



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:53 AM UTC

PDB ID : 7PC8 / pdb_00007pc8
Title : The PDZ domain of SNTG1 complexed with the phosphomimetic mutant PDZ-binding motif of RSK1
Authors : Cousido-Siah, A.; Trave, G.; Gogl, G.
Deposited on : 2021-08-03
Resolution : 2.50 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

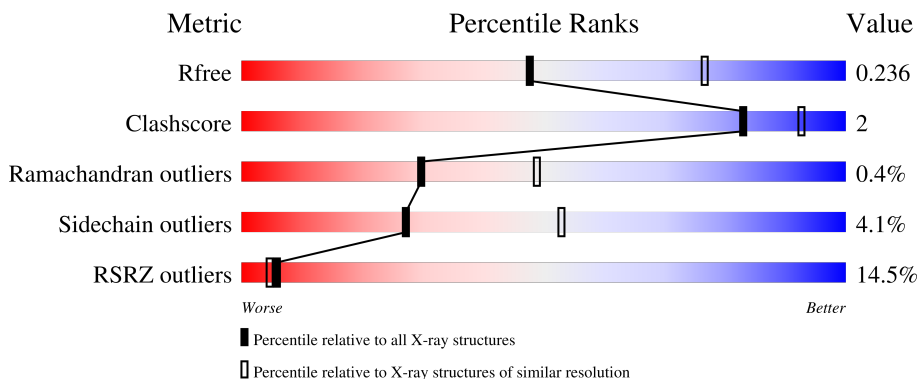
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	414	
1	B	414	
2	C	10	
2	D	10	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 6914 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 Gamma-1-syntrophin,Annexin A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	413	Total 3281	C 2056	N 578	O 634	S 13	0	1	0
1	B	409	Total 3253	C 2040	N 572	O 629	S 12	0	1	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	GLY	-	expression tag	UNP Q9NSN8
A	50	SER	-	expression tag	UNP Q9NSN8
A	51	HIS	-	expression tag	UNP Q9NSN8
A	52	MET	-	expression tag	UNP Q9NSN8
A	53	GLY	-	expression tag	UNP Q9NSN8
A	144	GLY	-	linker	UNP Q9NSN8
A	189	GLU	ALA	conflict	UNP P07355
B	49	GLY	-	expression tag	UNP Q9NSN8
B	50	SER	-	expression tag	UNP Q9NSN8
B	51	HIS	-	expression tag	UNP Q9NSN8
B	52	MET	-	expression tag	UNP Q9NSN8
B	53	GLY	-	expression tag	UNP Q9NSN8
B	144	GLY	-	linker	UNP Q9NSN8
B	189	GLU	ALA	conflict	UNP P07355

- Molecule 2 is a protein called Ribosomal protein S6 kinase alpha-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	8	Total 67	C 42	N 12	O 13	0	0	0
2	D	6	Total 47	C 30	N 6	O 11	0	0	0

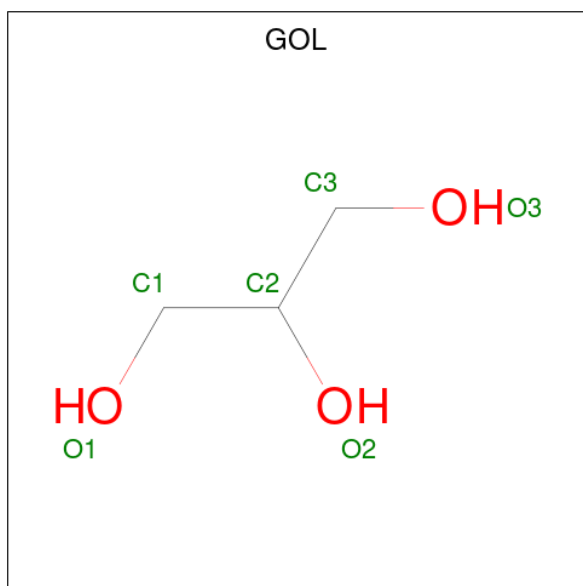
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	186	GLU	SER	conflict	UNP Q15418
D	186	GLU	SER	conflict	UNP Q15418

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	5	Total Ca 5 5	0	0
3	B	4	Total Ca 4 4	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

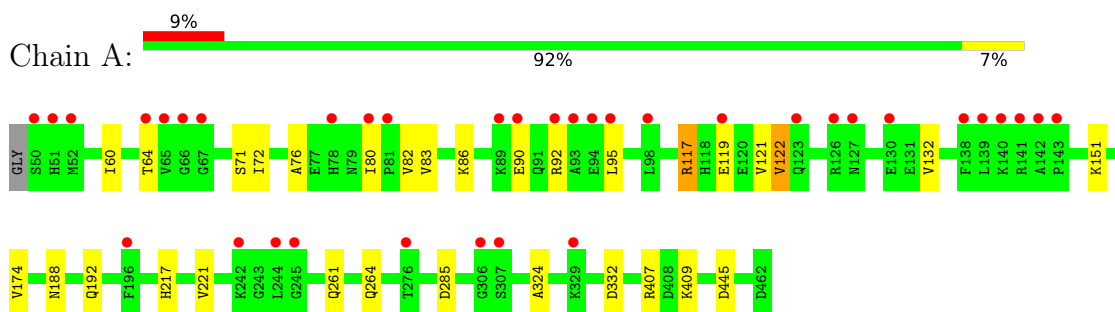
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	137	Total 137	O 137	0	0
5	B	83	Total 83	O 83	0	0
5	C	1	Total 1	O 1	0	0

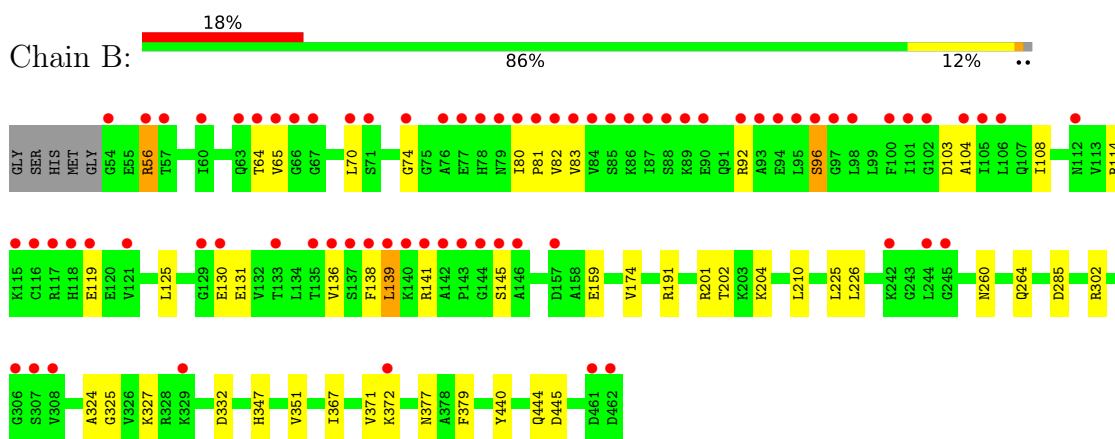
3 Residue-property plots [i](#)

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.

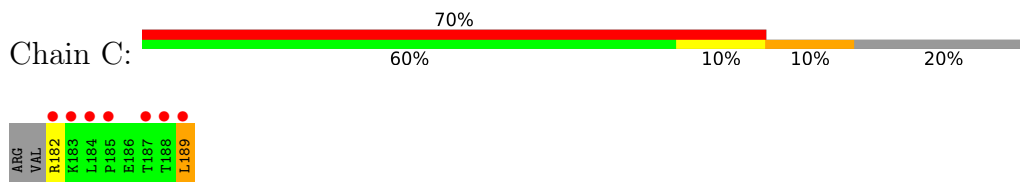
- Molecule 1: Gamma-1-syntrophin,Annexin A2



- Molecule 1: Gamma-1-syntrophin,Annexin A2



- Molecule 2: Ribosomal protein S6 kinase alpha-1



- Molecule 2: Ribosomal protein S6 kinase alpha-1



ARG	
VAL	
ARG	
LYS	
L184	●
P185	●
E186	●
T187	●
T188	●
L189	●

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	226.58Å 59.82Å 125.21Å 90.00° 117.84° 90.00°	Depositor
Resolution (Å)	48.33 – 2.50 48.33 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.33-2.50) 99.7 (48.33-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.202 , 0.232 0.211 , 0.236	Depositor DCC
R_{free} test set	2584 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtrriage
Anisotropy	0.215	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6914	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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: CA, GOL

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	0.18	0/3326	0.34	0/4465
1	B	0.14	0/3297	0.33	0/4427
2	C	0.12	0/67	0.30	0/88
2	D	0.08	0/47	0.25	0/63
All	All	0.16	0/6737	0.34	0/9043

There are no bond length outliers.

There are no bond angle outliers.

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	3281	0	3341	11	0
1	B	3253	0	3317	21	0
2	C	67	0	74	2	0
2	D	47	0	48	0	0
3	A	5	0	0	0	0
3	B	4	0	0	0	0
4	A	18	0	24	0	0
4	B	18	0	24	0	0
5	A	137	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	83	0	0	3	0
5	C	1	0	0	1	0
All	All	6914	0	6828	33	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 (33) 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:C:182:ARG:NH2	5:C:200:HOH:O	2.24	0.66
1:B:201:ARG:HG3	1:B:202:THR:HG23	1.87	0.56
1:A:72:ILE:HD11	1:A:122:VAL:HG12	1.86	0.56
1:B:377:ASN:ND2	5:B:606:HOH:O	2.38	0.56
1:B:324:ALA:HB1	1:B:332:ASP:HB3	1.90	0.53
1:A:60:ILE:HG22	1:A:95:LEU:HD11	1.90	0.53
1:B:92:ARG:HH21	1:B:96:SER:HA	1.76	0.51
1:B:104:ALA:HB2	1:B:139:LEU:HD23	1.93	0.51
1:B:367:ILE:HD13	1:B:379:PHE:HB3	1.93	0.51
1:B:202:THR:HB	1:B:204:LYS:HE3	1.93	0.50
1:A:71:SER:HB2	1:A:86:LYS:HB3	1.93	0.50
1:A:122:VAL:HB	2:C:189:LEU:HD21	1.96	0.48
1:A:324:ALA:HB1	1:A:332:ASP:HB3	1.97	0.47
1:A:82:VAL:HG21	1:A:121:VAL:HG21	1.96	0.47
1:B:210:LEU:HD12	1:B:226:LEU:HD11	1.98	0.46
1:A:217:HIS:O	1:A:221:VAL:HG23	2.17	0.44
1:B:56:ARG:HH22	1:B:103:ASP:CG	2.26	0.44
1:B:327:LYS:NZ	5:B:613:HOH:O	2.47	0.44
1:A:407:ARG:HE	1:A:409:LYS:HB3	1.83	0.44
1:B:130:GLU:OE1	5:B:601:HOH:O	2.21	0.44
1:B:108:ILE:HD13	1:B:125:LEU:HG	2.00	0.43
1:B:81:PRO:O	1:B:83:VAL:HG23	2.19	0.43
1:B:191:ARG:NH2	1:B:225:LEU:HD22	2.33	0.43
1:A:151:LYS:NZ	5:A:601:HOH:O	2.33	0.43
1:B:74:GLY:HA3	1:B:82:VAL:HA	2.01	0.42
1:A:76:ALA:H	1:A:117:ARG:HA	1.84	0.42
1:B:347:HIS:O	1:B:351:VAL:HG23	2.20	0.42
1:B:260:ASN:ND2	1:B:302:ARG:O	2.50	0.41
1:B:371:VAL:O	1:B:372:LYS:HD3	2.20	0.41
1:B:104:ALA:O	1:B:136:VAL:HA	2.20	0.41
1:B:440:TYR:O	1:B:444:GLN:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ASN:O	1:A:192:GLN:HG2	2.21	0.40
1:B:70:LEU:HD23	1:B:70:LEU:HA	1.87	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	412/414 (100%)	406 (98%)	5 (1%)	1 (0%)	43	63
1	B	408/414 (99%)	396 (97%)	10 (2%)	2 (0%)	24	43
2	C	6/10 (60%)	6 (100%)	0	0	100	100
2	D	4/10 (40%)	4 (100%)	0	0	100	100
All	All	830/848 (98%)	812 (98%)	15 (2%)	3 (0%)	30	49

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	174	VAL
1	A	174	VAL
1	B	325	GLY

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	358/357 (100%)	345 (96%)	13 (4%)	31	58
1	B	355/357 (99%)	339 (96%)	16 (4%)	24	49
2	C	8/10 (80%)	7 (88%)	1 (12%)	4	9
2	D	6/10 (60%)	6 (100%)	0	100	100
All	All	727/734 (99%)	697 (96%)	30 (4%)	27	53

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	THR
1	A	80	ILE
1	A	83	VAL
1	A	90	GLU
1	A	92	ARG
1	A	117	ARG
1	A	119	GLU
1	A	122	VAL
1	A	132	VAL
1	A	261	GLN
1	A	264	GLN
1	A	285	ASP
1	A	445	ASP
1	B	56	ARG
1	B	64	THR
1	B	65	VAL
1	B	80	ILE
1	B	96	SER
1	B	114	ARG
1	B	119	GLU
1	B	131	GLU
1	B	138	PHE
1	B	139	LEU
1	B	141	ARG
1	B	145	SER
1	B	159	GLU
1	B	264	GLN
1	B	285	ASP
1	B	445	ASP
2	C	189	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	HIS
1	A	217	HIS
1	A	267	ASN

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](#)

Of 15 ligands modelled in this entry, 9 are monoatomic - leaving 6 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	$\# Z > 2$
4	GOL	A	508	-	5,5,5	0.96	0	5,5,5	1.09	1 (20%)
4	GOL	B	507	-	5,5,5	0.92	0	5,5,5	1.07	0
4	GOL	A	507	-	5,5,5	0.93	0	5,5,5	1.04	0
4	GOL	B	506	-	5,5,5	0.88	0	5,5,5	1.07	0
4	GOL	A	506	-	5,5,5	0.93	0	5,5,5	1.07	0
4	GOL	B	505	-	5,5,5	0.89	0	5,5,5	1.08	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	508	-	-	2/4/4/4	-
4	GOL	B	507	-	-	2/4/4/4	-
4	GOL	A	507	-	-	2/4/4/4	-
4	GOL	B	506	-	-	0/4/4/4	-
4	GOL	A	506	-	-	0/4/4/4	-
4	GOL	B	505	-	-	1/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	508	GOL	C3-C2-C1	-2.02	104.39	111.80

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	507	GOL	C1-C2-C3-O3
4	A	508	GOL	C1-C2-C3-O3
4	A	508	GOL	O2-C2-C3-O3
4	B	507	GOL	O1-C1-C2-C3
4	A	507	GOL	O2-C2-C3-O3
4	B	507	GOL	O1-C1-C2-O2
4	B	505	GOL	C1-C2-C3-O3

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	413/414 (99%)	0.17	36 (8%) 16 14	26, 51, 103, 135	1 (0%)
1	B	409/414 (98%)	0.67	73 (17%) 4 3	32, 58, 105, 133	1 (0%)
2	C	8/10 (80%)	3.31	7 (87%) 0 0	113, 120, 128, 129	0
2	D	6/10 (60%)	3.40	5 (83%) 0 0	117, 123, 125, 129	0
All	All	836/848 (98%)	0.47	121 (14%) 6 5	26, 55, 111, 135	2 (0%)

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	54	GLY	8.3
1	B	139	LEU	7.2
2	D	184	LEU	7.0
1	B	95	LEU	6.4
1	B	87	ILE	5.6
1	B	98	LEU	5.5
1	A	50	SER	5.4
1	B	138	PHE	5.2
1	B	96	SER	5.1
1	B	101	ILE	5.1
1	B	65	VAL	4.7
1	B	64	THR	4.7
1	A	142	ALA	4.6
1	B	81	PRO	4.6
1	B	140	LYS	4.5
2	C	184	LEU	4.5
1	B	86	LYS	4.4
1	B	102	GLY	4.4
1	B	244	LEU	4.3
1	B	84	VAL	4.3
1	B	141	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	80	ILE	4.1
1	A	143	PRO	4.1
1	B	90	GLU	4.1
2	C	187	THR	4.1
2	C	182	ARG	4.0
1	B	66	GLY	4.0
1	B	97	GLY	4.0
2	C	183	LYS	3.9
2	D	185	PRO	3.8
1	A	64	THR	3.6
1	B	88	SER	3.6
1	A	65	VAL	3.6
1	A	244	LEU	3.6
1	B	94	GLU	3.5
1	A	307	SER	3.5
2	C	188	THR	3.5
1	A	66	GLY	3.5
1	B	306	GLY	3.4
1	A	52	MET	3.4
1	B	63	GLN	3.4
1	B	115	LYS	3.3
1	B	144	GLY	3.3
1	B	89	LYS	3.3
1	B	82	VAL	3.3
1	B	145	SER	3.2
1	B	133	THR	3.2
1	B	372	LYS	3.2
1	B	57	THR	3.2
1	A	93	ALA	3.2
1	A	89	LYS	3.1
1	A	95	LEU	3.1
1	B	70	LEU	3.1
1	A	80	ILE	3.1
1	B	67	GLY	3.1
1	B	100	PHE	3.0
1	A	92	ARG	3.0
1	B	104	ALA	3.0
2	D	189	LEU	3.0
1	B	83	VAL	3.0
2	C	189	LEU	3.0
1	A	51	HIS	3.0
1	B	118	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	93	ALA	2.9
1	A	306	GLY	2.9
1	B	76	ALA	2.9
1	B	106	LEU	2.9
1	B	245	GLY	2.9
1	B	307	SER	2.8
1	A	127	ASN	2.8
1	B	56	ARG	2.8
1	B	142	ALA	2.7
2	D	187	THR	2.7
1	A	242	LYS	2.7
2	C	185	PRO	2.7
1	A	139	LEU	2.7
1	B	105	ILE	2.6
1	B	137	SER	2.6
1	B	92	ARG	2.6
1	B	121	VAL	2.6
1	B	146	ALA	2.6
1	B	329	LYS	2.6
1	A	67	GLY	2.5
1	A	98	LEU	2.5
1	B	136	VAL	2.5
1	A	81	PRO	2.5
1	B	143	PRO	2.5
1	A	90	GLU	2.5
1	A	94	GLU	2.5
1	B	119	GLU	2.5
1	B	130	GLU	2.5
1	B	77	GLU	2.5
1	A	119	GLU	2.4
1	B	60	ILE	2.4
1	A	196	PHE	2.4
1	A	138	PHE	2.4
1	B	74	GLY	2.3
1	B	462	ASP	2.3
1	B	308	VAL	2.3
1	B	135	THR	2.3
1	A	126	ARG	2.3
1	A	141	ARG	2.3
1	A	78	HIS	2.3
1	A	123	GLN	2.3
1	B	242	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	116	CYS	2.2
1	A	130	GLU	2.2
1	A	140	LYS	2.2
1	B	79	ASN	2.1
1	B	117	ARG	2.1
1	B	157	ASP	2.1
1	A	329	LYS	2.1
1	B	78	HIS	2.1
1	B	71	SER	2.1
1	B	461	ASP	2.1
1	B	129	GLY	2.1
1	A	276	THR	2.1
1	B	112	ASN	2.0
1	A	245	GLY	2.0
2	D	188	THR	2.0
1	B	85	SER	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
3	CA	B	502	1/1	0.83	0.10	109,109,109,109	0
4	GOL	A	507	6/6	0.86	0.16	52,59,69,74	0
3	CA	A	501	1/1	0.87	0.09	101,101,101,101	0
3	CA	A	502	1/1	0.88	0.19	90,90,90,90	0
3	CA	A	503	1/1	0.88	0.10	84,84,84,84	0
4	GOL	B	506	6/6	0.88	0.19	67,70,84,89	0
3	CA	B	501	1/1	0.92	0.16	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	B	503	1/1	0.94	0.07	86,86,86,86	0
4	GOL	A	508	6/6	0.95	0.10	43,47,49,52	0
4	GOL	B	507	6/6	0.96	0.12	69,70,71,72	0
4	GOL	A	506	6/6	0.97	0.07	39,41,43,45	0
4	GOL	B	505	6/6	0.97	0.07	45,47,49,53	0
3	CA	A	505	1/1	0.98	0.03	42,42,42,42	0
3	CA	A	504	1/1	0.98	0.05	79,79,79,79	0
3	CA	B	504	1/1	0.98	0.04	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.