



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:07 PM UTC

PDB ID : 9QCI / pdb_00009qci
Title : Crystal structure of PhoC mutant acid phosphatase
Authors : Levy, C.W.; Ortmayer, M.
Deposited on : 2025-03-04
Resolution : 2.00 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

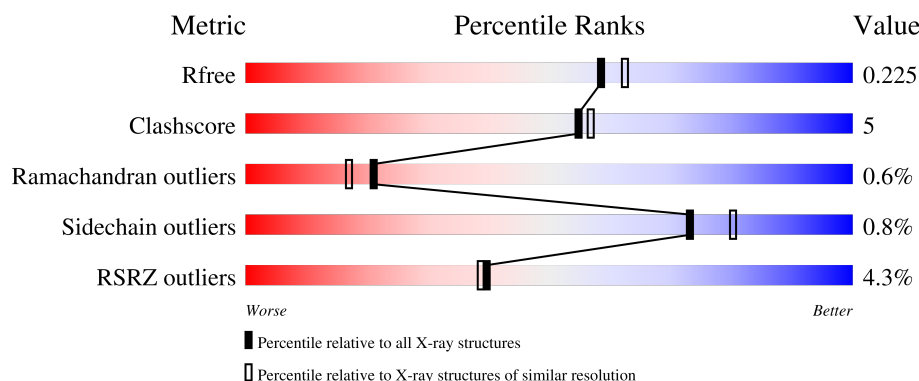
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	249	
1	B	249	
1	C	249	

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	PEG	A	304	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10665 atoms, of which 5206 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.

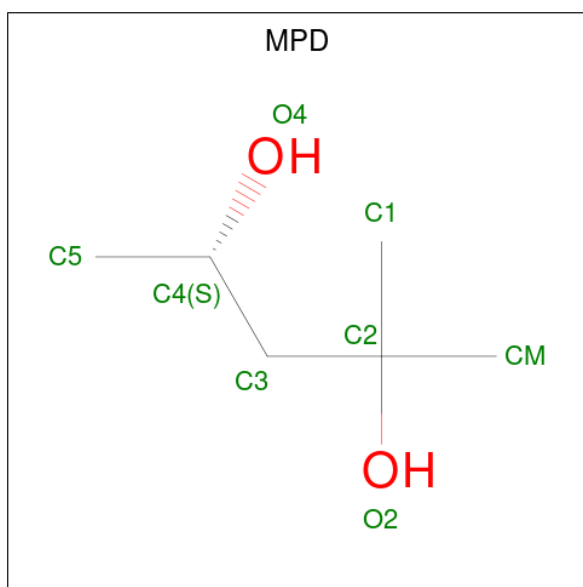
- Molecule 1 is a protein called Major phosphate-irrepressible acid phosphatase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	227	Total	C	H	N	O	S	0	9	0
			3520	1114	1742	306	350	8			
1	B	224	Total	C	H	N	O	S	0	8	0
			3473	1101	1715	304	345	8			
1	C	224	Total	C	H	N	O	S	0	5	0
			3435	1089	1697	301	341	7			

There are 15 discrepancies between the modelled and reference sequences:

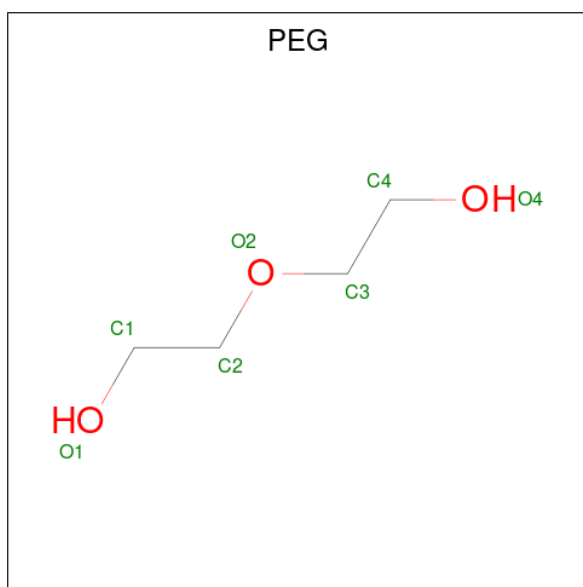
Chain	Residue	Modelled	Actual	Comment	Reference
A	90	GLU	ALA	conflict	UNP P28581
A	92	ASP	GLY	conflict	UNP P28581
A	151	ALA	ASN	conflict	UNP P28581
A	154	LEU	ASP	conflict	UNP P28581
A	171	THR	ILE	conflict	UNP P28581
B	90	GLU	ALA	conflict	UNP P28581
B	92	ASP	GLY	conflict	UNP P28581
B	151	ALA	ASN	conflict	UNP P28581
B	154	LEU	ASP	conflict	UNP P28581
B	171	THR	ILE	conflict	UNP P28581
C	90	GLU	ALA	conflict	UNP P28581
C	92	ASP	GLY	conflict	UNP P28581
C	151	ALA	ASN	conflict	UNP P28581
C	154	LEU	ASP	conflict	UNP P28581
C	171	THR	ILE	conflict	UNP P28581

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



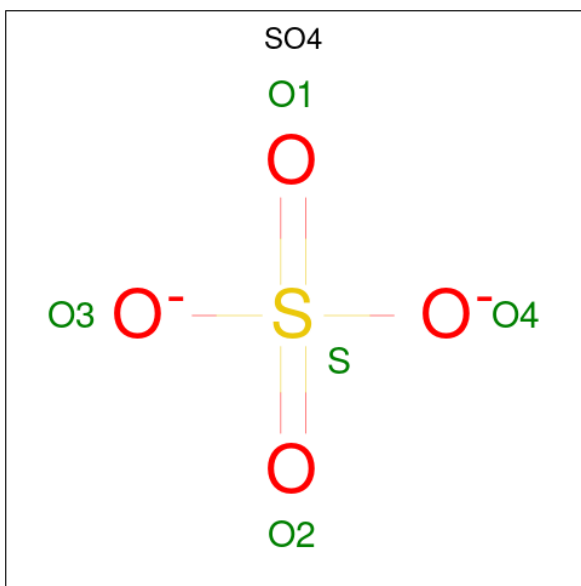
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			22	6	14	2		
2	A	1	Total	C	H	O	0	0
			22	6	14	2		
2	A	1	Total	C	H	O	0	0
			22	6	14	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

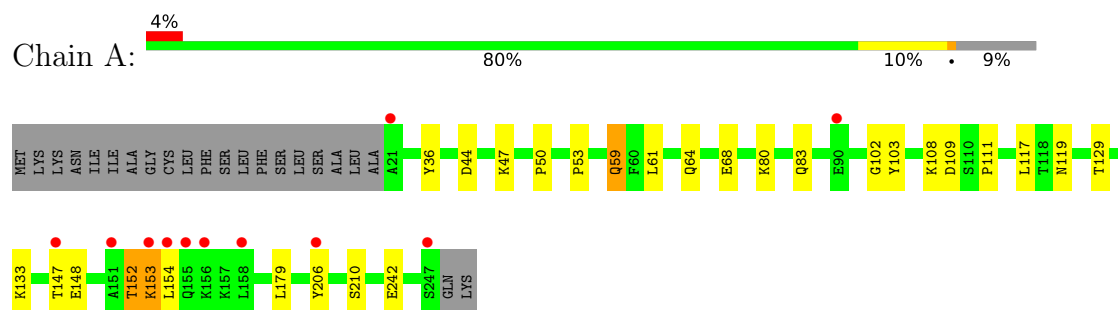
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	62	Total	O	0	0
			62	62		
5	B	46	Total	O	0	0
			46	46		
5	C	26	Total	O	0	0
			26	26		

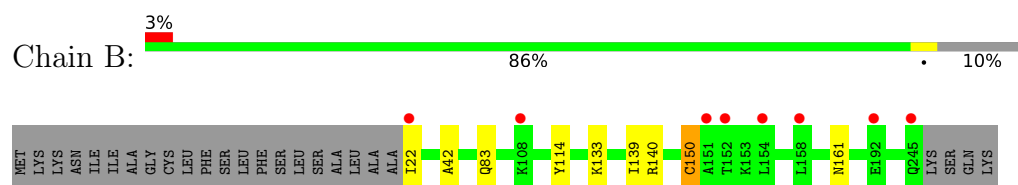
3 Residue-property plots

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.

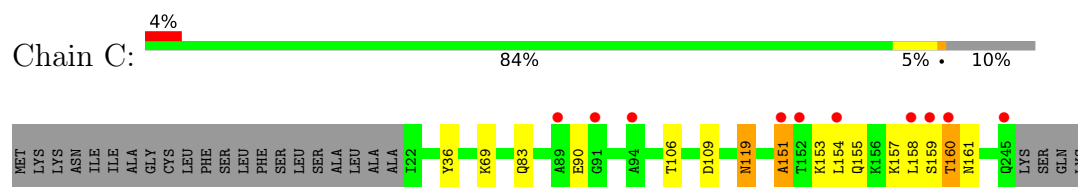
- Molecule 1: Major phosphate-irrepressible acid phosphatase



- Molecule 1: Major phosphate-irrepressible acid phosphatase



- Molecule 1: Major phosphate-irrepressible acid phosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.72Å 117.72Å 97.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	70.51 – 2.00 70.51 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (70.51-2.00) 91.0 (70.51-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.34 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.186 , 0.225 0.190 , 0.225	Depositor DCC
R_{free} test set	1936 reflections (3.64%)	wwPDB-VP
Wilson B-factor (Å ²)	39.6	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10665	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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, PEG, MPD

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	0/1835	0.76	0/2488
1	B	0.60	0/1814	0.68	0/2461
1	C	0.51	0/1786	0.61	0/2422
All	All	0.61	0/5435	0.69	0/7371

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	C	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	C	151	ALA	Peptide

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	1778	1742	1731	22	0
1	B	1758	1715	1703	7	0
1	C	1738	1697	1686	15	0
2	A	24	42	42	9	0
3	A	7	10	10	4	0
4	A	10	0	0	0	0
4	B	5	0	0	1	0
4	C	5	0	0	0	0
5	A	62	0	0	3	0
5	B	46	0	0	2	0
5	C	26	0	0	0	0
All	All	5459	5206	5172	50	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 5.

All (50) 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:A:303:MPD:HM2	5:A:439:HOH:O	1.61	1.00
1:A:64:GLN:OE1	2:A:303:MPD:HM1	1.74	0.87
1:C:83:GLN:HG3	1:C:151:ALA:HB2	1.63	0.80
2:A:303:MPD:H53	5:A:453:HOH:O	1.85	0.76
1:C:154:LEU:HG	1:C:158:LEU:HD21	1.66	0.76
2:A:301:MPD:H51	5:A:414:HOH:O	1.90	0.71
1:B:114:TYR:OH	5:B:401:HOH:O	2.10	0.69
1:A:154:LEU:HD23	1:A:206:TYR:HE1	1.61	0.65
1:A:210:SER:HB2	3:A:304:PEG:H31	1.80	0.63
2:A:301:MPD:HM1	2:A:301:MPD:H52	1.83	0.60
1:A:154:LEU:HD23	1:A:206:TYR:CE1	2.37	0.60
1:C:153:LYS:O	1:C:157:LYS:HE2	2.07	0.55
1:A:61:LEU:HD13	2:A:303:MPD:HM3	1.89	0.54
1:B:22:ILE:HD13	1:B:42:ALA:HB3	1.89	0.54
1:C:159:SER:O	1:C:160:THR:HG22	2.07	0.54
1:C:155:GLN:HA	1:C:158:LEU:HD23	1.88	0.53
1:A:50:PRO:HG2	3:A:304:PEG:H11	1.91	0.53
1:B:83:GLN:HG2	1:B:150[B]:CYS:HB3	1.91	0.52
2:A:301:MPD:H52	2:A:301:MPD:CM	2.39	0.52
1:A:152:THR:O	1:A:153:LYS:HB2	2.10	0.52
1:B:140[B]:ARG:NH1	1:B:161:ASN:O	2.43	0.51
1:C:159:SER:O	1:C:161:ASN:N	2.35	0.50
1:C:106:THR:HG23	1:C:109:ASP:H	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:LEU:HD11	1:A:179:LEU:HD21	1.95	0.48
1:A:152:THR:O	1:A:153:LYS:CB	2.60	0.48
1:A:210:SER:CB	3:A:304:PEG:H31	2.44	0.48
1:A:50:PRO:HG2	3:A:304:PEG:C1	2.43	0.48
1:A:53:PRO:HB3	1:A:59[A]:GLN:HB3	1.95	0.48
1:A:36:TYR:CE2	1:A:119:ASN:HB3	2.48	0.48
1:C:159:SER:C	1:C:160:THR:HG22	2.38	0.48
1:C:154:LEU:O	1:C:158:LEU:CD2	2.63	0.46
1:B:83:GLN:HG2	1:B:150[A]:CYS:HB2	1.97	0.46
1:C:153:LYS:O	1:C:154:LEU:C	2.55	0.46
1:A:147:THR:OG1	1:A:148:GLU:N	2.50	0.45
1:A:44:ASP:OD2	1:A:47:LYS:HD3	2.18	0.44
1:A:68:GLU:HG3	2:A:301:MPD:H52	2.00	0.44
1:A:108:LYS:HG3	1:A:109:ASP:N	2.32	0.43
1:A:111:PRO:HD2	1:A:242:GLU:OE2	2.19	0.43
1:A:80:LYS:NZ	1:A:83:GLN:HG2	2.33	0.43
1:C:36:TYR:CE2	1:C:119:ASN:HB3	2.54	0.43
1:C:154:LEU:O	1:C:158:LEU:HD22	2.19	0.43
1:B:133:LYS:NZ	4:B:301:SO4:O2	2.50	0.42
1:C:159:SER:O	1:C:160:THR:CG2	2.67	0.42
2:A:303:MPD:H52	2:A:303:MPD:O2	2.19	0.42
1:C:154:LEU:C	1:C:158:LEU:CD2	2.93	0.42
1:A:53:PRO:HB3	1:A:59[B]:GLN:HB3	2.02	0.41
1:B:139:ILE:HG22	5:B:432:HOH:O	2.20	0.41
1:A:129:THR:O	1:A:133:LYS:HB2	2.21	0.41
1:C:154:LEU:C	1:C:158:LEU:HD23	2.45	0.40
1:A:102:GLY:C	1:A:103:TYR:CD1	3.00	0.40

There are no symmetry-related clashes.

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	234/249 (94%)	226 (97%)	6 (3%)	2 (1%)	14	9
1	B	230/249 (92%)	225 (98%)	5 (2%)	0	100	100
1	C	227/249 (91%)	218 (96%)	7 (3%)	2 (1%)	14	9
All	All	691/747 (92%)	669 (97%)	18 (3%)	4 (1%)	21	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	LYS
1	A	152	THR
1	C	160	THR
1	C	90	GLU

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	186/197 (94%)	184 (99%)	2 (1%)	65	73
1	B	184/197 (93%)	182 (99%)	2 (1%)	65	73
1	C	180/197 (91%)	178 (99%)	2 (1%)	65	73
All	All	550/591 (93%)	544 (99%)	6 (1%)	73	73

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59[A]	GLN
1	A	59[B]	GLN
1	B	150[A]	CYS
1	B	150[B]	CYS
1	C	69	LYS
1	C	119	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	B	59	GLN
1	B	62	ASN
1	B	64	GLN
1	B	81	GLN
1	B	119	ASN
1	B	233	GLN
1	C	59	GLN
1	C	62	ASN
1	C	64	GLN
1	C	233	GLN
1	C	241	GLN
1	C	245	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](#)

8 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	$\# Z > 2$
4	SO4	B	301	-	4,4,4	1.29	0	6,6,6	0.40	0
2	MPD	A	301	-	7,7,7	0.57	0	9,10,10	1.02	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MPD	A	302	-	7,7,7	0.91	0	9,10,10	1.26	1 (11%)
3	PEG	A	304	-	6,6,6	0.66	0	5,5,5	0.65	0
4	SO4	C	301	-	4,4,4	1.07	0	6,6,6	0.55	0
2	MPD	A	303	-	7,7,7	0.59	0	9,10,10	0.70	0
4	SO4	A	305	-	4,4,4	1.67	1 (25%)	6,6,6	0.77	0
4	SO4	A	306	-	4,4,4	1.01	0	6,6,6	0.58	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
2	MPD	A	303	-	-	2/5/5/5	-
2	MPD	A	302	-	-	3/5/5/5	-
2	MPD	A	301	-	-	2/5/5/5	-
3	PEG	A	304	-	-	3/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	305	SO4	O1-S	2.37	1.58	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	302	MPD	CM-C2-C1	-2.57	104.87	110.63

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	MPD	C2-C3-C4-O4
2	A	301	MPD	C2-C3-C4-C5
2	A	303	MPD	C2-C3-C4-O4
2	A	303	MPD	C2-C3-C4-C5
3	A	304	PEG	O1-C1-C2-O2
3	A	304	PEG	O2-C3-C4-O4
2	A	302	MPD	C2-C3-C4-O4
2	A	302	MPD	C1-C2-C3-C4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	304	PEG	C1-C2-O2-C3
2	A	302	MPD	CM-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	301	SO4	1	0
2	A	301	MPD	4	0
3	A	304	PEG	4	0
2	A	303	MPD	5	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	227/249 (91%)	-0.15	11 (4%) 35 34	22, 48, 97, 184	7 (3%)
1	B	224/249 (89%)	0.12	8 (3%) 46 45	27, 59, 92, 185	6 (2%)
1	C	224/249 (89%)	0.33	10 (4%) 38 37	25, 70, 118, 166	3 (1%)
All	All	675/747 (90%)	0.10	29 (4%) 40 39	22, 58, 108, 185	16 (2%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	151	ALA	5.9
1	B	108	LYS	4.0
1	A	21	ALA	3.9
1	A	154	LEU	3.5
1	A	158	LEU	3.4
1	C	154	LEU	3.1
1	C	159	SER	2.9
1	A	247	SER	2.9
1	A	151[A]	ALA	2.8
1	C	152	THR	2.6
1	B	154	LEU	2.5
1	B	152	THR	2.4
1	A	153	LYS	2.4
1	C	245	GLN	2.3
1	A	147	THR	2.3
1	C	89	ALA	2.3
1	A	90	GLU	2.2
1	A	156	LYS	2.2
1	C	160	THR	2.2
1	B	192[A]	GLU	2.2
1	C	158	LEU	2.2
1	B	22	ILE	2.2
1	B	245	GLN	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	91	GLY	2.1
1	C	151	ALA	2.1
1	A	206	TYR	2.1
1	C	94	ALA	2.1
1	B	158	LEU	2.0
1	A	155	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
4	SO4	C	301	5/5	0.64	0.12	74,74,97,103	0
4	SO4	B	301	5/5	0.76	0.12	63,64,80,89	0
4	SO4	A	306	5/5	0.83	0.13	51,66,75,84	5
4	SO4	A	305	5/5	0.84	0.11	50,56,89,90	0
3	PEG	A	304	7/7	0.89	0.13	32,47,57,57	17
2	MPD	A	302	8/8	0.96	0.08	28,40,47,54	0
2	MPD	A	301	8/8	0.96	0.07	26,38,48,57	0
2	MPD	A	303	8/8	0.97	0.06	32,41,49,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.