



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 PM UTC

PDB ID : 1SW5 / pdb_00001sw5
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:

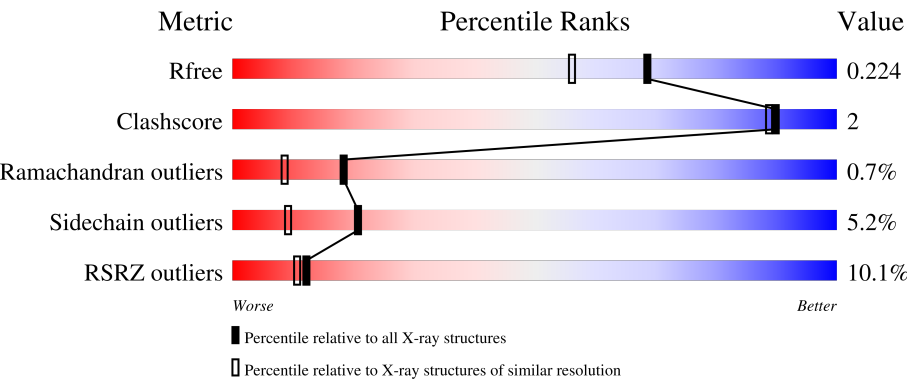
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 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}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (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	91% 7% .
1	B	275	89% 8% .
1	C	275	22% 87% 11% .
1	D	275	16% 89% 8% ..

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
1	A	270	Total	C	N	O	S	0	0	0
			2161	1386	349	421	5			
1	B	270	Total	C	N	O	S	0	0	0
			2161	1386	349	421	5			
1	C	270	Total	C	N	O	S	0	0	0
			2161	1386	349	421	5			
1	D	270	Total	C	N	O	S	0	0	0
			2161	1386	349	421	5			

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 (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

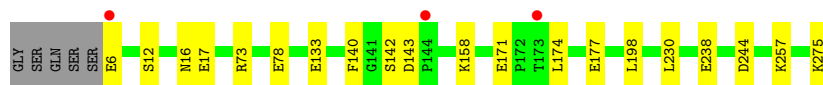
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	122	Total 122	O 122	0	0
4	B	89	Total 89	O 89	0	0
4	C	59	Total 59	O 59	0	0
4	D	57	Total 57	O 57	0	0

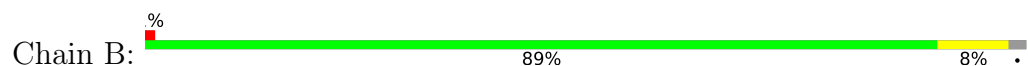
3 Residue-property plots [i](#)

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.

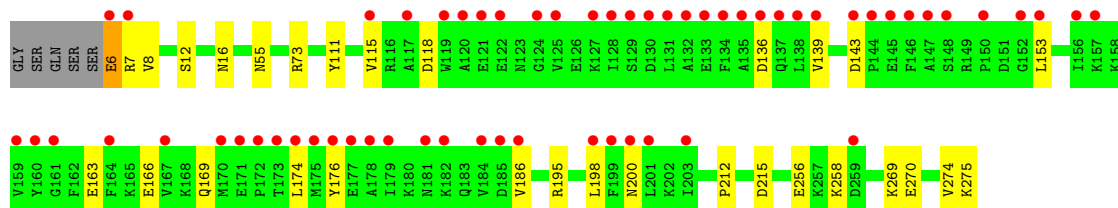
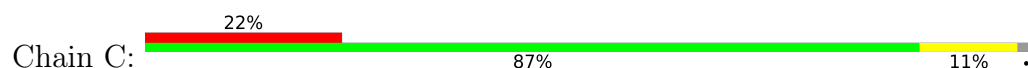
- Molecule 1: osmoprotection protein (proX)



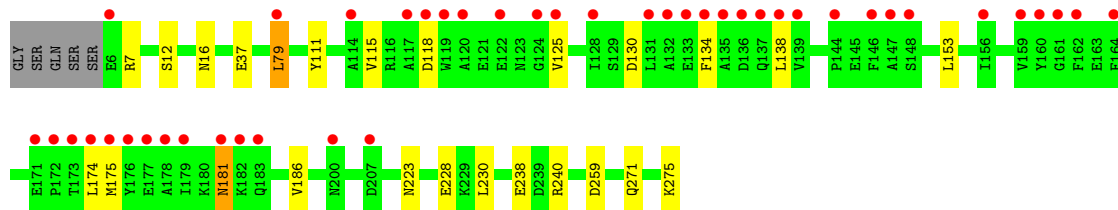
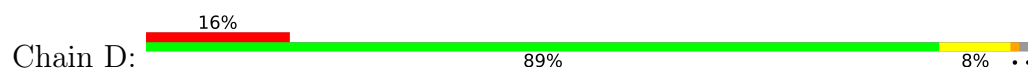
- Molecule 1: osmoprotection protein (proX)



- Molecule 1: osmoprotection protein (proX)



- Molecule 1: osmoprotection protein (proX)



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 50.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-1.80) 99.7 (50.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 1.79Å)	Xtriage
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	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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	0.82	0/2198	0.93	1/2971 (0.0%)
1	B	0.81	0/2198	0.91	0/2971
1	C	0.74	0/2198	0.91	1/2971 (0.0%)
1	D	0.74	0/2198	0.90	0/2971
All	All	0.78	0/8792	0.91	2/11884 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	212	PRO	O-C-N	5.50	123.73	121.15
1	A	17	GLU	N-CA-CB	-5.03	102.73	110.12

There are no chirality outliers.

There are no planarity outliers.

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	2161	0	2165	7	0
1	B	2161	0	2165	10	2
1	C	2161	0	2165	7	0
1	D	2161	0	2165	9	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
4	C	59	0	0	0	0
4	D	57	0	0	0	0
All	All	8980	0	8660	31	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 (31) 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:256:GLU:OE2	1:C:258:LYS:NZ	2.29	0.54
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:D:230:LEU:C	1:D:230:LEU:HD13	2.37	0.50
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:230:LEU:C	1:A:230:LEU:HD23	2.41	0.46
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: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:B:230:LEU:C	1:B:230:LEU:HD23	2.43	0.43
1:D:115:VAL:HG12	1:D:186:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:VAL:HG13	1:C:166:GLU:HB2	2.01	0.42
1:A:78:GLU:HG2	1:B:95:GLU:HG3	2.01	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

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	268/275 (98%)	263 (98%)	4 (2%)	1 (0%)	30	19
1	B	268/275 (98%)	264 (98%)	2 (1%)	2 (1%)	18	8
1	C	268/275 (98%)	261 (97%)	4 (2%)	3 (1%)	11	3
1	D	268/275 (98%)	262 (98%)	5 (2%)	1 (0%)	30	19
All	All	1072/1100 (98%)	1050 (98%)	15 (1%)	7 (1%)	18	8

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	7	ARG
1	B	7	ARG
1	C	16	ASN

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

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	231/235 (98%)	221 (96%)	10 (4%)	26	13
1	B	231/235 (98%)	220 (95%)	11 (5%)	23	11
1	C	231/235 (98%)	216 (94%)	15 (6%)	15	5
1	D	231/235 (98%)	219 (95%)	12 (5%)	21	9
All	All	924/940 (98%)	876 (95%)	48 (5%)	21	9

All (48) 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	275	LYS
1	B	7	ARG
1	B	12	SER
1	B	78	GLU
1	B	145	GLU
1	B	174	LEU
1	B	181	ASN
1	B	198	LEU

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Mol	Chain	Res	Type
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	136	ASP
1	C	143	ASP
1	C	153	LEU
1	C	163	GLU
1	C	169	GLN
1	C	174	LEU
1	C	198	LEU
1	C	215	ASP
1	C	270	GLU
1	C	275	LYS
1	D	12	SER
1	D	79	LEU
1	D	111	TYR
1	D	118	ASP
1	D	153	LEU
1	D	174	LEU
1	D	175	MET
1	D	181	ASN
1	D	228	GLU
1	D	238	GLU
1	D	259	ASP
1	D	275	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	GLN
1	A	181	ASN
1	A	183	GLN
1	A	252	GLN
1	B	69	ASN
1	B	82	GLN
1	B	181	ASN

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Mol	Chain	Res	Type
1	B	183	GLN
1	B	200	ASN
1	B	271	GLN
1	C	23	ASN
1	C	181	ASN
1	C	200	ASN
1	D	48	ASN
1	D	181	ASN
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 oligosaccharides 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 ⓘ

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%)	-0.27	3 (1%) 78 78	4, 12, 29, 37	0
1	B	270/275 (98%)	-0.21	2 (0%) 84 85	5, 14, 28, 38	0
1	C	270/275 (98%)	0.82	60 (22%) 2 2	7, 20, 57, 64	0
1	D	270/275 (98%)	0.66	44 (16%) 4 3	7, 20, 56, 60	0
All	All	1080/1100 (98%)	0.25	109 (10%) 12 11	4, 16, 54, 64	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	6	GLU	6.8
1	C	144	PRO	6.2
1	C	173	THR	5.3
1	C	125	VAL	5.2
1	C	134	PHE	5.2
1	B	6	GLU	5.0
1	D	174	LEU	4.9
1	D	6	GLU	4.5
1	C	161	GLY	4.4
1	C	117	ALA	4.3
1	C	159	VAL	4.2
1	D	125	VAL	4.2
1	D	128	ILE	4.1
1	D	132	ALA	4.1
1	C	172	PRO	4.0
1	C	146	PHE	3.9
1	D	131	LEU	3.8
1	D	134	PHE	3.8
1	C	7	ARG	3.7
1	D	172	PRO	3.7
1	C	174	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	179	ILE	3.4
1	C	120	ALA	3.4
1	C	171	GLU	3.3
1	C	135	ALA	3.3
1	C	147	ALA	3.3
1	C	178	ALA	3.2
1	C	131	LEU	3.2
1	D	144	PRO	3.2
1	C	115	VAL	3.2
1	D	159	VAL	3.2
1	C	121	GLU	3.2
1	C	198	LEU	3.2
1	D	161	GLY	3.2
1	C	186	VAL	3.1
1	D	162	PHE	3.1
1	D	117	ALA	3.1
1	D	120	ALA	3.1
1	D	173	THR	3.0
1	D	124	GLY	3.0
1	C	160	TYR	3.0
1	D	177	GLU	3.0
1	D	135	ALA	3.0
1	C	128	ILE	2.9
1	C	148	SER	2.9
1	C	143	ASP	2.9
1	D	175	MET	2.9
1	D	181	ASN	2.9
1	C	132	ALA	2.9
1	D	119	TRP	2.9
1	C	137	GLN	2.8
1	D	156	ILE	2.8
1	D	183	GLN	2.8
1	D	146	PHE	2.8
1	C	181	ASN	2.8
1	C	200	ASN	2.8
1	D	160	TYR	2.8
1	C	167	VAL	2.8
1	C	176	TYR	2.7
1	C	179	ILE	2.7
1	D	178	ALA	2.7
1	C	124	GLY	2.6
1	A	6	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	176	TYR	2.6
1	D	114	ALA	2.6
1	D	182	LYS	2.6
1	C	201	LEU	2.6
1	D	118	ASP	2.6
1	D	133	GLU	2.6
1	D	139	VAL	2.6
1	C	119	TRP	2.5
1	D	147	ALA	2.5
1	C	259	ASP	2.4
1	D	136	ASP	2.4
1	D	122	GLU	2.4
1	D	137	GLN	2.4
1	C	175	MET	2.4
1	D	148	SER	2.4
1	D	138	LEU	2.4
1	C	136	ASP	2.4
1	C	164	PHE	2.4
1	A	144	PRO	2.4
1	C	129	SER	2.3
1	C	145	GLU	2.3
1	C	177	GLU	2.3
1	C	182	LYS	2.3
1	C	133	GLU	2.3
1	C	156	ILE	2.2
1	C	203	ILE	2.2
1	B	122	GLU	2.2
1	C	139	VAL	2.2
1	C	127	LYS	2.2
1	C	184	VAL	2.2
1	D	207	ASP	2.2
1	C	199	PHE	2.1
1	C	150	PRO	2.1
1	C	157	LYS	2.1
1	C	122	GLU	2.1
1	D	171	GLU	2.1
1	C	138	LEU	2.1
1	C	153	LEU	2.1
1	D	164	PHE	2.1
1	C	170	MET	2.1
1	A	173	THR	2.0
1	D	79	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	130	ASP	2.0
1	C	185	ASP	2.0
1	C	152	GLY	2.0
1	D	200	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	MG	A	409	1/1	0.92	0.14	31,31,31,31	0
2	CL	B	406	1/1	0.98	0.06	22,22,22,22	0
2	CL	D	408	1/1	0.98	0.07	26,26,26,26	0
2	CL	B	401	1/1	0.98	0.03	20,20,20,20	0
2	CL	C	404	1/1	0.99	0.03	16,16,16,16	0
2	CL	C	407	1/1	0.99	0.06	23,23,23,23	0
2	CL	D	402	1/1	0.99	0.03	22,22,22,22	0
2	CL	A	403	1/1	0.99	0.02	15,15,15,15	0
2	CL	A	405	1/1	0.99	0.06	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.