



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:22 PM UTC

PDB ID : 5JN5 / pdb_00005jn5
Title : Crystal structure of the D263Y missense variant of human PGM1
Authors : Beamer, L.J.; Stiers, K.M.
Deposited on : 2016-04-29
Resolution : 1.75 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

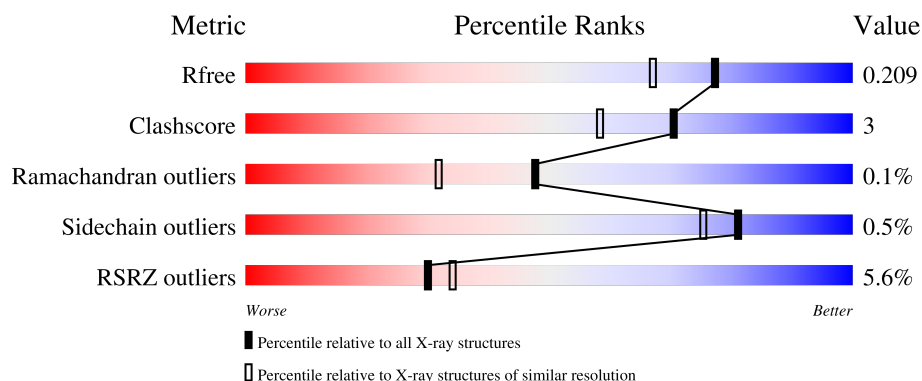
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	585	3% 89% 6% • •
1	B	585	8% 88% 7% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10013 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 Phosphoglucomutase-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	P	S	0	14	0
			4341	2758	736	829	1	17			
1	B	556	Total	C	N	O	P	S	0	10	0
			4212	2684	713	797	1	17			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	expression tag	UNP P36871
A	-21	HIS	-	expression tag	UNP P36871
A	-20	HIS	-	expression tag	UNP P36871
A	-19	HIS	-	expression tag	UNP P36871
A	-18	HIS	-	expression tag	UNP P36871
A	-17	HIS	-	expression tag	UNP P36871
A	-16	HIS	-	expression tag	UNP P36871
A	-15	SER	-	expression tag	UNP P36871
A	-14	SER	-	expression tag	UNP P36871
A	-13	GLY	-	expression tag	UNP P36871
A	-12	VAL	-	expression tag	UNP P36871
A	-11	ASP	-	expression tag	UNP P36871
A	-10	LEU	-	expression tag	UNP P36871
A	-9	GLY	-	expression tag	UNP P36871
A	-8	THR	-	expression tag	UNP P36871
A	-7	GLU	-	expression tag	UNP P36871
A	-6	ASN	-	expression tag	UNP P36871
A	-5	LEU	-	expression tag	UNP P36871
A	-4	TYR	-	expression tag	UNP P36871
A	-3	PHE	-	expression tag	UNP P36871
A	-2	GLN	-	expression tag	UNP P36871
A	-1	SER	-	expression tag	UNP P36871
A	0	ASN	-	expression tag	UNP P36871
A	263	TYR	ASP	engineered mutation	UNP P36871
B	-22	MET	-	expression tag	UNP P36871

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-21	HIS	-	expression tag	UNP P36871
B	-20	HIS	-	expression tag	UNP P36871
B	-19	HIS	-	expression tag	UNP P36871
B	-18	HIS	-	expression tag	UNP P36871
B	-17	HIS	-	expression tag	UNP P36871
B	-16	HIS	-	expression tag	UNP P36871
B	-15	SER	-	expression tag	UNP P36871
B	-14	SER	-	expression tag	UNP P36871
B	-13	GLY	-	expression tag	UNP P36871
B	-12	VAL	-	expression tag	UNP P36871
B	-11	ASP	-	expression tag	UNP P36871
B	-10	LEU	-	expression tag	UNP P36871
B	-9	GLY	-	expression tag	UNP P36871
B	-8	THR	-	expression tag	UNP P36871
B	-7	GLU	-	expression tag	UNP P36871
B	-6	ASN	-	expression tag	UNP P36871
B	-5	LEU	-	expression tag	UNP P36871
B	-4	TYR	-	expression tag	UNP P36871
B	-3	PHE	-	expression tag	UNP P36871
B	-2	GLN	-	expression tag	UNP P36871
B	-1	SER	-	expression tag	UNP P36871
B	0	ASN	-	expression tag	UNP P36871
B	263	TYR	ASP	engineered mutation	UNP P36871

- 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	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0

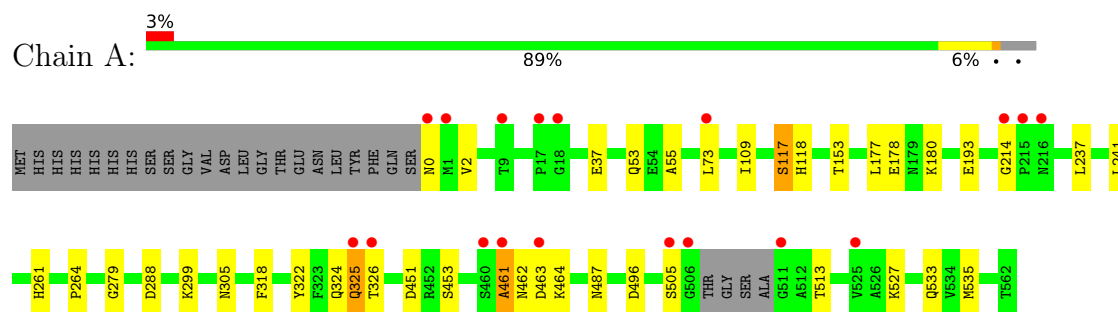
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	798	Total O 798 798	0	0
4	B	625	Total O 625 625	0	0

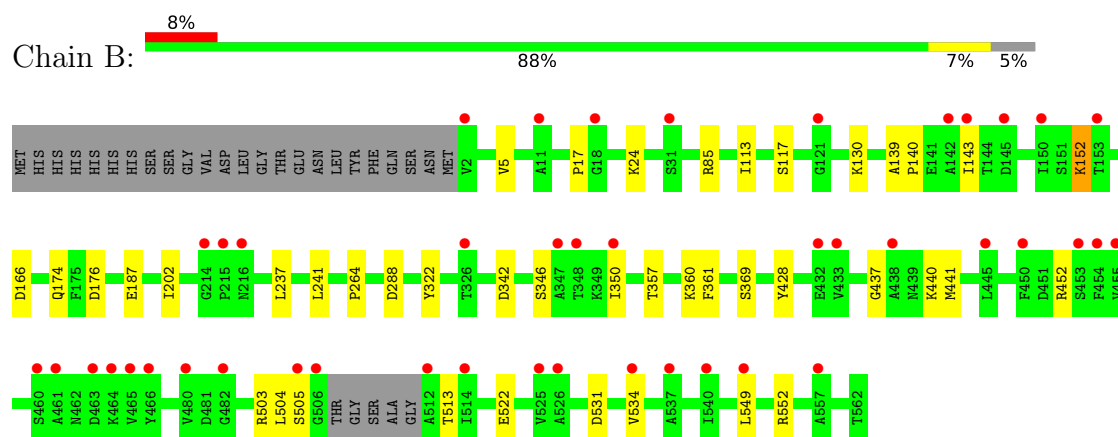
3 Residue-property plots

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: Phosphoglucumutase-1



• Molecule 1: Phosphoglucumutase-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.99Å 172.99Å 100.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.70 – 1.75 54.70 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.70-1.75) 100.0 (54.70-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.180 , 0.209 0.182 , 0.209	Depositor DCC
R_{free} test set	7553 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.3	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	0.96	EDS
Total number of atoms	10013	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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: CA, SEP, 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	0.53	0/4437	0.79	6/6006 (0.1%)
1	B	0.47	0/4305	0.77	0/5840
All	All	0.50	0/8742	0.78	6/11846 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	461	ALA	CA-C-N	6.98	134.26	121.70
1	A	461	ALA	C-N-CA	6.98	134.26	121.70
1	A	2	VAL	N-CA-C	5.20	117.34	108.86
1	A	214	GLY	CA-C-N	5.18	124.49	118.85
1	A	214	GLY	C-N-CA	5.18	124.49	118.85
1	A	461	ALA	CA-C-O	-5.08	115.55	120.89

There are no chirality outliers.

There are no planarity outliers.

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	4341	0	4278	30	0
1	B	4212	0	4104	28	0
2	A	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	15	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	798	0	0	14	7
4	B	625	0	0	11	5
All	All	10013	0	8382	58	7

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 (58) 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:A:117:SEP:O2P	4:A:701:HOH:O	1.92	0.87
1:B:522:GLU:OE2	4:B:701:HOH:O	1.99	0.80
1:B:369:SER:OG	4:B:702:HOH:O	2.03	0.76
1:B:174:GLN:OE1	4:B:703:HOH:O	2.04	0.76
1:A:53:GLN:OE1	4:A:703:HOH:O	2.04	0.75
1:A:305[A]:ASN:OD1	4:A:702:HOH:O	2.04	0.75
1:A:533:GLN:NE2	4:A:706:HOH:O	2.18	0.73
1:A:325[A]:GLN:NE2	4:A:709:HOH:O	2.21	0.72
1:A:0:ASN:N	4:A:704:HOH:O	2.11	0.72
1:A:451:ASP:OD2	1:A:453:SER:OG	2.08	0.70
1:A:153:THR:OG1	4:A:705:HOH:O	2.12	0.68
1:A:37:GLU:HG3	1:A:73:LEU:HD11	1.77	0.66
1:B:166:ASP:OD2	4:B:704:HOH:O	2.14	0.65
1:A:464:LYS:HD2	4:A:744:HOH:O	2.00	0.62
1:A:261:HIS:ND1	4:A:714:HOH:O	2.28	0.60
1:B:505:SER:HB2	1:B:513:THR:HB	1.84	0.59
1:B:24:LYS:NZ	4:B:718:HOH:O	2.34	0.56
1:B:441:MET:HE1	1:B:549:LEU:HD12	1.87	0.56
1:B:113:ILE:HD12	1:B:130:LYS:HE3	1.89	0.55
1:B:357[B]:THR:HG21	1:B:503:ARG:CZ	2.37	0.55
1:A:461:ALA:HB3	1:A:462:ASN:C	2.32	0.54
1:B:237:LEU:HD23	1:B:241:LEU:HD12	1.92	0.52
1:B:152:LYS:HB2	1:B:152:LYS:HZ2	1.75	0.52
1:B:428:TYR:OH	4:B:705:HOH:O	2.19	0.52
1:B:531:ASP:O	1:B:534:VAL:HG12	2.11	0.50
1:B:152:LYS:HB2	1:B:152:LYS:NZ	2.27	0.50
1:B:452:ARG:O	4:B:706:HOH:O	2.19	0.49
1:A:527:LYS:HD3	1:A:535:MET:HE1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:LYS:HG2	1:B:552:ARG:HD3	1.94	0.49
1:B:85:ARG:HH11	1:B:187[B]:GLU:CD	2.21	0.49
1:A:487[B]:ASN:ND2	4:A:727:HOH:O	2.42	0.48
1:A:193[B]:GLU:OE1	4:A:707:HOH:O	2.20	0.47
1:A:464:LYS:HE2	1:A:496:ASP:OD2	2.15	0.46
1:A:322:TYR:O	1:A:326:THR:HG23	2.16	0.46
1:A:178:GLU:HB3	4:A:876:HOH:O	2.16	0.46
1:A:513:THR:OG1	4:A:708:HOH:O	2.20	0.45
1:B:140:PRO:HD2	1:B:143:ILE:HD12	1.97	0.45
1:A:464:LYS:HE3	4:A:770:HOH:O	2.16	0.44
1:B:139:ALA:HA	1:B:140:PRO:HD3	1.85	0.44
1:B:264:PRO:HD3	1:B:288:ASP:HB3	2.00	0.44
1:B:346[A]:SER:HB2	4:B:936:HOH:O	2.16	0.44
1:B:437:GLY:N	4:B:731:HOH:O	2.48	0.44
1:B:85:ARG:NH1	1:B:187[B]:GLU:OE1	2.50	0.44
1:A:37:GLU:HA	1:A:73:LEU:HD21	1.98	0.44
1:B:504:LEU:HD23	1:B:504:LEU:HA	1.85	0.43
1:A:279:GLY:O	1:A:299:LYS:HE2	2.18	0.43
1:A:55:ALA:HB1	1:A:109:ILE:HD13	2.00	0.43
1:A:264:PRO:HD3	1:A:288:ASP:HB3	2.00	0.43
1:A:505:SER:HB3	1:A:513:THR:HB	2.01	0.43
1:B:202:ILE:HG23	1:B:322:TYR:HB2	2.01	0.43
1:A:117:SEP:OG	1:A:118:HIS:N	2.50	0.42
1:B:176:ASP:OD2	4:B:707:HOH:O	2.21	0.42
1:A:237:LEU:HD23	1:A:241:LEU:HD12	2.02	0.42
1:A:462:ASN:HB3	1:A:463:ASP:H	1.51	0.42
1:A:318:PHE:O	1:A:324:GLN:NE2	2.52	0.42
1:B:350:ILE:HA	4:B:715:HOH:O	2.20	0.41
1:A:177:LEU:HB2	1:A:180:LYS:HB2	2.03	0.40
1:B:360:LYS:HE3	1:B:361:PHE:CZ	2.56	0.40

All (7) 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)
4:A:1041:HOH:O	4:B:834:HOH:O[4_544]	1.87	0.33
4:A:1129:HOH:O	4:B:1266:HOH:O[4_545]	1.96	0.24
4:A:1037:HOH:O	4:B:1224:HOH:O[6_544]	1.99	0.21
4:A:1471:HOH:O	4:B:1196:HOH:O[4_544]	2.06	0.14
4:A:1362:HOH:O	4:A:1373:HOH:O[3_445]	2.13	0.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1471:HOH:O	4:B:1171:HOH:O[4_544]	2.13	0.07
4:A:1183:HOH:O	4:A:1359:HOH:O[8_555]	2.14	0.06

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	568/585 (97%)	558 (98%)	10 (2%)	0	100	100
1	B	561/585 (96%)	551 (98%)	9 (2%)	1 (0%)	43	27
All	All	1129/1170 (96%)	1109 (98%)	19 (2%)	1 (0%)	48	32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	17	PRO

5.3.2 Protein sidechains [i](#)

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	457/482 (95%)	455 (100%)	2 (0%)	84	80
1	B	431/482 (89%)	428 (99%)	3 (1%)	76	67
All	All	888/964 (92%)	883 (99%)	5 (1%)	81	71

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	325[A]	GLN
1	A	325[B]	GLN
1	B	5	VAL
1	B	152	LYS
1	B	342	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	294	ASN
1	A	300	HIS
1	B	30	GLN
1	B	174	GLN
1	B	423	ASN
1	B	548	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SEP	A	117	1,3	8,9,10	1.61	1 (12%)	7,12,14	2.58	2 (28%)
1	SEP	B	117	1,3	8,9,10	1.64	1 (12%)	7,12,14	1.76	2 (28%)

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
1	SEP	A	117	1,3	-	5/6/8/10	-
1	SEP	B	117	1,3	-	4/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	117	SEP	P-O1P	3.57	1.61	1.50
1	A	117	SEP	P-O1P	3.19	1.60	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	117	SEP	OG-CB-CA	5.72	113.71	108.14
1	B	117	SEP	OG-CB-CA	3.54	111.59	108.14
1	A	117	SEP	O2P-P-OG	3.33	115.36	106.67
1	B	117	SEP	O2P-P-OG	2.63	113.52	106.67

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	117	SEP	C-CA-CB-OG
1	A	117	SEP	CB-OG-P-O1P
1	A	117	SEP	CB-OG-P-O3P
1	B	117	SEP	CB-OG-P-O1P
1	B	117	SEP	CB-OG-P-O2P
1	B	117	SEP	CB-OG-P-O3P
1	A	117	SEP	N-CA-CB-OG
1	B	117	SEP	N-CA-CB-OG
1	A	117	SEP	CB-OG-P-O2P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	117	SEP	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	$\# Z > 2$
2	SO4	B	601	-	4,4,4	0.20	0	6,6,6	0.21	0
2	SO4	A	604	-	4,4,4	0.22	0	6,6,6	0.14	0
2	SO4	B	602	-	4,4,4	0.23	0	6,6,6	0.20	0
2	SO4	A	603	-	4,4,4	0.21	0	6,6,6	0.14	0
2	SO4	B	603	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	A	601	-	4,4,4	0.19	0	6,6,6	0.31	0
2	SO4	A	602	-	4,4,4	0.35	0	6,6,6	0.38	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	558/585 (95%)	-0.12	18 (3%) 50 57	7, 18, 35, 65	14 (2%)
1	B	555/585 (94%)	0.47	44 (7%) 18 22	9, 26, 45, 79	10 (1%)
All	All	1113/1170 (95%)	0.17	62 (5%) 30 34	7, 22, 42, 79	24 (2%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	ASP	4.9
1	A	215	PRO	4.8
1	A	461	ALA	4.6
1	B	480	VAL	3.7
1	B	465	VAL	3.7
1	A	73	LEU	3.5
1	A	511	GLY	3.5
1	B	214	GLY	3.5
1	B	350	ILE	3.5
1	B	534	VAL	3.4
1	B	525	VAL	3.4
1	A	1	MET	3.4
1	A	0	ASN	3.3
1	B	347	ALA	3.2
1	B	512	ALA	3.2
1	B	215	PRO	3.2
1	A	325[A]	GLN	3.1
1	B	348	THR	3.0
1	B	2	VAL	3.0
1	B	142	ALA	3.0
1	A	18	GLY	3.0
1	A	216[A]	ASN	2.9
1	B	216	ASN	2.9
1	B	506	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	432	GLU	2.7
1	B	461	ALA	2.7
1	B	464	LYS	2.7
1	B	143	ILE	2.6
1	B	526	ALA	2.6
1	A	214	GLY	2.6
1	B	463	ASP	2.6
1	B	482	GLY	2.5
1	B	445	LEU	2.5
1	B	433	VAL	2.5
1	B	11	ALA	2.5
1	B	145	ASP	2.4
1	B	537	ALA	2.4
1	B	450	PHE	2.4
1	B	505	SER	2.4
1	B	150	ILE	2.4
1	B	438	ALA	2.4
1	B	455	VAL	2.3
1	B	460	SER	2.3
1	B	454	PHE	2.3
1	A	525	VAL	2.2
1	A	17	PRO	2.2
1	B	453	SER	2.2
1	B	153	THR	2.2
1	B	326	THR	2.2
1	A	9	THR	2.1
1	A	506	GLY	2.1
1	B	121	GLY	2.1
1	B	549	LEU	2.1
1	B	31[A]	SER	2.1
1	B	514	ILE	2.1
1	A	460	SER	2.1
1	B	466	TYR	2.1
1	B	18	GLY	2.0
1	B	557	ALA	2.0
1	A	326	THR	2.0
1	B	540	ILE	2.0
1	A	505	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	B	117	10/11	0.91	0.11	20,28,38,39	10
1	SEP	A	117	10/11	0.92	0.10	16,24,31,31	10

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	B	603	5/5	0.84	0.12	33,40,47,48	5
2	SO4	A	602	5/5	0.85	0.16	14,19,30,31	5
2	SO4	A	604	5/5	0.91	0.11	22,33,35,37	5
2	SO4	A	603	5/5	0.93	0.09	29,29,32,33	5
2	SO4	B	602	5/5	0.96	0.07	20,23,28,29	5
2	SO4	B	601	5/5	0.96	0.07	35,36,41,43	0
2	SO4	A	601	5/5	0.99	0.04	22,23,28,28	0
3	CA	A	605	1/1	0.99	0.02	9,9,9,9	0
3	CA	B	604	1/1	0.99	0.02	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.