



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:33 PM BST

PDB ID : 4M0P
Title : Crystal structure of human PRS1 M115T mutant
Authors : Chen, P.; Teng, M.; Li, X.
Deposited on : 2013-08-01
Resolution : 2.11 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

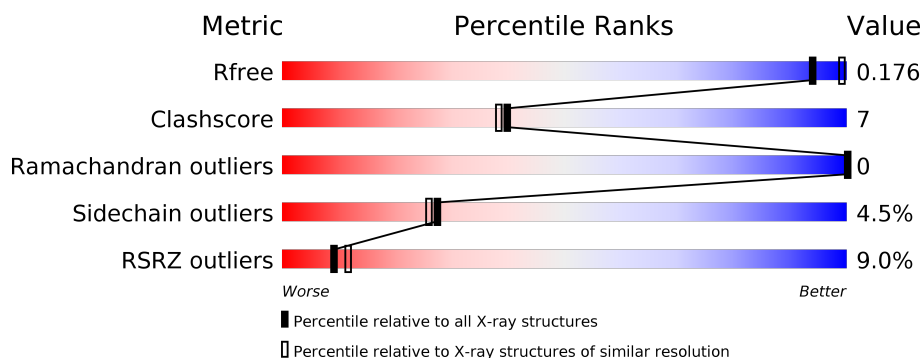
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 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	326	<div> <div>10%</div> <div> <div></div> <div>77%</div> <div>15%</div> <div>• 7%</div> </div> </div>
1	B	326	<div> <div>7%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	1003	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4751 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 Ribose-phosphate pyrophosphokinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	4	0	0
			2324	1457	408	443	16			
1	B	308	Total	C	N	O	S	0	0	0
			2345	1470	411	448	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	THR	MET	ENGINEERED MUTATION	UNP P60891
A	319	LEU	-	EXPRESSION TAG	UNP P60891
A	320	GLU	-	EXPRESSION TAG	UNP P60891
A	321	HIS	-	EXPRESSION TAG	UNP P60891
A	322	HIS	-	EXPRESSION TAG	UNP P60891
A	323	HIS	-	EXPRESSION TAG	UNP P60891
A	324	HIS	-	EXPRESSION TAG	UNP P60891
A	325	HIS	-	EXPRESSION TAG	UNP P60891
A	326	HIS	-	EXPRESSION TAG	UNP P60891
B	115	THR	MET	ENGINEERED MUTATION	UNP P60891
B	319	LEU	-	EXPRESSION TAG	UNP P60891
B	320	GLU	-	EXPRESSION TAG	UNP P60891
B	321	HIS	-	EXPRESSION TAG	UNP P60891
B	322	HIS	-	EXPRESSION TAG	UNP P60891
B	323	HIS	-	EXPRESSION TAG	UNP P60891
B	324	HIS	-	EXPRESSION TAG	UNP P60891
B	325	HIS	-	EXPRESSION TAG	UNP P60891
B	326	HIS	-	EXPRESSION TAG	UNP P60891

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

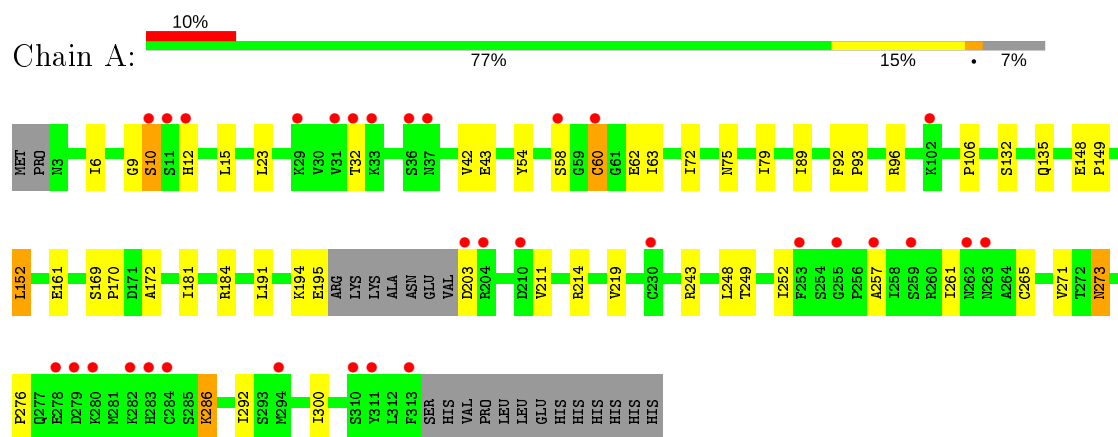
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	22	Total	O	0	0
			22	22		
3	B	30	Total	O	0	0
			30	30		

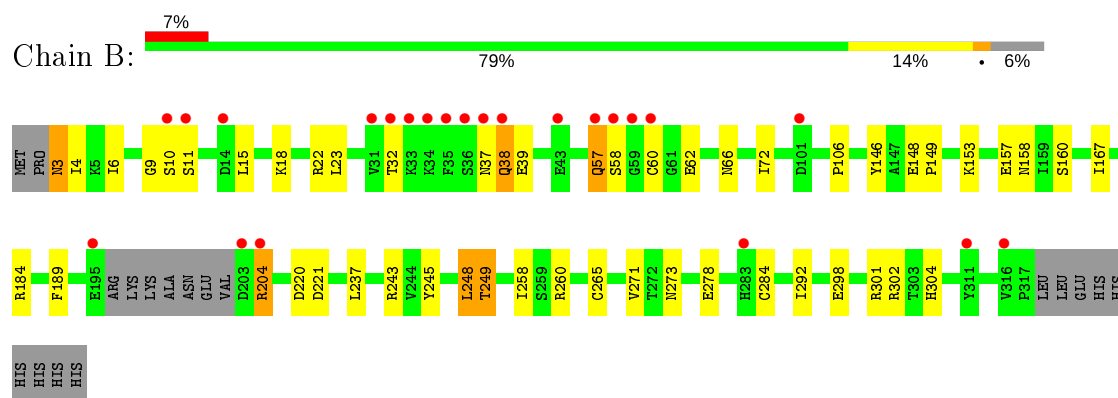
3 Residue-property plots [i](#)

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: Ribose-phosphate pyrophosphokinase 1



- Molecule 1: Ribose-phosphate pyrophosphokinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	170.08 Å 170.08 Å 61.62 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.10 – 2.11 49.10 – 2.11	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.10-2.11) 99.8 (49.10-2.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.12 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.171 , 0.191 0.163 , 0.176	Depositor DCC
R_{free} test set	1906 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 21.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.309 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.673 for H, K, L 0.327 for K, H, -L	Depositor
Outliers	0 of 38071 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4751	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.42	0/2356	0.57	1/3186 (0.0%)
1	B	0.46	0/2379	0.59	1/3222 (0.0%)
All	All	0.44	0/4735	0.58	2/6408 (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	B	38	GLN	CB-CA-C	-5.25	99.91	110.40
1	A	10	SER	N-CA-C	5.09	124.74	111.00

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	2324	0	2358	40	0
1	B	2345	0	2359	38	0
2	A	15	0	0	2	0
2	B	15	0	0	1	0
3	A	22	0	0	0	0
3	B	30	0	0	0	0
All	All	4751	0	4717	69	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 7.

All (69) 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:204:ARG:HH11	1:B:204:ARG:HG3	1.41	0.83
1:A:63:ILE:HG22	1:B:38:GLN:O	1.83	0.79
1:A:273:ASN:HD21	1:A:292:ILE:H	1.32	0.76
1:B:60:CYS:O	1:B:66:ASN:ND2	2.19	0.75
1:A:9:GLY:HA3	1:A:58:SER:HB2	1.70	0.71
1:B:243:ARG:NH1	1:B:245:TYR:OH	2.21	0.69
1:B:9:GLY:O	1:B:58:SER:HB2	2.00	0.62
1:B:157:GLU:HG3	1:B:158:ASN:ND2	2.16	0.61
1:A:273:ASN:H	1:A:273:ASN:HD22	1.49	0.61
1:B:298:GLU:O	1:B:302:ARG:HG2	2.01	0.61
1:A:63:ILE:CG2	1:B:38:GLN:O	2.50	0.59
1:A:248:LEU:O	1:A:271:VAL:HA	2.03	0.59
1:A:152:LEU:CD2	1:A:184:ARG:HG2	2.36	0.56
1:A:12:HIS:CD2	1:A:276:PRO:HG3	2.41	0.55
1:A:135:GLN:NE2	2:A:1003:SO4:O4	2.40	0.54
1:A:106:PRO:HG3	1:B:72:ILE:HG23	1.89	0.54
1:A:148:GLU:HB3	1:A:149:PRO:HD3	1.90	0.53
1:A:181:ILE:CD1	1:A:219:VAL:HG11	2.40	0.52
1:B:278:GLU:CD	1:B:278:GLU:H	2.13	0.52
1:A:152:LEU:HD21	1:A:184:ARG:HG2	1.92	0.51
1:A:9:GLY:CA	1:A:58:SER:HB2	2.40	0.51
1:A:6:ILE:HD11	1:A:23:LEU:CD1	2.40	0.51
1:A:132:SER:OG	2:A:1003:SO4:O1	2.27	0.50
1:B:9:GLY:C	1:B:58:SER:HB2	2.32	0.50
1:A:248:LEU:HB2	1:A:271:VAL:HG12	1.94	0.49
1:A:32:THR:HG22	1:A:42:VAL:HG22	1.93	0.49
1:A:60:CYS:SG	1:A:60:CYS:O	2.67	0.49
1:B:3:ASN:HB3	1:B:304:HIS:HE1	1.77	0.49
1:A:106:PRO:HG3	1:B:72:ILE:CG2	2.43	0.49
1:A:261:ILE:HG22	1:A:286:LYS:HD2	1.94	0.49
1:B:60:CYS:HB3	1:B:66:ASN:OD1	2.13	0.48
1:A:273:ASN:ND2	1:A:292:ILE:H	2.07	0.48
1:B:204:ARG:HH11	1:B:204:ARG:CG	2.16	0.48
1:A:72:ILE:HG23	1:B:106:PRO:HG3	1.96	0.48
1:B:273:ASN:OD1	1:B:292:ILE:HG13	2.14	0.48
1:A:63:ILE:HD13	1:B:39:GLU:HG2	1.96	0.48
1:A:161:GLU:OE1	1:A:243:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ILE:CD1	1:B:39:GLU:HG2	2.43	0.47
1:B:10:SER:OG	1:B:11:SER:N	2.42	0.47
1:B:298:GLU:OE2	1:B:301:ARG:NH1	2.48	0.47
1:A:273:ASN:N	1:A:273:ASN:HD22	2.10	0.47
1:B:237:LEU:HD12	1:B:265:CYS:SG	2.55	0.46
1:B:153:LYS:O	1:B:157:GLU:HG2	2.15	0.46
1:A:6:ILE:HD11	1:A:23:LEU:HD13	1.97	0.46
1:B:6:ILE:HD11	1:B:23:LEU:CD1	2.45	0.45
1:B:258:ILE:HG23	1:B:284:CYS:HB2	1.98	0.45
1:B:146:TYR:OH	2:B:403:SO4:O2	2.35	0.45
1:B:167:ILE:O	1:B:189:PHE:HA	2.16	0.45
1:B:6:ILE:HD11	1:B:23:LEU:HD12	1.99	0.45
1:B:18:LYS:O	1:B:22:ARG:HG3	2.16	0.45
1:A:194:LYS:HE2	1:A:203:ASP:HB2	1.99	0.44
1:B:248:LEU:O	1:B:271:VAL:HA	2.17	0.44
1:B:220:ASP:HB3	1:B:248:LEU:HD12	1.99	0.44
1:A:89:ILE:HG21	1:A:93:PRO:HD3	2.00	0.43
1:B:221:ASP:O	1:B:249:THR:HG23	2.19	0.43
1:A:152:LEU:HD23	1:A:184:ARG:HG2	2.01	0.43
1:A:257:ALA:O	1:A:261:ILE:HG13	2.19	0.42
1:B:148:GLU:HB3	1:B:149:PRO:HD3	2.01	0.42
1:A:172:ALA:HA	1:A:191:LEU:HD11	2.02	0.42
1:B:148:GLU:OE2	1:B:184:ARG:NH1	2.53	0.41
1:B:57:GLN:O	1:B:57:GLN:HG3	2.20	0.41
1:A:211:VAL:O	1:A:214:ARG:HG2	2.21	0.41
1:A:54:TYR:CD2	1:A:300:ILE:HG12	2.55	0.41
1:A:75:ASN:O	1:A:79:ILE:HG12	2.20	0.41
1:A:252:ILE:HG21	1:B:37:ASN:CB	2.51	0.41
1:A:252:ILE:HG21	1:B:37:ASN:HB2	2.02	0.40
1:A:92:PHE:HA	1:A:93:PRO:HD3	1.88	0.40
1:A:169:SER:HA	1:A:170:PRO:HD3	1.88	0.40
1:B:37:ASN:CG	1:B:37:ASN:O	2.59	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	300/326 (92%)	285 (95%)	15 (5%)	0	100	100
1	B	304/326 (93%)	291 (96%)	13 (4%)	0	100	100
All	All	604/652 (93%)	576 (95%)	28 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	257/278 (92%)	245 (95%)	12 (5%)	26	24
1	B	258/278 (93%)	247 (96%)	11 (4%)	29	28
All	All	515/556 (93%)	492 (96%)	23 (4%)	27	26

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	15	LEU
1	A	43	GLU
1	A	60	CYS
1	A	62	GLU
1	A	96	ARG
1	A	152	LEU
1	A	195	GLU
1	A	249	THR
1	A	265	CYS
1	A	273	ASN
1	A	286	LYS
1	B	3	ASN
1	B	4	ILE

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Mol	Chain	Res	Type
1	B	15	LEU
1	B	32	THR
1	B	57	GLN
1	B	62	GLU
1	B	160	SER
1	B	204	ARG
1	B	248	LEU
1	B	249	THR
1	B	260	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	273	ASN
1	A	277	GLN
1	B	57	GLN
1	B	64	ASN
1	B	277	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](#)

6 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	A	1002	-	4,4,4	0.14	0	6,6,6	0.14	0
2	SO4	B	401	-	4,4,4	0.25	0	6,6,6	0.35	0
2	SO4	A	1001	-	4,4,4	0.20	0	6,6,6	0.15	0
2	SO4	B	402	-	4,4,4	0.14	0	6,6,6	0.10	0
2	SO4	A	1003	-	4,4,4	0.19	0	6,6,6	0.26	0
2	SO4	B	403	-	4,4,4	0.17	0	6,6,6	0.17	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1003	SO4	2	0
2	B	403	SO4	1	0

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	303/326 (92%)	0.47	32 (10%) 6 7	20, 42, 65, 74	40 (13%)
1	B	308/326 (94%)	0.35	23 (7%) 14 18	19, 34, 51, 59	44 (14%)
All	All	611/652 (93%)	0.41	55 (9%) 9 12	19, 37, 59, 74	84 (13%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	35	PHE	13.0
1	B	36	SER	11.9
1	B	33	LYS	11.1
1	A	60	CYS	10.8
1	B	37	ASN	10.3
1	B	203	ASP	7.0
1	A	36	SER	6.5
1	B	10	SER	5.5
1	A	283	HIS	5.4
1	A	33	LYS	5.2
1	A	10	SER	4.9
1	B	11	SER	4.3
1	B	60	CYS	4.1
1	A	12	HIS	4.1
1	B	32	THR	3.9
1	B	34	LYS	3.9
1	A	282	LYS	3.7
1	A	313	PHE	3.4
1	A	284	CYS	3.2
1	B	101	ASP	3.1
1	A	29	LYS	3.1
1	B	38	GLN	3.1
1	A	31	VAL	3.1
1	A	279	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	195	GLU	2.8
1	B	14	ASP	2.8
1	A	280	LYS	2.8
1	A	278	GLU	2.7
1	A	257	ALA	2.7
1	A	11	SER	2.6
1	A	253	PHE	2.6
1	A	310	SER	2.6
1	B	316	VAL	2.6
1	A	32	THR	2.5
1	A	311	TYR	2.5
1	A	58	SER	2.5
1	A	255	GLY	2.5
1	A	37	ASN	2.4
1	A	294	MET	2.4
1	B	58	SER	2.4
1	A	259	SER	2.3
1	A	102	LYS	2.2
1	B	57	GLN	2.2
1	A	230	CYS	2.2
1	B	204	ARG	2.1
1	A	204	ARG	2.1
1	A	263	ASN	2.1
1	B	31	VAL	2.1
1	A	262	ASN	2.1
1	B	311	TYR	2.1
1	B	43	GLU	2.1
1	A	210	ASP	2.0
1	B	283	HIS	2.0
1	B	59	GLY	2.0
1	A	203	ASP	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(\AA^2)	Q<0.9
2	SO4	A	1002	5/5	0.85	0.11	93,93,93,94	0
2	SO4	B	402	5/5	0.96	0.10	60,60,61,62	0
2	SO4	A	1003	5/5	0.96	0.16	43,44,44,45	5
2	SO4	B	403	5/5	0.98	0.12	38,39,39,40	5
2	SO4	A	1001	5/5	0.99	0.11	36,36,37,38	0
2	SO4	B	401	5/5	0.99	0.12	32,32,33,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.