



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 03:33 AM GMT

PDB ID : 3S3N
Title : Crystal structure of the Prototype Foamy Virus (PFV) S217H mutant in some in complex with magnesium and Dolutegravir (S/GSK1349572)
Authors : Hare, S.; Cherepanov, P.
Deposited on : 2011-05-18
Resolution : 2.49 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

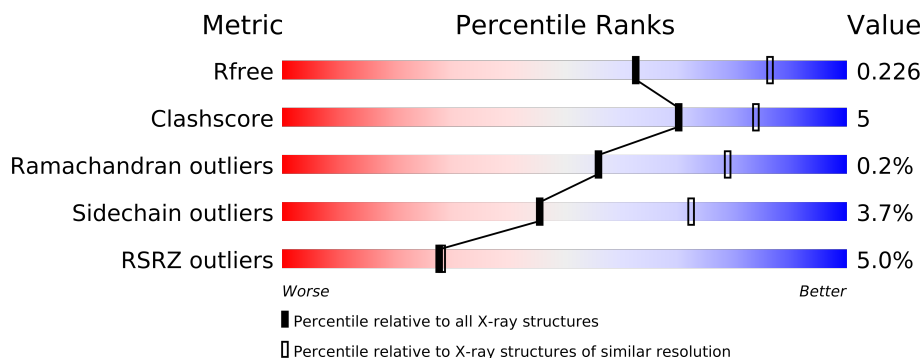
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.49 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	395	
1	B	395	
2	C	19	
3	D	17	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
6	GOL	A	801	-	X
6	GOL	A	805	-	X
7	NH4	A	395	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 5411 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PFV integrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	1	0
			2936	1882	518	532	4			
1	B	181	Total	C	N	O	S	0	0	0
			1421	924	230	266	1			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P14350
A	-1	PRO	-	EXPRESSION TAG	UNP P14350
A	0	GLY	-	EXPRESSION TAG	UNP P14350
A	217	HIS	GLY	ENGINEERED MUTATION	UNP P14350
A	218	GLY	SER	VARIANT	UNP P14350
B	-2	GLY	-	EXPRESSION TAG	UNP P14350
B	-1	PRO	-	EXPRESSION TAG	UNP P14350
B	0	GLY	-	EXPRESSION TAG	UNP P14350
B	217	HIS	GLY	VARIANT	UNP P14350
B	218	GLY	SER	VARIANT	UNP P14350

- Molecule 2 is a DNA chain called 5'-D(*AP*TP*TP*GP*TP*CP*AP*TP*GP*GP*AP*A P*TP*TP*TP*CP*GP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	19	Total	C	N	O	P	0	1	0
			405	197	73	117	18			

- Molecule 3 is a DNA chain called 5'-D(*TP*GP*CP*GP*AP*AP*AP*TP*TP*CP*CP*A P*TP*GP*AP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	17	Total	C	N	O	P	0	1	0
			366	176	70	103	17			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 7 is AMMONIUM ION (three-letter code: NH4) (formula: H₄N).

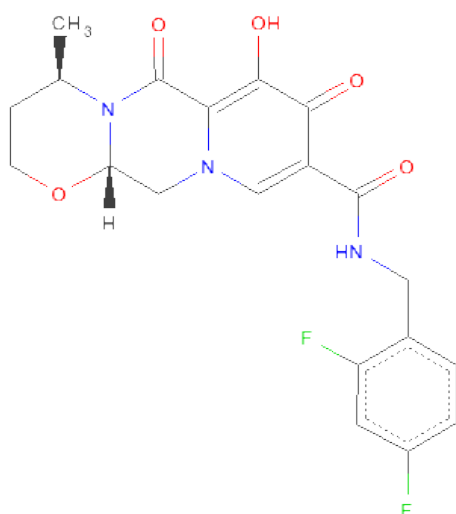


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total N 1 1	0	0

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	2	Total Mg 2 2	0	0

- Molecule 9 is (4R,12AS)-N-(2,4-DIFLUOROBENZYL)-7-HYDROXY-4-METHYL-6,8-DIOXO-3,4,6,8,12,12A-HEXAHYDRO-2H-PYRIDO[1',2':4,5]PYRAZINO[2,1-B][1,3]OXAZINE-9-CARBOXAMIDE (three-letter code: DLU) (formula: C₂₀H₁₉F₂N₃O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C F N O 30 20 2 3 5	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	143	Total O 143 143	0	0
10	B	30	Total O 30 30	0	0
10	C	21	Total O 21 21	0	0

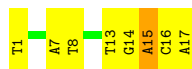
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	16	Total	O	0	0
			16	16		

- Molecule 3: 5'-D(*TP*GP*CP*GP*AP*AP*AP*TP*TP*CP*CP*AP*TP*GP*AP*CP*A)-3',

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	160.05Å 160.05Å 123.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.16 – 2.49 39.16 – 2.49	Depositor EDS
% Data completeness (in resolution range)	94.0 (39.16-2.49) 94.0 (39.16-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.209 , 0.232 0.204 , 0.226	Depositor DCC
R_{free} test set	2720 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.537	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 53251 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5411	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: GOL, ZN, MG, NH4, SO4, DLU

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	0.61	0/3019	0.70	3/4120 (0.1%)
1	B	0.63	0/1459	0.62	0/1994
2	C	1.02	0/454	1.71	11/700 (1.6%)
3	D	1.05	0/410	1.99	10/628 (1.6%)
All	All	0.70	0/5342	0.99	24/7442 (0.3%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	15	DA	O4'-C1'-N9	15.31	118.72	108.00
3	D	1	DT	P-O3'-C3'	9.18	130.71	119.70
2	C	7	DA	O4'-C1'-N9	-7.88	102.49	108.00
2	C	8	DT	O4'-C4'-C3'	-7.77	101.34	106.00
3	D	8	DT	O4'-C1'-N1	-6.66	103.34	108.00
3	D	7	DA	O4'-C1'-N9	-6.39	103.53	108.00
3	D	15	DA	P-O3'-C3'	6.28	127.23	119.70
3	D	14	DG	N1-C6-O6	-6.25	116.15	119.90
1	A	69	ARG	NE-CZ-NH2	-6.09	117.25	120.30
2	C	11	DA	O4'-C1'-N9	-6.09	103.74	108.00
1	A	69	ARG	NE-CZ-NH1	6.02	123.31	120.30
3	D	15	DA	P-O5'-C5'	5.93	130.39	120.90
2	C	14	DT	P-O3'-C3'	5.72	126.56	119.70
2	C	18	DC	C1'-O4'-C4'	-5.64	104.46	110.10
2	C	14	DT	N3-C4-O4	5.56	123.23	119.90
2	C	17	DG	O4'-C1'-N9	-5.48	104.16	108.00
2	C	1[A]	DA	O4'-C4'-C3'	-5.34	102.36	104.50
2	C	1[B]	DA	O4'-C4'-C3'	-5.34	102.36	104.50
2	C	8	DT	OP2-P-O3'	5.34	116.94	105.20
2	C	6	DC	O4'-C1'-N1	5.22	111.65	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	14	DG	O4'-C1'-N9	-5.18	104.37	108.00
1	A	173	LEU	CA-CB-CG	5.14	127.13	115.30
3	D	8	DT	N1-C1'-C2'	5.11	122.31	112.60
3	D	13	DT	C5-C4-O4	-5.08	121.34	124.90

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2936	0	2966	29	0
1	B	1421	0	1401	11	0
2	C	405	0	230	6	0
3	D	366	0	205	2	0
4	A	1	0	0	0	0
5	A	10	0	0	1	0
5	B	5	0	0	1	0
6	A	24	0	32	1	0
7	A	1	0	0	0	0
8	A	2	0	0	0	0
9	A	30	0	18	2	0
10	A	143	0	0	1	0
10	B	30	0	0	0	0
10	C	21	0	0	0	0
10	D	16	0	0	0	0
All	All	5411	0	4852	46	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (46) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:174:THR:HB	1:A:178:ILE:HD13	1.59	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:258:SER:O	1:B:261:LEU:O	2.06	0.73
1:A:358:LEU:N	1:A:359:GLY:HA2	2.08	0.69
1:A:221:GLU:O	1:A:224:ASN:HB2	1.93	0.68
3:D:15:DA:H4'	3:D:16:DC:OP1	1.93	0.66
1:B:233:LYS:O	1:B:236:VAL:HG22	1.97	0.63
1:A:162:SER:HB2	6:A:801:GOL:H2	1.82	0.61
1:A:108:ALA:O	1:A:314:SER:HA	2.03	0.58
1:B:155:LEU:HD12	1:B:250:GLN:HG3	1.84	0.58
1:B:127:ILE:HG22	1:B:145:VAL:HG22	1.87	0.56
2:C:1[A]:DA:C2'	2:C:2:DT:OP1	2.55	0.55
1:A:73:LEU:HD13	1:A:86:ARG:HG3	1.88	0.55
1:A:295:LEU:HD21	1:A:299:ARG:CZ	2.37	0.54
1:A:215[A]:GLN:HG3	9:A:398:DLU:FAF	1.98	0.54
1:B:127:ILE:HA	1:B:144:VAL:O	2.08	0.53
1:A:174:THR:HB	1:A:178:ILE:CD1	2.35	0.52
1:A:114:ARG:NH1	5:A:399:SO4:O3	2.36	0.51
1:A:76:ILE:HG22	1:A:85:MET:CE	2.42	0.50
1:A:295:LEU:HD21	1:A:299:ARG:NH2	2.28	0.49
1:B:283:THR:C	1:B:285:ASP:H	2.17	0.49
1:A:67:THR:HB	1:A:71:ALA:HB3	1.94	0.48
2:C:1[A]:DA:N3	2:C:1[A]:DA:O4'	2.45	0.48
1:A:145:VAL:HG11	1:A:173:LEU:HD21	1.97	0.47
1:B:290:GLU:HA	1:B:293:SER:HB2	1.97	0.47
1:A:221:GLU:OE1	1:A:221:GLU:HA	2.16	0.46
1:B:120:LYS:O	1:B:123:ASP:HB2	2.16	0.45
1:A:219:LYS:HE3	2:C:6:DC:OP1	2.17	0.45
1:A:157:PRO:HD3	1:A:246:LEU:HD12	1.99	0.45
1:B:222:ARG:NE	5:B:393:SO4:O3	2.33	0.45
1:A:358:LEU:H	1:A:359:GLY:HA2	1.81	0.44
2:C:8:DT:H2''	2:C:9:DG:H5'	2.00	0.44
1:A:366:ILE:HD13	1:A:366:ILE:HG21	1.65	0.43
2:C:1[B]:DA:H2''	2:C:2:DT:C6	2.52	0.43
9:A:398:DLU:CAR	3:D:17[A]:DA:H2'	2.49	0.43
2:C:8:DT:H2'	2:C:9:DG:C8	2.53	0.43
1:A:163:THR:HG23	1:A:195:PHE:HB2	2.01	0.43
1:A:358:LEU:N	1:A:359:GLY:CA	2.80	0.42
1:A:122:PHE:O	1:A:179:PRO:HA	2.19	0.42
1:A:276:THR:HG22	1:B:178:ILE:HD12	2.01	0.42
1:A:246:LEU:HD23	1:A:246:LEU:HA	1.90	0.42
1:A:97:GLN:OE1	1:A:339:LYS:HG2	2.19	0.42
1:A:315:TRP:CE2	1:A:371:PRO:HD3	2.55	0.41
1:B:163:THR:HG23	1:B:195:PHE:HB2	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:341:SER:HB2	1:A:355:LEU:O	2.20	0.41
1:A:69:ARG:HD2	1:A:70:GLU:OE2	2.21	0.41
1:A:112:ILE:HG23	10:A:435:HOH:O	2.21	0.41

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	367/395 (93%)	355 (97%)	11 (3%)	1 (0%)	50	73
1	B	177/395 (45%)	168 (95%)	9 (5%)	0	100	100
All	All	544/790 (69%)	523 (96%)	20 (4%)	1 (0%)	56	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	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	329/354 (93%)	321 (98%)	8 (2%)	61	86
1	B	156/354 (44%)	146 (94%)	10 (6%)	25	43
All	All	485/708 (68%)	467 (96%)	18 (4%)	45	72

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	73	LEU
1	A	137	GLN
1	A	149	MET
1	A	312	SER
1	A	356	ASP
1	A	357	HIS
1	A	361	ASN
1	B	149	MET
1	B	164	SER
1	B	261	LEU
1	B	274	SER
1	B	281	GLN
1	B	285	ASP
1	B	286	LEU
1	B	288	ARG
1	B	293	SER
1	B	297	GLU

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 1 is modelled with single atom and 3 are monoatomic - leaving 8 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
5	SO4	A	394	-	4,4,4	0.30	0	6,6,6	0.25	0
9	DLU	A	398	8	33,33,33	2.53	4 (12%)	47,49,49	2.19	16 (34%)
5	SO4	A	399	-	4,4,4	0.23	0	6,6,6	0.42	0
6	GOL	A	801	-	5,5,5	0.43	0	5,5,5	0.81	0
6	GOL	A	802	-	5,5,5	0.46	0	5,5,5	0.50	0
6	GOL	A	803	-	5,5,5	0.35	0	5,5,5	0.45	0
6	GOL	A	805	-	5,5,5	0.41	0	5,5,5	0.34	0
5	SO4	B	393	-	4,4,4	0.24	0	6,6,6	0.13	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
5	SO4	A	394	-	-	0/0/0/0	0/0/0/0
9	DLU	A	398	8	-	0/9/35/35	0/1/4/4
5	SO4	A	399	-	-	0/0/0/0	0/0/0/0
6	GOL	A	801	-	-	0/4/4/4	0/0/0/0
6	GOL	A	802	-	-	0/4/4/4	0/0/0/0
6	GOL	A	803	-	-	0/4/4/4	0/0/0/0
6	GOL	A	805	-	-	0/4/4/4	0/0/0/0
5	SO4	B	393	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	398	DLU	CAS-NBC	13.13	1.43	1.36
9	A	398	DLU	OAQ-CAL	2.25	1.50	1.44
9	A	398	DLU	CAO-CBB	-2.18	1.47	1.51
9	A	398	DLU	CAH-CAT	2.06	1.41	1.36

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	398	DLU	OAQ-CAL-CAM	5.49	123.06	110.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	398	DLU	CAZ-CAX-CAR	5.11	123.07	120.17
9	A	398	DLU	CAW-CAY-CAS	5.01	123.66	118.47
9	A	398	DLU	OAQ-CBB-NBC	-4.70	103.11	110.42
9	A	398	DLU	OAC-CAS-NBC	-3.12	119.34	121.86
9	A	398	DLU	CAA-CBA-CAM	-2.92	107.50	112.66
9	A	398	DLU	CAO-NBD-CAK	-2.79	115.77	118.26
9	A	398	DLU	CAY-CAS-NBC	2.75	118.64	113.75
9	A	398	DLU	CAO-NBD-CAY	2.73	122.82	118.76
9	A	398	DLU	CBB-CAO-NBD	2.64	113.17	109.22
9	A	398	DLU	CBA-NBC-CAS	2.58	123.31	118.71
9	A	398	DLU	CAZ-CAW-CAY	2.56	121.20	119.05
9	A	398	DLU	CAH-CAI-CAV	-2.36	118.10	121.40
9	A	398	DLU	CAK-NBD-CAY	-2.10	121.41	122.48
9	A	398	DLU	CAN-CAV-CAI	-2.07	116.47	121.02
9	A	398	DLU	CAO-CBB-NBC	2.05	115.67	111.74

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	368/395 (93%)	0.09	10 (2%) 52 54	36, 52, 94, 125	0
1	B	181/395 (45%)	0.15	20 (11%) 6 6	45, 60, 139, 147	0
2	C	19/19 (100%)	-0.27	0 100 100	42, 56, 68, 73	0
3	D	17/17 (100%)	-0.41	0 100 100	51, 53, 69, 98	0
All	All	585/826 (70%)	0.08	30 (5%) 28 27	36, 55, 113, 147	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	8	LEU	7.1
1	B	280	ASN	4.3
1	A	15	LEU	4.0
1	B	260	VAL	4.0
1	B	279	ALA	3.9
1	B	295	LEU	3.8
1	A	358	LEU	3.7
1	B	289	GLU	3.5
1	B	298	ILE	3.5
1	B	296	GLN	3.3
1	A	17	GLN	3.2
1	B	237	GLY	3.1
1	B	288	ARG	3.0
1	B	297	GLU	3.0
1	A	20	TYR	3.0
1	B	116	ASP	2.9
1	B	292	LEU	2.9
1	A	9	ASP	2.9
1	B	294	LEU	2.9
1	A	16	LEU	2.8
1	A	21	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	281	GLN	2.7
1	A	19	HIS	2.6
1	B	283	THR	2.5
1	B	299	ARG	2.5
1	A	29	THR	2.4
1	B	286	LEU	2.4
1	B	293	SER	2.1
1	B	212	TYR	2.0
1	B	282	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q < 0.9
7	NH4	A	395	1/1	0.47	40.90	37,37,37,37	0
6	GOL	A	805	6/6	0.20	4.78	85,88,89,90	0
6	GOL	A	801	6/6	0.18	3.78	72,76,76,77	0
6	GOL	A	803	6/6	0.25	1.59	73,75,76,79	0
5	SO4	A	399	5/5	0.18	1.28	76,76,76,78	0
6	GOL	A	802	6/6	0.15	0.25	86,88,89,89	0
4	ZN	A	393	1/1	0.13	-0.15	45,45,45,45	0
5	SO4	B	393	5/5	0.16	-0.33	105,106,106,106	0
9	DLU	A	398	30/30	0.12	-0.80	39,45,48,50	0
8	MG	A	397	1/1	0.12	-0.89	46,46,46,46	0
5	SO4	A	394	5/5	0.12	-0.90	82,82,83,84	0
8	MG	A	396	1/1	0.09	-1.47	41,41,41,41	0

6.5 Other polymers ⓘ

There are no such residues in this entry.