Full wwPDB X-ray Structure Validation Report

Sep 8, 2016 – 05:14 PM EDT

PDB ID	:	5IMT
Title	:	Toxin receptor complex
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Deposited on	:	2016-03-06
Resolution	:	2.70 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

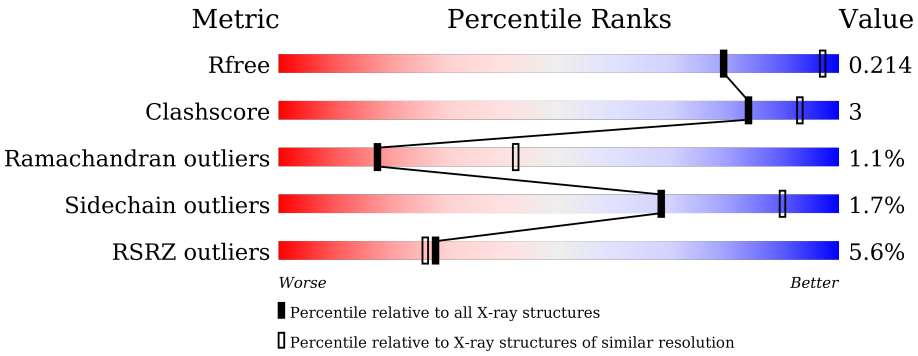
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

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 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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. 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 <=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	534	4% 81% • • 14%
2	D	77	12% 91% 9%

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
3	PGE	A	601	-	-	-	X
5	ZN	A	605	-	-	-	X
5	ZN	A	608	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8516 atoms, of which 4159 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 Intermedilysin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	460	7158	2261	3571	631	690	5	0	2	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9LCB8
A	0	GLY	-	expression tag	UNP Q9LCB8
A	1	SER	-	expression tag	UNP Q9LCB8
A	2	HIS	-	expression tag	UNP Q9LCB8
A	3	HIS	-	expression tag	UNP Q9LCB8
A	4	HIS	-	expression tag	UNP Q9LCB8
A	5	HIS	-	expression tag	UNP Q9LCB8
A	6	HIS	-	expression tag	UNP Q9LCB8
A	7	HIS	-	expression tag	UNP Q9LCB8
A	8	GLY	-	expression tag	UNP Q9LCB8
A	9	MET	-	expression tag	UNP Q9LCB8
A	10	ALA	-	expression tag	UNP Q9LCB8
A	11	SER	-	expression tag	UNP Q9LCB8
A	12	MET	-	expression tag	UNP Q9LCB8
A	13	THR	-	expression tag	UNP Q9LCB8
A	14	GLY	-	expression tag	UNP Q9LCB8
A	15	GLY	-	expression tag	UNP Q9LCB8
A	16	GLN	-	expression tag	UNP Q9LCB8
A	17	GLN	-	expression tag	UNP Q9LCB8
A	18	MET	-	expression tag	UNP Q9LCB8
A	19	GLY	-	expression tag	UNP Q9LCB8
A	20	ARG	-	expression tag	UNP Q9LCB8
A	21	ASP	-	expression tag	UNP Q9LCB8
A	22	LEU	-	expression tag	UNP Q9LCB8
A	23	TYR	-	expression tag	UNP Q9LCB8
A	24	ASP	-	expression tag	UNP Q9LCB8
A	25	ASP	-	expression tag	UNP Q9LCB8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ASP	-	expression tag	UNP Q9LCB8
A	27	ASP	-	expression tag	UNP Q9LCB8
A	28	LYS	-	expression tag	UNP Q9LCB8
A	29	ASP	-	expression tag	UNP Q9LCB8
A	30	ARG	-	expression tag	UNP Q9LCB8
A	31	TRP	-	expression tag	UNP Q9LCB8
A	32	GLY	-	expression tag	UNP Q9LCB8
A	33	SER	-	expression tag	UNP Q9LCB8
A	48	PRO	THR	conflict	UNP Q9LCB8
A	346	CYS	THR	conflict	UNP Q9LCB8
A	361	CYS	ILE	conflict	UNP Q9LCB8
A	445	GLU	ASP	conflict	UNP Q9LCB8

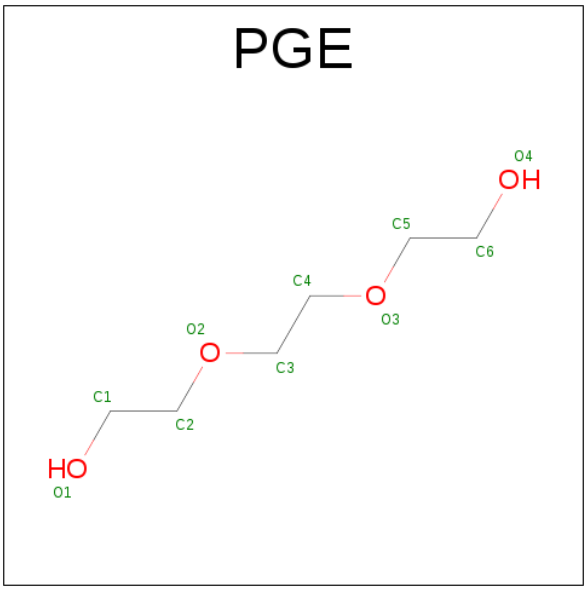
- Molecule 2 is a protein called CD59 glycoprotein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	D	77	Total	C	H	N	O	S	0	0	0
			1192	383	574	105	120	10			

There is a discrepancy between the modelled and reference sequences:

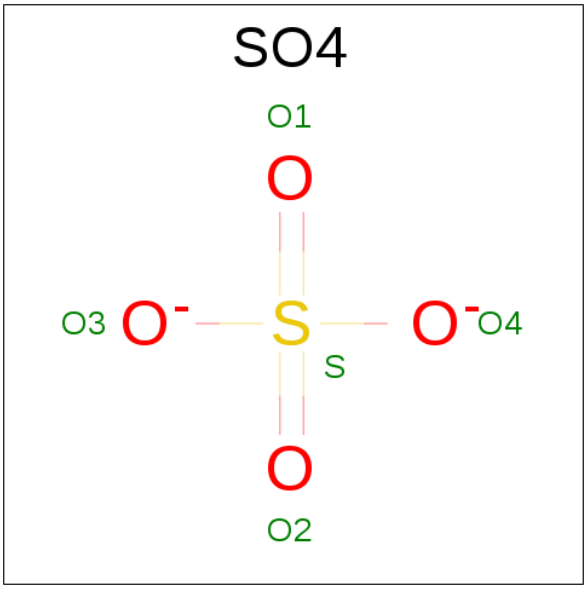
Chain	Residue	Modelled	Actual	Comment	Reference
D	22	ALA	ASP	conflict	UNP P13987

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C H O 24 6 14 4	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	5	Total Zn 5 5	0	0
5	D	2	Total Zn 2 2	0	0

- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Cu 2 2	0	0

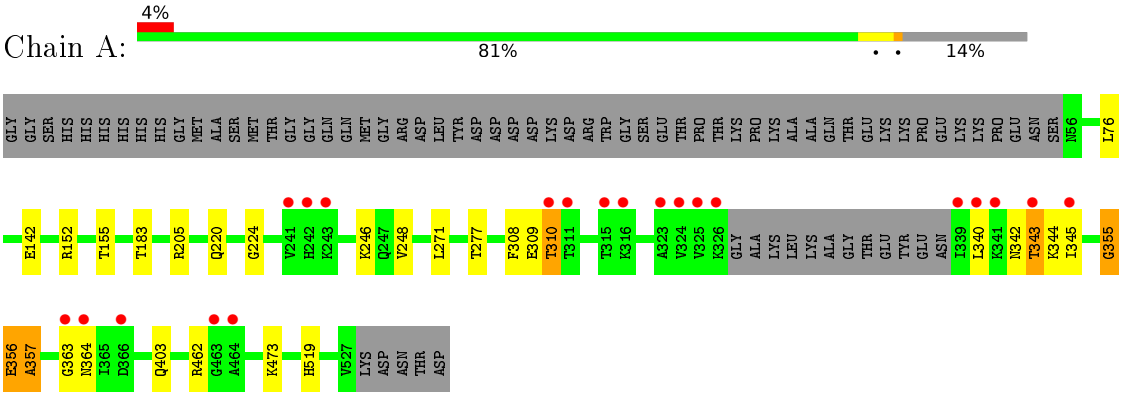
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	103	Total O 103 103	0	0
7	D	15	Total O 15 15	0	0

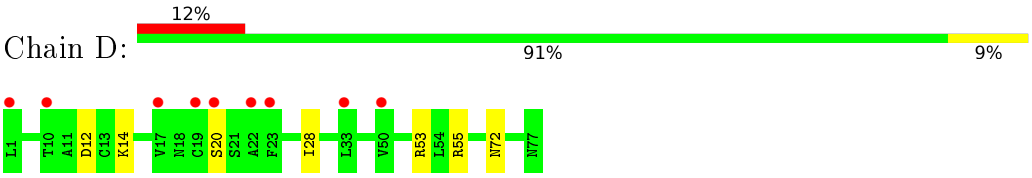
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Intermedilysin



- Molecule 2: CD59 glycoprotein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	93.73Å 166.56Å 118.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.21 – 2.70 48.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.21-2.70) 93.3 (48.21-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.208 , 0.257 0.208 , 0.214	Depositor DCC
R_{free} test set	1246 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	30.9	Xtriage
Anisotropy	0.880	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 30.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.028 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.043 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	8516	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN, PGE, SO4, CU

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	0.25	0/3666	0.47	0/4975
2	D	0.25	0/630	0.43	0/853
All	All	0.25	0/4296	0.46	0/5828

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	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	462	ARG	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	3587	3571	3566	19	0
2	D	618	574	574	5	0
3	A	10	14	14	0	0
4	A	10	0	0	0	0
4	D	5	0	0	1	0
5	A	5	0	0	0	0
5	D	2	0	0	0	0
6	A	2	0	0	0	0
7	A	103	0	0	3	1
7	D	15	0	0	4	1
All	All	4357	4159	4154	25	1

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 3.

All (25) 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)
2:D:14:LYS:NZ	7:D:202:HOH:O	2.20	0.65
1:A:473:LYS:NZ	7:A:705:HOH:O	2.38	0.56
1:A:152[B]:ARG:NH1	1:A:271:LEU:O	2.39	0.56
1:A:152[B]:ARG:NH2	7:A:707:HOH:O	2.40	0.55
1:A:309:GLU:N	1:A:343:THR:HG23	2.23	0.54
1:A:363:GLY:HA2	1:A:364:ASN:HB3	1.90	0.54
4:D:101:SO4:O3	7:D:201:HOH:O	2.18	0.51
2:D:28:ILE:HD11	2:D:72:ASN:HA	1.92	0.50
1:A:356:GLU:O	1:A:357:ALA:CB	2.60	0.49
2:D:53:ARG:NH2	7:D:203:HOH:O	2.48	0.47
1:A:310:THR:HG22	1:A:343:THR:OG1	2.15	0.47
1:A:152[B]:ARG:NH2	1:A:155:THR:OG1	2.50	0.44
1:A:220:GLN:O	1:A:224:GLY:N	2.50	0.44
1:A:340:LEU:N	1:A:340:LEU:HD12	2.32	0.43
1:A:345:ILE:H	1:A:363:GLY:H	1.65	0.43
1:A:248:VAL:HA	1:A:308:PHE:O	2.18	0.43
1:A:310:THR:OG1	1:A:310:THR:O	2.34	0.43
2:D:28:ILE:CD1	2:D:72:ASN:HA	2.48	0.43
1:A:363:GLY:HA2	1:A:364:ASN:CB	2.49	0.42
1:A:205:ARG:NH1	7:A:710:HOH:O	2.52	0.42
1:A:342:ASN:O	1:A:343:THR:O	2.37	0.42
2:D:53:ARG:NH1	7:D:204:HOH:O	2.51	0.41
1:A:76:LEU:HD23	1:A:76:LEU:H	1.85	0.41
1:A:246:LYS:HB2	1:A:310:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:GLY:O	1:A:356:GLU:HB2	2.21	0.41

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	Interatomic distance (Å)	Clash overlap (Å)
7:A:734:HOH:O	7:D:202:HOH:O[5_545]	1.99	0.21

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	458/534 (86%)	425 (93%)	29 (6%)	4 (1%)	21 49
2	D	75/77 (97%)	72 (96%)	1 (1%)	2 (3%)	6 16
All	All	533/611 (87%)	497 (93%)	30 (6%)	6 (1%)	17 42

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	THR
1	A	357	ALA
2	D	12	ASP
2	D	20	SER
1	A	356	GLU
1	A	355	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	396/456 (87%)	389 (98%)	7 (2%)	66 89
2	D	71/71 (100%)	70 (99%)	1 (1%)	74 92
All	All	467/527 (89%)	459 (98%)	8 (2%)	68 90

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	GLU
1	A	183	THR
1	A	277	THR
1	A	310	THR
1	A	344	LYS
1	A	403	GLN
1	A	519	HIS
2	D	55	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 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	PGE	A	601	-	9,9,9	0.31	0	8,8,8	0.53	0
4	SO4	A	602	-	4,4,4	0.21	0	6,6,6	0.09	0
4	SO4	A	603	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	101	-	4,4,4	0.22	0	6,6,6	0.07	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	PGE	A	601	-	-	0/7/7/7	0/0/0/0
4	SO4	A	602	-	-	0/0/0/0	0/0/0/0
4	SO4	A	603	-	-	0/0/0/0	0/0/0/0
4	SO4	D	101	-	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	101	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, 95^{th} 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	460/534 (86%)	0.24	21 (4%) 36 35	17, 33, 67, 78	0
2	D	77/77 (100%)	0.79	9 (11%) 6 5	28, 46, 63, 69	0
All	All	537/611 (87%)	0.32	30 (5%) 28 26	17, 35, 67, 78	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	340	LEU	4.4
1	A	364	ASN	4.1
2	D	1	LEU	3.9
1	A	324	VAL	3.8
2	D	22	ALA	3.8
1	A	326	LYS	3.6
1	A	323	ALA	3.5
1	A	343	THR	3.4
1	A	339	ILE	3.3
2	D	10	THR	3.1
2	D	33	LEU	3.1
1	A	241	VAL	3.0
1	A	311	THR	2.9
2	D	19	CYS	2.8
1	A	316	LYS	2.8
1	A	363	GLY	2.8
1	A	243	LYS	2.7
1	A	366	ASP	2.7
1	A	341	LYS	2.6
2	D	23	PHE	2.6
1	A	310	THR	2.5
2	D	20	SER	2.5
1	A	325	VAL	2.5
1	A	242	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	463	GLY	2.3
2	D	17	VAL	2.3
1	A	464	ALA	2.2
1	A	315	THR	2.2
2	D	50	VAL	2.1
1	A	345	ILE	2.1

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 carbohydrates 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. 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, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
5	ZN	A	608	1/1	0.75	0.38	7.98	120,120,120,120	0
3	PGE	A	601	10/10	0.88	0.27	7.09	28,56,69,78	0
5	ZN	A	605	1/1	0.99	0.22	4.35	38,38,38,38	0
5	ZN	A	604	1/1	0.98	0.22	0.97	60,60,60,60	0
5	ZN	A	606	1/1	0.98	0.20	0.77	50,50,50,50	0
4	SO4	A	603	5/5	0.91	0.19	-0.92	58,66,79,90	0
4	SO4	A	602	5/5	0.87	0.13	-0.93	31,32,55,82	0
4	SO4	D	101	5/5	0.93	0.13	-1.09	42,55,65,99	0
6	CU	A	609	1/1	0.97	0.07	-4.29	52,52,52,52	0
6	CU	A	610	1/1	0.88	0.21	-	113,113,113,113	0
5	ZN	A	607	1/1	0.99	0.18	-	53,53,53,53	0
5	ZN	D	103	1/1	0.90	0.15	-	115,115,115,115	0
5	ZN	D	102	1/1	0.99	0.13	-	52,52,52,52	0

6.5 Other polymers (i)

There are no such residues in this entry.