



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:56 AM UTC

PDB ID : 3B5M / pdb_00003b5m
Title : Crystal structure of conserved uncharacterized protein from *Rhodopirellula baltica*
Authors : Patskovsky, Y.; Bonanno, J.B.; Sridhar, V.; Rutter, M.; Powell, A.; Maletic, M.; Rodgers, R.; Wasserman, S.; Smith, D.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-10-26
Resolution : 1.21 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

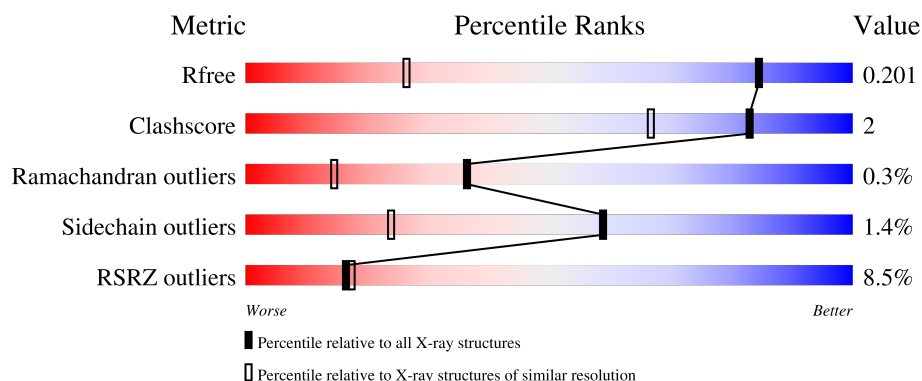
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.21 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	2002 (1.24-1.20)
Clashscore	190562	2061 (1.24-1.20)
Ramachandran outliers	187476	2009 (1.24-1.20)
Sidechain outliers	187428	2008 (1.24-1.20)
RSRZ outliers	180081	2000 (1.24-1.20)

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	205	7% 90% • 5%
1	B	205	8% 88% 6% • 5%
1	C	205	7% 88% 5% 6%
1	D	205	10% 90% 5% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7588 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	15	0
			1575	1000	285	286	4			
1	B	195	Total	C	N	O	S	0	13	0
			1573	996	281	292	4			
1	C	192	Total	C	N	O	S	0	8	0
			1521	965	276	277	3			
1	D	195	Total	C	N	O	S	0	11	0
			1558	988	281	285	4			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP Q7UTD8
A	0	SER	-	expression tag	UNP Q7UTD8
A	1	LEU	-	expression tag	UNP Q7UTD8
A	196	GLU	-	expression tag	UNP Q7UTD8
A	197	GLY	-	expression tag	UNP Q7UTD8
A	198	HIS	-	expression tag	UNP Q7UTD8
A	199	HIS	-	expression tag	UNP Q7UTD8
A	200	HIS	-	expression tag	UNP Q7UTD8
A	201	HIS	-	expression tag	UNP Q7UTD8
A	202	HIS	-	expression tag	UNP Q7UTD8
A	203	HIS	-	expression tag	UNP Q7UTD8
B	-1	MET	-	expression tag	UNP Q7UTD8
B	0	SER	-	expression tag	UNP Q7UTD8
B	1	LEU	-	expression tag	UNP Q7UTD8
B	196	GLU	-	expression tag	UNP Q7UTD8
B	197	GLY	-	expression tag	UNP Q7UTD8
B	198	HIS	-	expression tag	UNP Q7UTD8
B	199	HIS	-	expression tag	UNP Q7UTD8
B	200	HIS	-	expression tag	UNP Q7UTD8
B	201	HIS	-	expression tag	UNP Q7UTD8
B	202	HIS	-	expression tag	UNP Q7UTD8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	203	HIS	-	expression tag	UNP Q7UTD8
C	-1	MET	-	expression tag	UNP Q7UTD8
C	0	SER	-	expression tag	UNP Q7UTD8
C	1	LEU	-	expression tag	UNP Q7UTD8
C	196	GLU	-	expression tag	UNP Q7UTD8
C	197	GLY	-	expression tag	UNP Q7UTD8
C	198	HIS	-	expression tag	UNP Q7UTD8
C	199	HIS	-	expression tag	UNP Q7UTD8
C	200	HIS	-	expression tag	UNP Q7UTD8
C	201	HIS	-	expression tag	UNP Q7UTD8
C	202	HIS	-	expression tag	UNP Q7UTD8
C	203	HIS	-	expression tag	UNP Q7UTD8
D	-1	MET	-	expression tag	UNP Q7UTD8
D	0	SER	-	expression tag	UNP Q7UTD8
D	1	LEU	-	expression tag	UNP Q7UTD8
D	196	GLU	-	expression tag	UNP Q7UTD8
D	197	GLY	-	expression tag	UNP Q7UTD8
D	198	HIS	-	expression tag	UNP Q7UTD8
D	199	HIS	-	expression tag	UNP Q7UTD8
D	200	HIS	-	expression tag	UNP Q7UTD8
D	201	HIS	-	expression tag	UNP Q7UTD8
D	202	HIS	-	expression tag	UNP Q7UTD8
D	203	HIS	-	expression tag	UNP Q7UTD8

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

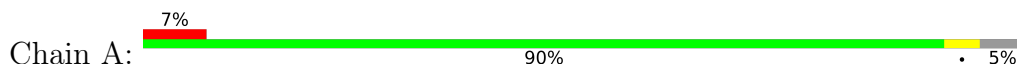
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	370	Total O 370 370	0	0
3	B	313	Total O 313 313	0	0
3	C	346	Total O 346 346	0	0
3	D	312	Total O 312 312	0	0

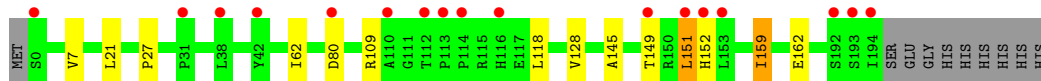
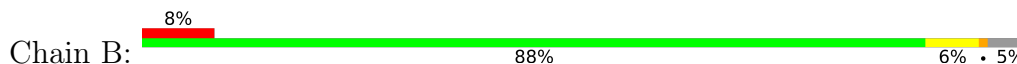
3 Residue-property plots [i](#)

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.

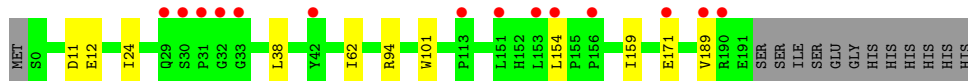
- Molecule 1: Uncharacterized protein



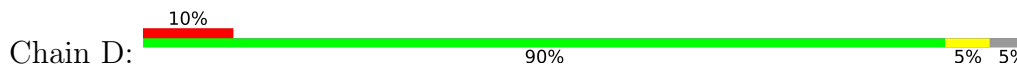
- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.27Å 58.31Å 73.80Å 93.89° 91.12° 90.10°	Depositor
Resolution (Å)	20.00 – 1.21 20.00 – 1.21	Depositor EDS
% Data completeness (in resolution range)	93.6 (20.00-1.21) 93.5 (20.00-1.21)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 1.21Å)	Xtriage
Refinement program	REFMAC 5.3.0034	Depositor
R, R_{free}	0.176 , 0.202 0.175 , 0.201	Depositor DCC
R_{free} test set	6990 reflections (2.82%)	wwPDB-VP
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7588	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.78	2/1643 (0.1%)	0.79	0/2236
1	B	0.76	0/1629	0.78	1/2218 (0.0%)
1	C	0.84	2/1574 (0.1%)	0.81	0/2143
1	D	0.69	0/1620	0.80	0/2204
All	All	0.77	4/6466 (0.1%)	0.80	1/8801 (0.0%)

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	D	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	12	GLU	C-O	-6.71	1.15	1.24
1	C	11	ASP	C-O	-6.47	1.17	1.23
1	A	40[A]	ARG	C-O	-5.19	1.18	1.24
1	A	40[B]	ARG	C-O	-5.19	1.18	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27	PRO	O-C-N	5.21	123.71	121.31

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	112	THR	Peptide

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	1575	0	1655	8	0
1	B	1573	0	1629	7	0
1	C	1521	0	1586	5	0
1	D	1558	0	1629	12	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	370	0	0	1	0
3	B	313	0	0	0	0
3	C	346	0	0	0	0
3	D	312	0	0	1	0
All	All	7588	0	6499	31	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 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:C:159[B]:ILE:HD13	1:C:189:VAL:HG11	1.68	0.74
1:A:153[B]:LEU:N	1:A:153[B]:LEU:HD23	2.03	0.73
1:C:159[B]:ILE:CD1	1:C:189:VAL:HG11	2.22	0.70
1:D:113:PRO:N	1:D:114:PRO:CD	2.58	0.66
1:D:172:LYS:HG3	3:D:294:HOH:O	1.97	0.63
1:D:112:THR:HG22	1:D:114:PRO:HD2	1.82	0.62
1:A:150:ARG:HG2	1:A:150:ARG:HH11	1.66	0.59
1:D:112:THR:CG2	1:D:113:PRO:CD	2.83	0.56
1:A:153[B]:LEU:N	1:A:153[B]:LEU:CD2	2.67	0.55
1:B:7[B]:VAL:HG21	1:B:21:LEU:HD22	1.89	0.54
1:D:113:PRO:N	1:D:114:PRO:HD2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:112:THR:HG22	1:D:113:PRO:HD2	1.90	0.54
1:D:112:THR:CG2	1:D:113:PRO:HD2	2.40	0.52
1:D:151:LEU:HD23	1:D:159[A]:ILE:HD13	1.92	0.51
1:B:7[B]:VAL:HG21	1:B:21:LEU:CD2	2.42	0.50
1:A:150:ARG:HG2	1:A:150:ARG:NH1	2.29	0.48
1:C:94:ARG:HD3	1:C:101:TRP:CD1	2.48	0.47
1:A:153[B]:LEU:HD22	3:A:340:HOH:O	2.13	0.47
1:A:122[B]:CYS:SG	1:A:124:ALA:O	2.71	0.47
1:B:151:LEU:HD12	1:B:159[B]:ILE:HD13	1.97	0.46
1:D:112:THR:C	1:D:114:PRO:HD2	2.41	0.46
1:D:112:THR:HG22	1:D:113:PRO:CD	2.45	0.45
1:B:145:ALA:O	1:B:149:THR:HG23	2.16	0.45
1:A:165[A]:ARG:NH1	1:B:162:GLU:OE2	2.40	0.45
1:D:112:THR:HG23	1:D:113:PRO:CD	2.49	0.43
1:D:155:PRO:HA	1:D:156:PRO:HD2	1.90	0.41
1:B:109:ARG:HD3	1:B:118:LEU:HD22	2.02	0.41
1:C:24:ILE:HB	1:C:38:LEU:HB3	2.02	0.41
1:C:154:LEU:HB2	1:C:159[B]:ILE:CG2	2.50	0.41
1:B:152:HIS:CD2	1:B:152:HIS:H	2.38	0.40
1:A:24:ILE:HB	1:A:38:LEU:HB3	2.04	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	207/205 (101%)	203 (98%)	4 (2%)	0	100	100
1	B	206/205 (100%)	204 (99%)	1 (0%)	1 (0%)	24	6
1	C	198/205 (97%)	195 (98%)	3 (2%)	0	100	100
1	D	204/205 (100%)	201 (98%)	2 (1%)	1 (0%)	24	6
All	All	815/820 (99%)	803 (98%)	10 (1%)	2 (0%)	36	16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	128	VAL
1	D	128	VAL

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	176/171 (103%)	175 (99%)	1 (1%)	78	52
1	B	175/171 (102%)	169 (97%)	6 (3%)	32	4
1	C	167/171 (98%)	165 (99%)	2 (1%)	63	28
1	D	173/171 (101%)	171 (99%)	2 (1%)	63	28
All	All	691/684 (101%)	680 (98%)	11 (2%)	59	19

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	B	62	ILE
1	B	80[A]	ASP
1	B	80[B]	ASP
1	B	151	LEU
1	B	159[A]	ILE
1	B	159[B]	ILE
1	C	62	ILE
1	C	171	GLU
1	D	62	ILE
1	D	115	ARG

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

Mol	Chain	Res	Type
1	A	17	ASN
1	A	36	GLN

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Mol	Chain	Res	Type
1	A	183	GLN
1	B	50	ASN
1	B	152	HIS
1	B	188	HIS
1	C	13	GLN
1	C	29	GLN
1	C	36	GLN
1	C	183	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](#)

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	$\# Z > 2$
2	SO4	C	204	-	4,4,4	0.40	0	6,6,6	0.33	0
2	SO4	A	204	-	4,4,4	0.37	0	6,6,6	0.53	0
2	SO4	D	204	-	4,4,4	0.27	0	6,6,6	0.21	0
2	SO4	B	204	-	4,4,4	0.18	0	6,6,6	0.28	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.

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	194/205 (94%)	0.39	14 (7%)	21	22	4, 13, 36, 71	15 (7%)
1	B	195/205 (95%)	0.56	17 (8%)	16	17	5, 14, 41, 62	13 (6%)
1	C	192/205 (93%)	0.34	14 (7%)	21	22	5, 13, 36, 50	8 (4%)
1	D	195/205 (95%)	0.54	21 (10%)	11	12	7, 14, 51, 86	11 (5%)
All	All	776/820 (94%)	0.46	66 (8%)	16	17	4, 13, 39, 86	47 (6%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	194	ILE	6.0
1	B	194	ILE	5.7
1	D	113	PRO	5.2
1	D	42	TYR	4.9
1	B	0	SER	4.8
1	B	192[A]	SER	4.6
1	D	193	SER	4.4
1	D	114	PRO	4.3
1	D	112	THR	4.1
1	D	152	HIS	3.8
1	B	113	PRO	3.8
1	B	42	TYR	3.7
1	D	115	ARG	3.6
1	B	149	THR	3.5
1	C	42	TYR	3.5
1	C	156	PRO	3.5
1	A	193	SER	3.4
1	B	110	ALA	3.4
1	B	151	LEU	3.2
1	D	153	LEU	3.2
1	A	192	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	111	GLY	3.2
1	C	189	VAL	3.1
1	C	31	PRO	3.1
1	B	152	HIS	3.0
1	D	192	SER	3.0
1	A	156	PRO	3.0
1	D	109	ARG	2.9
1	C	153	LEU	2.9
1	A	113	PRO	2.9
1	A	42	TYR	2.8
1	A	115	ARG	2.8
1	A	73	ILE	2.7
1	C	154	LEU	2.7
1	D	0	SER	2.7
1	A	157	GLU	2.7
1	A	151[A]	LEU	2.7
1	B	80[A]	ASP	2.6
1	A	30[A]	SER	2.6
1	B	193	SER	2.6
1	C	151	LEU	2.6
1	C	30	SER	2.6
1	D	31	PRO	2.5
1	B	114	PRO	2.4
1	A	190	ARG	2.4
1	D	151	LEU	2.4
1	D	149	THR	2.4
1	C	190	ARG	2.4
1	D	1	LEU	2.3
1	A	32	GLY	2.3
1	C	32	GLY	2.3
1	A	31	PRO	2.3
1	C	113	PRO	2.3
1	B	112	THR	2.2
1	D	44	GLY	2.2
1	D	156	PRO	2.2
1	B	153	LEU	2.2
1	B	31	PRO	2.2
1	C	33	GLY	2.1
1	D	150	ARG	2.1
1	B	116	HIS	2.1
1	B	38	LEU	2.1
1	C	171	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	157	GLU	2.0
1	C	29	GLN	2.0
1	A	183	GLN	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(Å ²)	Q<0.9
2	SO4	A	204	5/5	0.84	0.13	7,12,17,19	5
2	SO4	C	204	5/5	0.90	0.12	7,11,15,19	5
2	SO4	B	204	5/5	0.93	0.12	12,15,20,21	5
2	SO4	D	204	5/5	0.96	0.10	13,16,17,24	5

6.5 Other polymers [i](#)

There are no such residues in this entry.