0.45
1:C:186:LYS:HG2	1:C:199:GLY:HA2	1.99	0.44
1:A:55:LYS:HE3	1:A:55:LYS:HB3	1.78	0.44
1:A:157:HIS:O	1:A:249:ILE:HG12	2.19	0.43
1:D:49:PRO:HG3	1:D:180:LEU:HD22	2.00	0.43
1:D:74:MSE:HE2	6:D:2028:HOH:O	2.18	0.43
1:D:33:GLU:C	1:D:117:GLN:HE22	2.21	0.43
1:D:149:ASP:O	1:D:152:ASN:HB2	2.20	0.42
1:D:28:MSE:HE3	1:D:123:LEU:HD22	2.01	0.42
1:D:39:ARG:NH1	1:D:39:ARG:HG3	2.27	0.41
1:C:38:TRP:HZ2	1:C:55:LYS:O	2.03	0.41
1:D:48:SER:HB3	1:D:184:GLU:HB2	2.03	0.41
1:A:165:MSE:HB3	1:A:242:LYS:HB3	2.03	0.41
1:B:162:VAL:HB	1:B:246:VAL:HG12	2.03	0.41
1:D:112:GLU:HG2	1:D:242:LYS:CE	2.52	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	Distance(Å)	Clash(Å)
1:D:150:PRO:CB	1:D:150:PRO:CB[8_554]	2.03	0.17

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	174/233 (75%)	171 (98%)	3 (2%)	0	100	100
1	B	166/233 (71%)	166 (100%)	0	0	100	100
1	C	179/233 (77%)	174 (97%)	5 (3%)	0	100	100
1	D	184/233 (79%)	178 (97%)	5 (3%)	1 (0%)	38	22
All	All	703/932 (75%)	689 (98%)	13 (2%)	1 (0%)	59	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	175	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	154/192 (80%)	152 (99%)	2 (1%)	80	75
1	B	147/192 (77%)	147 (100%)	0	100	100
1	C	158/192 (82%)	158 (100%)	0	100	100
1	D	164/192 (85%)	161 (98%)	3 (2%)	71	63
All	All	623/768 (81%)	618 (99%)	5 (1%)	89	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	THR
1	A	185	GLN
1	D	39	ARG
1	D	166	LEU
1	D	242	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN
1	B	185	GLN
1	D	117	GLN

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 ⓘ

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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	$\# Z > 2$
3	GOL	A	1251	-	5,5,5	0.29	0	5,5,5	0.91	0
4	SO4	A	1252	-	4,4,4	0.40	0	6,6,6	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	1251	-	5,5,5	0.37	0	5,5,5	0.27	0
5	DMS	B	1252	-	3,3,3	2.65	1 (33%)	3,3,3	0.69	0
5	DMS	B	1253	-	3,3,3	2.67	1 (33%)	3,3,3	0.49	0
3	GOL	C	1251	-	5,5,5	0.31	0	5,5,5	0.41	0
3	GOL	D	1251	-	5,5,5	0.40	0	5,5,5	0.36	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
3	GOL	A	1251	-	-	0/4/4/4	0/0/0/0
4	SO4	A	1252	-	-	0/0/0/0	0/0/0/0
3	GOL	B	1251	-	-	0/4/4/4	0/0/0/0
5	DMS	B	1252	-	-	0/0/0/0	0/0/0/0
5	DMS	B	1253	-	-	0/0/0/0	0/0/0/0
3	GOL	C	1251	-	-	0/4/4/4	0/0/0/0
3	GOL	D	1251	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1253	DMS	O-S	4.47	1.80	1.50
5	B	1252	DMS	O-S	4.43	1.80	1.50

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	182/233 (78%)	0.96	24 (13%) 4 4	20, 26, 31, 43	0
1	B	174/233 (74%)	0.87	21 (12%) 5 5	21, 26, 31, 35	0
1	C	187/233 (80%)	1.19	42 (22%) 1 1	20, 26, 31, 37	0
1	D	194/233 (83%)	1.30	51 (26%) 1 1	11, 26, 31, 34	0
All	All	737/932 (79%)	1.09	138 (18%) 2 1	11, 26, 31, 43	0

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	94	THR	7.1
1	D	140	TYR	6.8
1	D	173	GLU	6.3
1	A	157	HIS	6.1
1	C	188	THR	5.9
1	C	36	GLU	5.8
1	D	29	VAL	5.8
1	D	232	THR	5.8
1	D	234	LYS	5.7
1	C	76	LYS	5.3
1	D	189	GLY	5.3
1	D	190	ASP	5.1
1	D	188	THR	4.8
1	C	192	TRP	4.8
1	C	153	ALA	4.7
1	D	233	LEU	4.7
1	A	190	ASP	4.7
1	A	36	GLU	4.7
1	C	174	GLU	4.6
1	C	155	PRO	4.6
1	D	191	GLY	4.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	154	GLY	4.5
1	D	148	HIS	4.4
1	D	146	TYR	4.3
1	D	174	GLU	4.3
1	B	29	VAL	4.3
1	D	147	PHE	4.3
1	D	33	GLU	4.2
1	B	249	ILE	4.2
1	D	153	ALA	4.1
1	A	66	ILE	4.1
1	C	152	ASN	4.1
1	A	108	ILE	4.0
1	D	156	GLU	4.0
1	D	155	PRO	4.0
1	C	35	LYS	4.0
1	C	34	LEU	3.9
1	B	159	GLY	3.9
1	D	157	HIS	3.9
1	A	32	GLY	3.8
1	C	189	GLY	3.8
1	D	28	MSE	3.8
1	D	198	ARG	3.8
1	C	157	HIS	3.7
1	B	39	ARG	3.7
1	B	169	LEU	3.6
1	C	135	HIS	3.6
1	B	234	LYS	3.6
1	B	115	VAL	3.6
1	C	187	VAL	3.6
1	A	240	ALA	3.5
1	C	185	GLN	3.5
1	C	234	LYS	3.5
1	C	99	TRP	3.5
1	B	66	ILE	3.5
1	C	198	ARG	3.4
1	D	99	TRP	3.3
1	D	144	TYR	3.3
1	A	168	TYR	3.3
1	B	135	HIS	3.3
1	B	240	ALA	3.2
1	C	178	THR	3.1
1	D	32	GLY	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	156	GLU	3.1
1	D	235	GLY	3.1
1	D	185	GLN	3.1
1	A	94	THR	3.1
1	D	135	HIS	3.0
1	C	156	GLU	3.0
1	D	192	TRP	2.9
1	B	95	SER	2.9
1	B	190	ASP	2.9
1	A	111	ILE	2.9
1	C	233	LEU	2.9
1	C	195	CYS	2.9
1	D	150	PRO	2.9
1	C	249	ILE	2.8
1	A	166	LEU	2.8
1	D	194	GLU	2.8
1	A	67	VAL	2.8
1	D	115	VAL	2.8
1	D	37	GLU	2.8
1	C	194	GLU	2.7
1	A	51	ALA	2.7
1	D	240	ALA	2.7
1	C	226	LEU	2.7
1	A	178	THR	2.6
1	D	72	PRO	2.6
1	D	141	GLU	2.6
1	A	201	ALA	2.6
1	D	231	PRO	2.6
1	C	199	GLY	2.6
1	A	169	LEU	2.6
1	C	196	ALA	2.5
1	B	233	LEU	2.5
1	B	99	TRP	2.5
1	C	173	GLU	2.5
1	A	210	LEU	2.5
1	A	115	VAL	2.5
1	D	187	VAL	2.5
1	C	32	GLY	2.5
1	B	51	ALA	2.5
1	A	202	VAL	2.4
1	C	210	LEU	2.4
1	B	210	LEU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	235	GLY	2.3
1	C	232	THR	2.3
1	D	184	GLU	2.3
1	C	244	ILE	2.3
1	D	243	TRP	2.3
1	A	129	LEU	2.3
1	C	181	PRO	2.3
1	C	28	MSE	2.2
1	D	95	SER	2.2
1	D	143	HIS	2.2
1	D	149	ASP	2.2
1	C	37	GLU	2.2
1	D	197	LYS	2.2
1	B	96	THR	2.1
1	C	241	THR	2.1
1	D	38	TRP	2.1
1	D	30	GLY	2.1
1	B	168	TYR	2.1
1	D	145	ASP	2.1
1	A	65	TYR	2.1
1	B	198	ARG	2.1
1	D	73	LYS	2.1
1	D	142	PRO	2.1
1	C	95	SER	2.1
1	A	57	PHE	2.1
1	D	104	GLU	2.0
1	B	111	ILE	2.0
1	C	166	LEU	2.0
1	B	63	CYS	2.0
1	D	226	LEU	2.0
1	C	186	LYS	2.0
1	A	167	MSE	2.0
1	D	68	GLU	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
3	GOL	D	1251	6/6	0.20	2.37	54,56,57,58	0
3	GOL	B	1251	6/6	0.21	2.14	55,56,57,57	0
3	GOL	A	1251	6/6	0.18	0.99	49,50,51,52	0
5	DMS	B	1252	4/4	0.19	0.72	57,58,58,59	0
3	GOL	C	1251	6/6	0.17	0.56	45,47,48,48	0
5	DMS	B	1253	4/4	0.17	-0.40	68,69,69,69	0
2	CL	A	1250	1/1	0.11	-0.69	28,28,28,28	0
2	CL	D	1250	1/1	0.12	-0.78	45,45,45,45	0
4	SO4	A	1252	5/5	0.09	-1.14	31,32,35,36	0
2	CL	C	1250	1/1	0.10	-1.30	35,35,35,35	0
2	CL	B	1250	1/1	0.06	-2.22	28,28,28,28	0

6.5 Other polymers ⓘ

There are no such residues in this entry.