



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 15, 2023 – 05:21 AM EDT

PDB ID : 1SW5
Title : Crystal structure of ProX from Archeoglobus fulgidus in the ligand free form
Authors : Schiefner, A.; Holtmann, G.; Diederichs, K.; Welte, W.; Bremer, E.
Deposited on : 2004-03-30
Resolution : 1.80 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

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
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

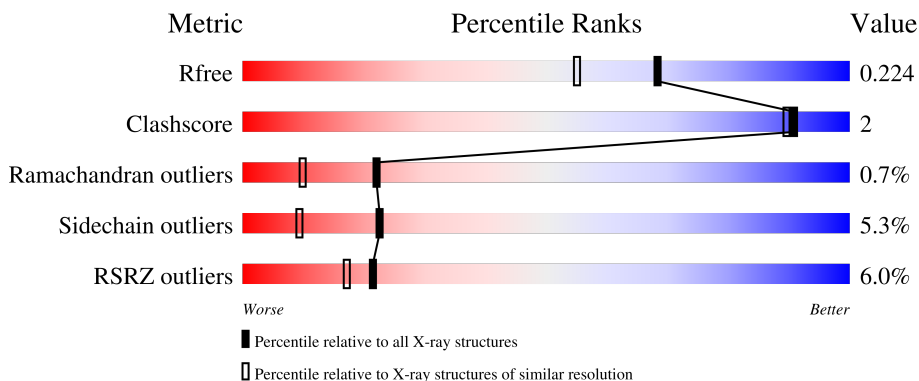
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	275	
1	B	275	
1	C	275	
1	D	275	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8980 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 osmoprotection protein (proX).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	270	2161	1386	349	421	5	0	0	0
1	B	270	2161	1386	349	421	5	0	0	0
1	C	270	2161	1386	349	421	5	0	0	0
1	D	270	2161	1386	349	421	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	CYS	engineered mutation	UNP O29280
B	1	GLY	CYS	engineered mutation	UNP O29280
C	1	GLY	CYS	engineered mutation	UNP O29280
D	1	GLY	CYS	engineered mutation	UNP O29280

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

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0


- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	122	Total O 122 122	0	0
4	B	89	Total O 89 89	0	0
4	C	59	Total O 59 59	0	0
4	D	57	Total O 57 57	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: osmoprotection protein (proX)

Chain A: 




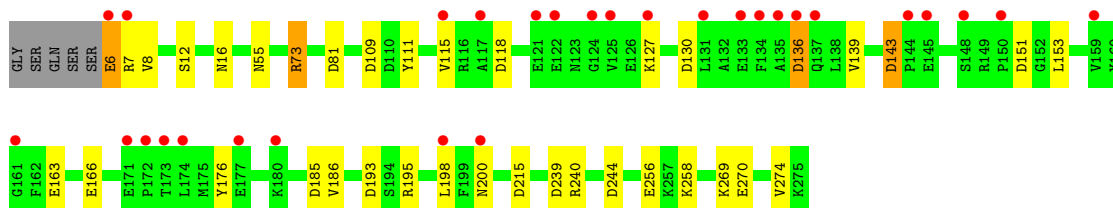
- Molecule 1: osmoprotection protein (proX)

Chain B: 




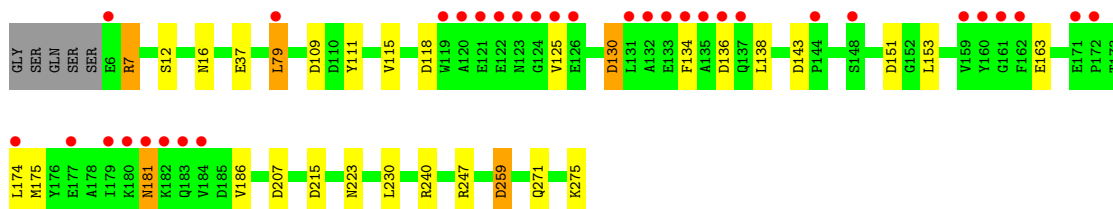
- Molecule 1: osmoprotection protein (proX)

Chain C: 



- Molecule 1: osmoprotection protein (proX)

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	161.50Å 56.50Å 116.10Å 90.00° 110.60° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 45.43 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-1.80) 99.8 (45.43-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 1.79Å)	Xtrriage
Refinement program	REFMAC 5.1.25	Depositor
R, R_{free}	0.186 , 0.214 0.199 , 0.224	Depositor DCC
R_{free} test set	4551 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtrriage
Anisotropy	0.029	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8980	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.4303e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MG, 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	0.69	0/2198	0.85	9/2971 (0.3%)
1	B	0.65	1/2198 (0.0%)	0.84	5/2971 (0.2%)
1	C	0.57	0/2198	0.82	11/2971 (0.4%)
1	D	0.59	0/2198	0.81	9/2971 (0.3%)
All	All	0.63	1/8792 (0.0%)	0.83	34/11884 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	244	ASP	CB-CG	-5.76	1.39	1.51

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	ARG	NE-CZ-NH1	7.18	123.89	120.30
1	D	215	ASP	CB-CG-OD2	7.18	124.76	118.30
1	C	239	ASP	CB-CG-OD2	6.92	124.53	118.30
1	A	118	ASP	CB-CG-OD2	6.86	124.48	118.30
1	C	193	ASP	CB-CG-OD2	6.80	124.42	118.30
1	B	143	ASP	CB-CG-OD2	6.62	124.25	118.30
1	A	239	ASP	CB-CG-OD2	6.53	124.17	118.30
1	D	259	ASP	CB-CG-OD2	6.40	124.06	118.30
1	D	109	ASP	CB-CG-OD2	6.37	124.04	118.30
1	C	244	ASP	CB-CG-OD2	6.25	123.92	118.30
1	A	81	ASP	CB-CG-OD2	6.08	123.77	118.30
1	C	109	ASP	CB-CG-OD2	5.93	123.64	118.30
1	A	136	ASP	CB-CG-OD2	5.92	123.63	118.30
1	D	247	ARG	NE-CZ-NH2	-5.91	117.35	120.30
1	A	247	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	B	185	ASP	CB-CG-OD2	5.81	123.53	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	143	ASP	CB-CG-OD2	5.71	123.44	118.30
1	D	136	ASP	CB-CG-OD2	5.62	123.36	118.30
1	B	247	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	B	215	ASP	CB-CG-OD2	5.42	123.18	118.30
1	C	136	ASP	CB-CG-OD2	5.38	123.15	118.30
1	C	151	ASP	CB-CG-OD2	5.34	123.10	118.30
1	B	81	ASP	CB-CG-OD2	5.33	123.10	118.30
1	A	87	ASP	CB-CG-OD2	5.28	123.05	118.30
1	D	130	ASP	CB-CG-OD2	5.23	123.01	118.30
1	D	151	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	185	ASP	CB-CG-OD2	5.20	122.97	118.30
1	C	73	ARG	NE-CZ-NH2	-5.17	117.71	120.30
1	D	207	ASP	CB-CG-OD2	5.16	122.94	118.30
1	D	143	ASP	CB-CG-OD2	5.16	122.94	118.30
1	C	81	ASP	CB-CG-OD2	5.13	122.92	118.30
1	C	130	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	207	ASP	CB-CG-OD2	5.04	122.83	118.30
1	C	185	ASP	CB-CG-OD2	5.03	122.83	118.30

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	2161	0	2165	7	0
1	B	2161	0	2165	9	2
1	C	2161	0	2165	7	0
1	D	2161	0	2165	9	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
4	A	122	0	0	3	2
4	B	89	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	59	0	0	0	0
4	D	57	0	0	0	0
All	All	8980	0	8660	30	2

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 2.

All (30) 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:B:240:ARG:HH11	1:B:271:GLN:HE21	1.37	0.73
1:D:240:ARG:HH11	1:D:271:GLN:HE21	1.45	0.65
1:C:115:VAL:HG12	1:C:186:VAL:HG22	1.84	0.59
1:D:79:LEU:O	1:D:79:LEU:HD23	2.04	0.57
1:D:125:VAL:HG13	1:D:130:ASP:HB2	1.88	0.55
1:C:6:GLU:O	1:C:8:VAL:HG23	2.07	0.53
1:D:181:ASN:HD22	1:D:181:ASN:N	2.07	0.53
1:B:140:PHE:CE2	1:B:142:SER:HB2	2.45	0.52
1:B:7:ARG:NH1	1:B:37:GLU:OE2	2.44	0.51
1:A:171:GLU:OE2	4:A:475:HOH:O	2.20	0.48
1:D:134:PHE:O	1:D:138:LEU:HG	2.14	0.48
1:A:257:LYS:NZ	4:A:507:HOH:O	2.49	0.46
1:C:176:TYR:CD2	1:C:195:ARG:HD2	2.51	0.46
1:B:169:GLN:HG3	4:B:473:HOH:O	2.16	0.46
1:B:69:ASN:HD21	1:B:80:TRP:HH2	1.65	0.45
1:D:230:LEU:C	1:D:230:LEU:HD13	2.37	0.45
1:C:55:ASN:ND2	1:D:223:ASN:OD1	2.49	0.45
1:B:69:ASN:ND2	4:B:458:HOH:O	2.50	0.45
1:D:7:ARG:CZ	1:D:37:GLU:HB2	2.47	0.45
1:C:269:LYS:HG2	1:C:274:VAL:HG23	2.00	0.44
1:A:244:ASP:HB3	4:A:504:HOH:O	2.17	0.44
1:D:115:VAL:HG12	1:D:186:VAL:HG22	2.00	0.43
1:C:139:VAL:HG13	1:C:166:GLU:HB2	2.01	0.42
1:C:256:GLU:OE2	1:C:258:LYS:NZ	2.29	0.42
1:A:78:GLU:HG2	1:B:95:GLU:HG3	2.01	0.42
1:A:230:LEU:C	1:A:230:LEU:HD23	2.41	0.42
1:A:140:PHE:CE2	1:A:142:SER:HB2	2.55	0.41
1:A:177:GLU:H	1:A:177:GLU:HG2	1.67	0.41
1:B:111:TYR:CZ	1:B:188:PRO:HB2	2.56	0.40
1:B:142:SER:O	1:B:169:GLN:HA	2.21	0.40

All (2) 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:B:262:GLU:OE1	4:A:529:HOH:O[3_545]	1.78	0.42
1:B:6:GLU:OE1	4:A:489:HOH:O[1_545]	2.08	0.12

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	268/275 (98%)	263 (98%)	4 (2%)	1 (0%)	34	21
1	B	268/275 (98%)	264 (98%)	2 (1%)	2 (1%)	22	10
1	C	268/275 (98%)	261 (97%)	4 (2%)	3 (1%)	14	4
1	D	268/275 (98%)	262 (98%)	5 (2%)	1 (0%)	34	21
All	All	1072/1100 (98%)	1050 (98%)	15 (1%)	7 (1%)	22	10

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	7	ARG
1	B	7	ARG
1	C	16	ASN
1	D	16	ASN
1	C	200	ASN
1	A	16	ASN
1	B	16	ASN

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	231/235 (98%)	219 (95%)	12 (5%)	23	10
1	B	231/235 (98%)	220 (95%)	11 (5%)	25	11
1	C	231/235 (98%)	217 (94%)	14 (6%)	18	7
1	D	231/235 (98%)	219 (95%)	12 (5%)	23	10
All	All	924/940 (98%)	875 (95%)	49 (5%)	22	9

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	12	SER
1	A	73	ARG
1	A	133	GLU
1	A	143	ASP
1	A	158	LYS
1	A	174	LEU
1	A	198	LEU
1	A	238	GLU
1	A	244	ASP
1	A	261	ARG
1	A	275	LYS
1	B	12	SER
1	B	78	GLU
1	B	111	TYR
1	B	145	GLU
1	B	174	LEU
1	B	181	ASN
1	B	198	LEU
1	B	221	ASN
1	B	244	ASP
1	B	262	GLU
1	B	275	LYS
1	C	6	GLU
1	C	12	SER
1	C	73	ARG
1	C	111	TYR
1	C	118	ASP
1	C	127	LYS
1	C	136	ASP

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Mol	Chain	Res	Type
1	C	143	ASP
1	C	153	LEU
1	C	163	GLU
1	C	198	LEU
1	C	215	ASP
1	C	240	ARG
1	C	270	GLU
1	D	7	ARG
1	D	12	SER
1	D	79	LEU
1	D	111	TYR
1	D	118	ASP
1	D	153	LEU
1	D	163	GLU
1	D	174	LEU
1	D	175	MET
1	D	181	ASN
1	D	259	ASP
1	D	275	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	181	ASN
1	B	69	ASN
1	B	181	ASN
1	B	271	GLN
1	C	181	ASN
1	C	183	GLN
1	C	200	ASN
1	C	252	GLN
1	D	123	ASN
1	D	181	ASN
1	D	252	GLN
1	D	271	GLN

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 9 ligands modelled in this entry, 9 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, 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	270/275 (98%)	-0.36	1 (0%) 92 90	4, 12, 29, 37	0
1	B	270/275 (98%)	-0.39	2 (0%) 87 86	5, 14, 28, 38	0
1	C	270/275 (98%)	0.37	29 (10%) 6 4	7, 20, 57, 64	0
1	D	270/275 (98%)	0.31	33 (12%) 4 3	7, 20, 56, 60	0
All	All	1080/1100 (98%)	-0.02	65 (6%) 21 17	4, 16, 54, 64	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	6	GLU	11.3
1	B	6	GLU	8.8
1	D	6	GLU	8.0
1	C	134	PHE	8.0
1	C	144	PRO	6.9
1	D	172	PRO	6.4
1	D	161	GLY	5.2
1	C	125	VAL	5.1
1	C	171	GLU	5.0
1	D	174	LEU	4.9
1	D	122	GLU	4.9
1	C	172	PRO	4.8
1	A	6	GLU	4.7
1	D	133	GLU	4.7
1	D	134	PHE	4.3
1	C	161	GLY	4.1
1	D	135	ALA	4.0
1	D	183	GLN	3.9
1	D	125	VAL	3.7
1	D	124	GLY	3.6
1	D	159	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	171	GLU	3.4
1	D	137	GLN	3.4
1	C	7	ARG	3.4
1	C	198	LEU	3.4
1	C	148	SER	3.3
1	C	122	GLU	3.2
1	C	115	VAL	3.2
1	C	173	THR	3.1
1	C	137	GLN	3.0
1	D	131	LEU	2.9
1	C	117	ALA	2.9
1	C	150	PRO	2.8
1	D	162	PHE	2.8
1	D	126	GLU	2.8
1	C	135	ALA	2.7
1	C	131	LEU	2.7
1	C	136	ASP	2.7
1	C	133	GLU	2.7
1	C	200	ASN	2.7
1	D	148	SER	2.7
1	D	123	ASN	2.6
1	D	132	ALA	2.6
1	D	180	LYS	2.6
1	C	180	LYS	2.5
1	D	181	ASN	2.5
1	D	120	ALA	2.5
1	B	275	LYS	2.5
1	D	136	ASP	2.4
1	C	174	LEU	2.4
1	C	145	GLU	2.3
1	C	124	GLY	2.2
1	C	121	GLU	2.2
1	D	144	PRO	2.2
1	D	179	ILE	2.2
1	D	177	GLU	2.2
1	C	177	GLU	2.2
1	D	119	TRP	2.1
1	D	160	TYR	2.1
1	C	127	LYS	2.1
1	C	159	VAL	2.1
1	D	79	LEU	2.1
1	D	182	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	184	VAL	2.0
1	D	121	GLU	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, 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
3	MG	A	409	1/1	0.91	0.16	31,31,31,31	0
2	CL	B	406	1/1	0.98	0.04	22,22,22,22	0
2	CL	B	401	1/1	0.98	0.08	20,20,20,20	0
2	CL	C	407	1/1	0.99	0.06	23,23,23,23	0
2	CL	D	402	1/1	0.99	0.08	22,22,22,22	0
2	CL	D	408	1/1	0.99	0.03	26,26,26,26	0
2	CL	A	405	1/1	0.99	0.03	22,22,22,22	0
2	CL	A	403	1/1	1.00	0.08	15,15,15,15	0
2	CL	C	404	1/1	1.00	0.08	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.