



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:10 PM GMT

PDB ID : 4WZI
Title : Crystal structure of crosslink stabilized long-form PDE4B
Authors : Cedervall, P.; Pandit, J.
Deposited on : 2014-11-19
Resolution : 2.58 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

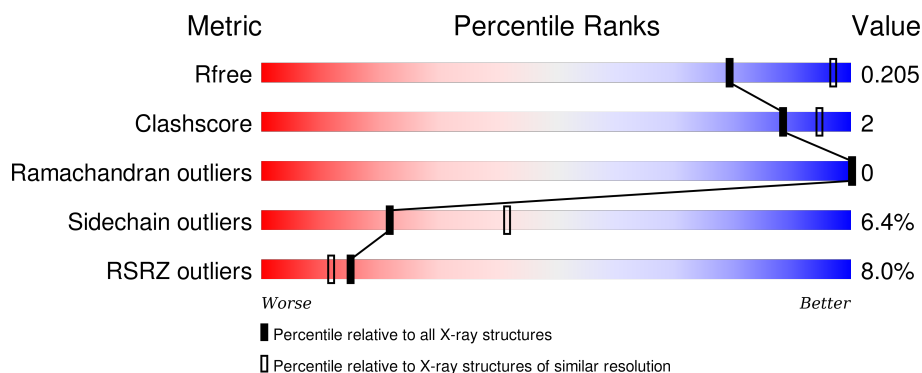
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	2636 (2.60-2.56)
Clashscore	102246	3003 (2.60-2.56)
Ramachandran outliers	100387	2956 (2.60-2.56)
Sidechain outliers	100360	2956 (2.60-2.56)
RSRZ outliers	91569	2642 (2.60-2.56)

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 $\leq 5\%$. 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	655	<div> <div>4%</div> <div>55%</div> <div>7%</div> <div>37%</div> </div>
1	B	655	<div> <div>6%</div> <div>58%</div> <div>6%</div> <div>35%</div> </div>

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	NA	B	802	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7124 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	1	0
			3336	2103	569	643	21			
1	B	424	Total	C	N	O	S	0	1	0
			3437	2167	584	665	21			

There are 106 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	MET	-	initiating methionine	UNP Q07343
A	83	ALA	-	expression tag	UNP Q07343
A	84	GLY	-	expression tag	UNP Q07343
A	85	LEU	-	expression tag	UNP Q07343
A	86	ASN	-	expression tag	UNP Q07343
A	87	ASP	-	expression tag	UNP Q07343
A	88	ILE	-	expression tag	UNP Q07343
A	89	PHE	-	expression tag	UNP Q07343
A	90	GLU	-	expression tag	UNP Q07343
A	91	ALA	-	expression tag	UNP Q07343
A	92	GLN	-	expression tag	UNP Q07343
A	93	LYS	-	expression tag	UNP Q07343
A	94	ILE	-	expression tag	UNP Q07343
A	95	GLU	-	expression tag	UNP Q07343
A	96	TRP	-	expression tag	UNP Q07343
A	97	HIS	-	expression tag	UNP Q07343
A	98	GLU	-	expression tag	UNP Q07343
A	99	ASN	-	expression tag	UNP Q07343
A	100	LEU	-	expression tag	UNP Q07343
A	101	TYR	-	expression tag	UNP Q07343
A	102	PHE	-	expression tag	UNP Q07343
A	103	GLN	-	expression tag	UNP Q07343
A	104	GLY	-	expression tag	UNP Q07343
A	105	SER	-	expression tag	UNP Q07343
A	106	ASP	-	expression tag	UNP Q07343

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Chain	Residue	Modelled	Actual	Comment	Reference
A	107	TYR	-	expression tag	UNP Q07343
A	108	LYS	-	expression tag	UNP Q07343
A	109	ASP	-	expression tag	UNP Q07343
A	110	ASP	-	expression tag	UNP Q07343
A	111	ASP	-	expression tag	UNP Q07343
A	112	ASP	-	expression tag	UNP Q07343
A	113	LYS	-	expression tag	UNP Q07343
A	114	ASP	-	expression tag	UNP Q07343
A	115	LEU	-	expression tag	UNP Q07343
A	116	VAL	-	expression tag	UNP Q07343
A	117	PRO	-	expression tag	UNP Q07343
A	118	ARG	-	expression tag	UNP Q07343
A	119	GLY	-	expression tag	UNP Q07343
A	120	SER	-	expression tag	UNP Q07343
A	121	MET	-	expression tag	UNP Q07343
A	133	ALA	SER	engineered mutation	UNP Q07343
A	229	ALA	CYS	engineered mutation	UNP Q07343
A	267	CYS	SER	engineered mutation	UNP Q07343
A	366	ALA	CYS	engineered mutation	UNP Q07343
A	492	ALA	CYS	engineered mutation	UNP Q07343
A	562	ALA	CYS	engineered mutation	UNP Q07343
A	604	ALA	CYS	engineered mutation	UNP Q07343
A	610	CYS	SER	engineered mutation	UNP Q07343
A	654	ALA	SER	engineered mutation	UNP Q07343
A	659	ALA	SER	engineered mutation	UNP Q07343
A	661	ALA	SER	engineered mutation	UNP Q07343
A	671	ALA	CYS	engineered mutation	UNP Q07343
A	709	ALA	CYS	engineered mutation	UNP Q07343
B	82	MET	-	initiating methionine	UNP Q07343
B	83	ALA	-	expression tag	UNP Q07343
B	84	GLY	-	expression tag	UNP Q07343
B	85	LEU	-	expression tag	UNP Q07343
B	86	ASN	-	expression tag	UNP Q07343
B	87	ASP	-	expression tag	UNP Q07343
B	88	ILE	-	expression tag	UNP Q07343
B	89	PHE	-	expression tag	UNP Q07343
B	90	GLU	-	expression tag	UNP Q07343
B	91	ALA	-	expression tag	UNP Q07343
B	92	GLN	-	expression tag	UNP Q07343
B	93	LYS	-	expression tag	UNP Q07343
B	94	ILE	-	expression tag	UNP Q07343
B	95	GLU	-	expression tag	UNP Q07343

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Chain	Residue	Modelled	Actual	Comment	Reference
B	96	TRP	-	expression tag	UNP Q07343
B	97	HIS	-	expression tag	UNP Q07343
B	98	GLU	-	expression tag	UNP Q07343
B	99	ASN	-	expression tag	UNP Q07343
B	100	LEU	-	expression tag	UNP Q07343
B	101	TYR	-	expression tag	UNP Q07343
B	102	PHE	-	expression tag	UNP Q07343
B	103	GLN	-	expression tag	UNP Q07343
B	104	GLY	-	expression tag	UNP Q07343
B	105	SER	-	expression tag	UNP Q07343
B	106	ASP	-	expression tag	UNP Q07343
B	107	TYR	-	expression tag	UNP Q07343
B	108	LYS	-	expression tag	UNP Q07343
B	109	ASP	-	expression tag	UNP Q07343
B	110	ASP	-	expression tag	UNP Q07343
B	111	ASP	-	expression tag	UNP Q07343
B	112	ASP	-	expression tag	UNP Q07343
B	113	LYS	-	expression tag	UNP Q07343
B	114	ASP	-	expression tag	UNP Q07343
B	115	LEU	-	expression tag	UNP Q07343
B	116	VAL	-	expression tag	UNP Q07343
B	117	PRO	-	expression tag	UNP Q07343
B	118	ARG	-	expression tag	UNP Q07343
B	119	GLY	-	expression tag	UNP Q07343
B	120	SER	-	expression tag	UNP Q07343
B	121	MET	-	expression tag	UNP Q07343
B	133	ALA	SER	engineered mutation	UNP Q07343
B	229	ALA	CYS	engineered mutation	UNP Q07343
B	267	CYS	SER	engineered mutation	UNP Q07343
B	366	ALA	CYS	engineered mutation	UNP Q07343
B	492	ALA	CYS	engineered mutation	UNP Q07343
B	562	ALA	CYS	engineered mutation	UNP Q07343
B	604	ALA	CYS	engineered mutation	UNP Q07343
B	610	CYS	SER	engineered mutation	UNP Q07343
B	654	ALA	SER	engineered mutation	UNP Q07343
B	659	ALA	SER	engineered mutation	UNP Q07343
B	661	ALA	SER	engineered mutation	UNP Q07343
B	671	ALA	CYS	engineered mutation	UNP Q07343
B	709	ALA	CYS	engineered mutation	UNP Q07343

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	I	0	0
			1	1		
5	A	1	Total	I	0	0
			1	1		

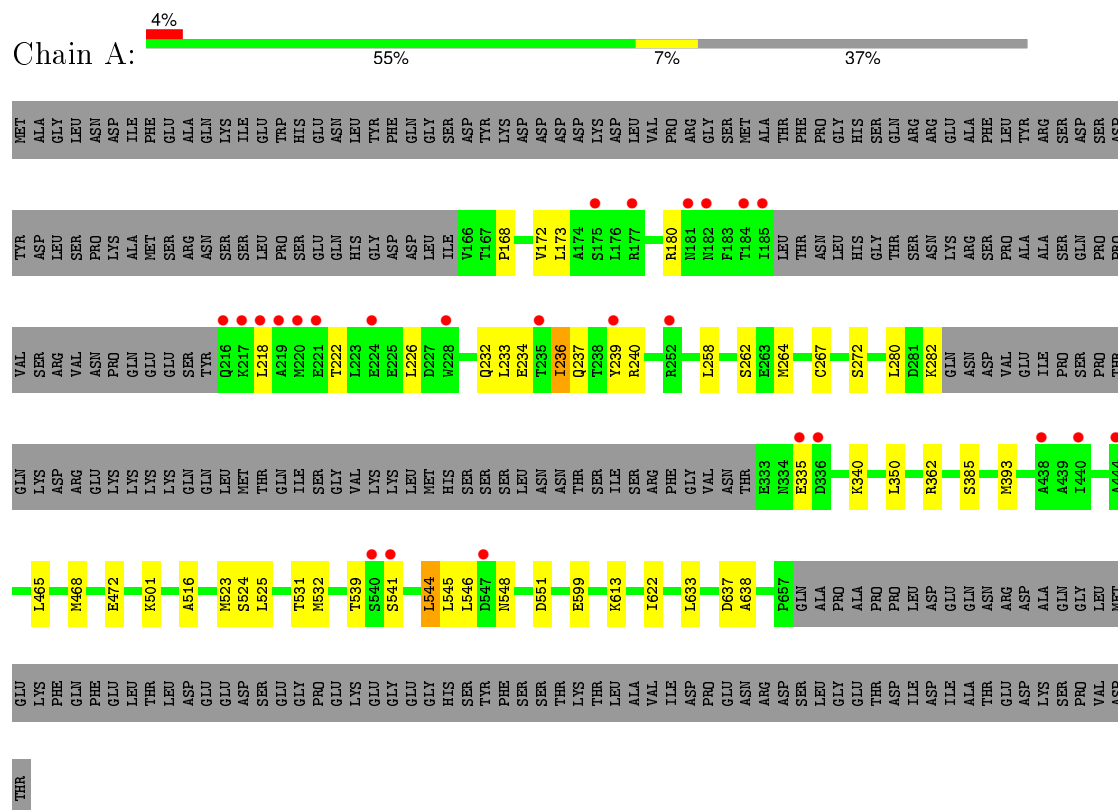
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	197	Total	O	0	0
			197	197		
6	B	145	Total	O	0	0
			145	145		

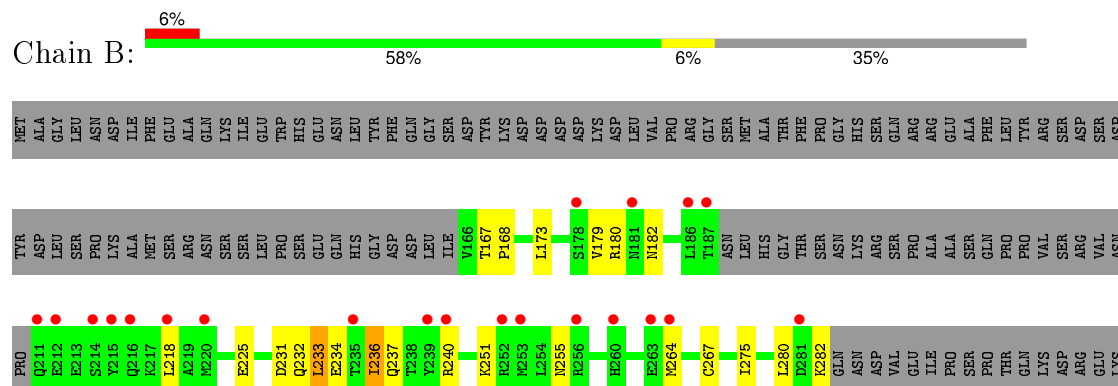
3 Residue-property plots

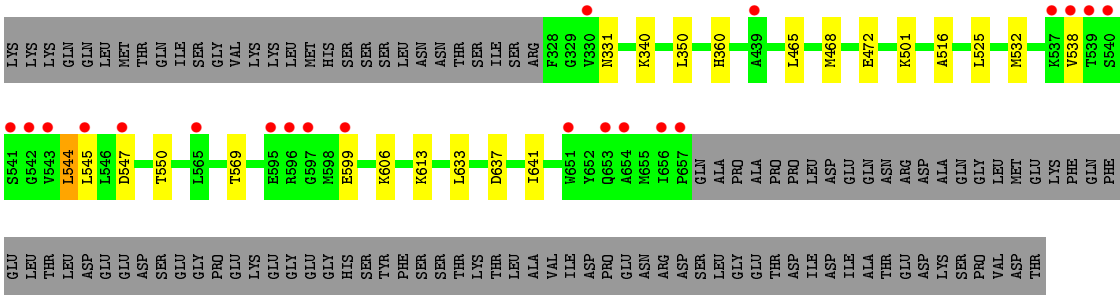
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: cAMP-specific 3',5'-cyclic phosphodiesterase 4B



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4B





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	137.83Å 137.83Å 141.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	26.01 – 2.58 25.62 – 2.58	Depositor EDS
% Data completeness (in resolution range)	98.4 (26.01-2.58) 98.6 (25.62-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.57Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.172 , 0.206 0.175 , 0.205	Depositor DCC
R_{free} test set	2453 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 73.8	EDS
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 48548 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7124	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, ZN, IOD, MG

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	0.51	0/3402	0.65	0/4608
1	B	0.48	0/3505	0.62	0/4747
All	All	0.50	0/6907	0.63	0/9355

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

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	3336	0	3260	28	0
1	B	3437	0	3357	22	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	197	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	145	0	0	0	0
All	All	7124	0	6617	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)
1:A:168:PRO:CB	1:B:236:ILE:HG12	2.15	0.77
1:A:168:PRO:HB2	1:B:236:ILE:HG12	1.76	0.67
1:A:622:ILE:HD11	1:B:275:ILE:HG23	1.85	0.59
1:A:613:LYS:HD2	1:B:267:CYS:HB3	1.85	0.58
1:A:546:LEU:HD22	1:A:551:ASP:HB3	1.85	0.58
1:A:173:LEU:HD11	1:A:234:GLU:HG2	1.87	0.57
1:A:226:LEU:HD13	1:B:179:VAL:HG11	1.86	0.56
1:A:168:PRO:HB3	1:B:236:ILE:HG12	1.90	0.54
1:A:172:VAL:HG11	1:B:233:LEU:HG	1.90	0.54
1:A:544:LEU:HD11	1:A:633:LEU:HG	1.91	0.52
1:A:468:MET:SD	1:B:468:MET:SD	3.07	0.51
1:A:637:ASP:O	1:A:638:ALA:HB3	2.11	0.51
1:A:236:ILE:HG12	1:B:168:PRO:HB2	1.93	0.51
1:B:569:THR:HB	1:B:641:ILE:HG23	1.94	0.49
1:A:232:GLN:O	1:A:236:ILE:HB	2.14	0.48
1:B:544:LEU:HD11	1:B:633:LEU:HG	1.95	0.48
1:A:362:ARG:HH12	1:A:393:MET:HA	1.79	0.48
1:A:258:LEU:HD22	1:A:272:SER:HA	1.96	0.47
1:B:516:ALA:HB1	1:B:525:LEU:HD11	1.98	0.46
1:B:232:GLN:O	1:B:236:ILE:HB	2.14	0.46
1:A:222:THR:HG21	1:B:182:ASN:HB3	1.96	0.46
1:A:258:LEU:HB3	1:A:272:SER:HB2	1.98	0.45
1:A:524:SER:HB3	1:B:240:ARG:HH12	1.81	0.45
1:A:531:THR:HG22	1:B:167:THR:HG21	2.00	0.44
1:A:236:ILE:HG12	1:B:168:PRO:CB	2.48	0.43
1:B:173:LEU:HD11	1:B:234:GLU:HG2	2.00	0.43
1:A:539:THR:HG22	1:A:541:SER:H	1.83	0.43
1:A:222:THR:HG21	1:B:182:ASN:CB	2.49	0.43
1:A:239:TYR:CD1	1:B:550:THR:HG21	2.55	0.41
1:A:523:MET:HB2	1:B:251:LYS:HE3	2.03	0.41
1:A:516:ALA:HB1	1:A:525:LEU:HD11	2.03	0.41
1:A:637:ASP:O	1:A:638:ALA:CB	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:CYS:HB3	1:B:613:LYS:HD2	2.03	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	407/655 (62%)	403 (99%)	4 (1%)	0	100	100
1	B	419/655 (64%)	413 (99%)	6 (1%)	0	100	100
All	All	826/1310 (63%)	816 (99%)	10 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	371/589 (63%)	349 (94%)	22 (6%)	24	46
1	B	383/589 (65%)	357 (93%)	26 (7%)	20	38
All	All	754/1178 (64%)	706 (94%)	48 (6%)	22	42

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	ARG
1	A	218	LEU
1	A	233	LEU
1	A	236	ILE
1	A	237	GLN
1	A	240	ARG
1	A	262	SER
1	A	264	MET
1	A	280	LEU
1	A	282	LYS
1	A	335	GLU
1	A	340	LYS
1	A	350	LEU
1	A	385	SER
1	A	465	LEU
1	A	472	GLU
1	A	501	LYS
1	A	532	MET
1	A	544	LEU
1	A	545	LEU
1	A	548	ASN
1	A	599	GLU
1	B	180	ARG
1	B	218	LEU
1	B	225	GLU
1	B	231	ASP
1	B	233	LEU
1	B	236	ILE
1	B	237	GLN
1	B	255	ASN
1	B	264	MET
1	B	280	LEU
1	B	282	LYS
1	B	331	ASN
1	B	340	LYS
1	B	350	LEU
1	B	360	HIS
1	B	465	LEU
1	B	472	GLU
1	B	501	LYS
1	B	532	MET
1	B	538	VAL
1	B	544	LEU

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Mol	Chain	Res	Type
1	B	545	LEU
1	B	547	ASP
1	B	599	GLU
1	B	606	LYS
1	B	637	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	548	ASN
1	A	567	ASN
1	A	635	GLN
1	B	269	ASN
1	B	567	ASN
1	B	635	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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

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	412/655 (62%)	-0.02	25 (6%) 25 20	20, 41, 103, 154	0
1	B	424/655 (64%)	0.21	42 (9%) 9 7	25, 58, 108, 185	0
All	All	836/1310 (63%)	0.09	67 (8%) 15 12	20, 50, 105, 185	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	MET	7.0
1	A	216	GLN	6.1
1	A	221	GLU	6.0
1	B	540	SER	5.9
1	B	215	TYR	5.5
1	A	218	LEU	4.5
1	B	547	ASP	4.4
1	B	541	SER	4.4
1	B	212	GLU	4.0
1	B	260	HIS	4.0
1	A	235	THR	4.0
1	B	539	THR	4.0
1	A	239	TYR	3.8
1	B	543	VAL	3.8
1	B	220	MET	3.7
1	B	281	ASP	3.7
1	A	182	ASN	3.6
1	B	264	MET	3.6
1	B	187	THR	3.5
1	A	184	THR	3.4
1	B	211	GLN	3.3
1	A	547	ASP	3.2
1	B	545	LEU	3.2
1	B	656	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	252	ARG	3.1
1	A	185	ILE	3.0
1	B	653	GLN	3.0
1	B	565	LEU	3.0
1	A	224	GLU	2.9
1	B	599	GLU	2.9
1	B	181	ASN	2.9
1	B	263	GLU	2.8
1	B	239	TYR	2.8
1	B	657	PRO	2.8
1	A	219	ALA	2.8
1	A	541	SER	2.7
1	B	542	GLY	2.7
1	A	217	LYS	2.7
1	B	651	TRP	2.6
1	B	538	VAL	2.6
1	A	177	ARG	2.6
1	B	240	ARG	2.5
1	B	597	GLY	2.5
1	B	235	THR	2.4
1	A	181	ASN	2.4
1	A	335	GLU	2.4
1	A	540	SER	2.4
1	B	596[A]	ARG	2.4
1	B	218	LEU	2.3
1	B	214	SER	2.3
1	B	252	ARG	2.3
1	B	256	ARG	2.3
1	B	216	GLN	2.2
1	A	228	TRP	2.2
1	B	253	MET	2.2
1	B	439	ALA	2.2
1	B	654	ALA	2.2
1	B	330	VAL	2.2
1	B	595	GLU	2.1
1	A	175	SER	2.1
1	A	336	ASP	2.1
1	B	537	LYS	2.0
1	B	186	LEU	2.0
1	A	440	ILE	2.0
1	B	178	SER	2.0
1	A	438	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	444	ALA	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 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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	NA	B	802	1/1	0.97	0.40	6.11	61,61,61,61	0
2	ZN	B	801	1/1	0.99	0.14	-0.80	39,39,39,39	0
2	ZN	A	801	1/1	1.00	0.13	-0.91	30,30,30,30	0
4	MG	B	803	1/1	0.99	0.09	-1.17	65,65,65,65	0
2	ZN	A	802	1/1	1.00	0.06	-1.20	37,37,37,37	0
4	MG	A	804	1/1	0.94	0.07	-1.86	53,53,53,53	0
5	IOD	A	805	1/1	0.99	0.07	-	59,59,59,59	0
3	NA	A	803	1/1	0.94	0.13	-	62,62,62,62	0
5	IOD	B	804	1/1	0.99	0.08	-	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.