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P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:27 PM GMT

PDB ID	:	4XY2
Title	:	Crystal structure of PDE10A in complex with ASP9436
Authors	:	Amano, Y.; Honbou, K.
Deposited on	:	2015-02-02
Resolution	:	2.03 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:

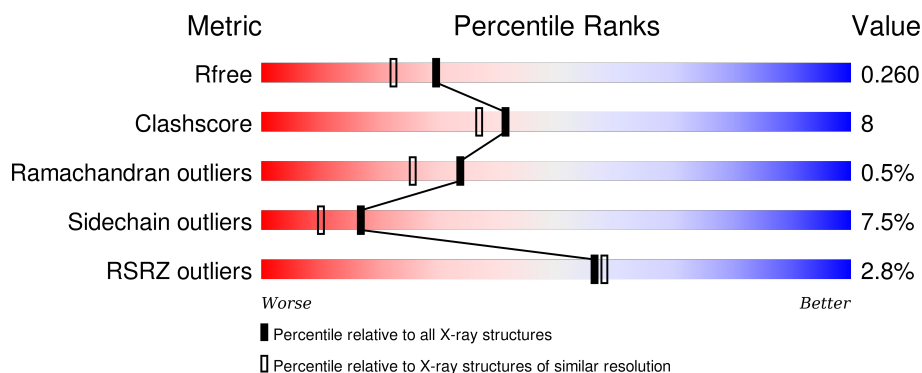|		
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	Percentile Ranks	Value
Rfree		0.260
Clashscore		8
Ramachandran outliers		0.5%
Sidechain outliers		7.5%
RSRZ outliers		2.8%

Worse   *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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 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 <=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	345	2% 71% 17% • 10%
1	B	345	3% 76% 14% • 7%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5404 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 and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total 2529	C 1610	N 431	O 463	S 25	0	0	0
1	B	322	Total 2611	C 1668	N 443	O 475	S 25	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	GLY	-	expression tag	UNP Q9Y233
A	446	SER	-	expression tag	UNP Q9Y233
A	447	HIS	-	expression tag	UNP Q9Y233
A	448	MET	-	expression tag	UNP Q9Y233
B	445	GLY	-	expression tag	UNP Q9Y233
B	446	SER	-	expression tag	UNP Q9Y233
B	447	HIS	-	expression tag	UNP Q9Y233
B	448	MET	-	expression tag	UNP Q9Y233

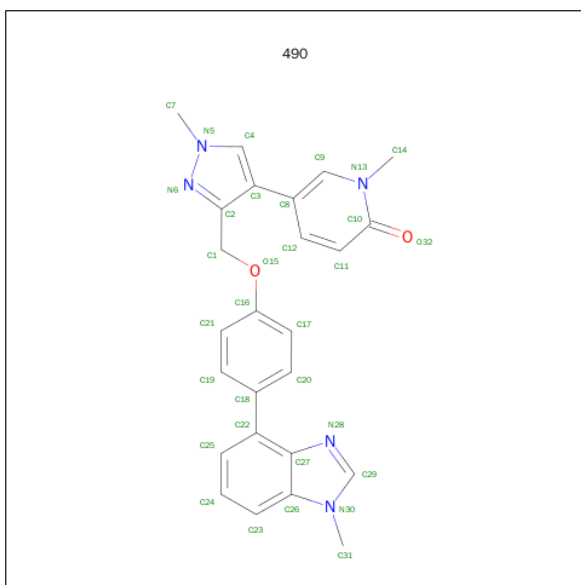- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Mg 1	0	0

- Molecule 4 is 1-methyl-5-(1-methyl-3-{[4-(1-methyl-1H-benzimidazol-4-yl)phenoxy]methyl}-1H-pyrazol-4-yl)pyridin-2(1H)-one (three-letter code: 490) (formula: $C_{25}H_{23}N_5O_2$).

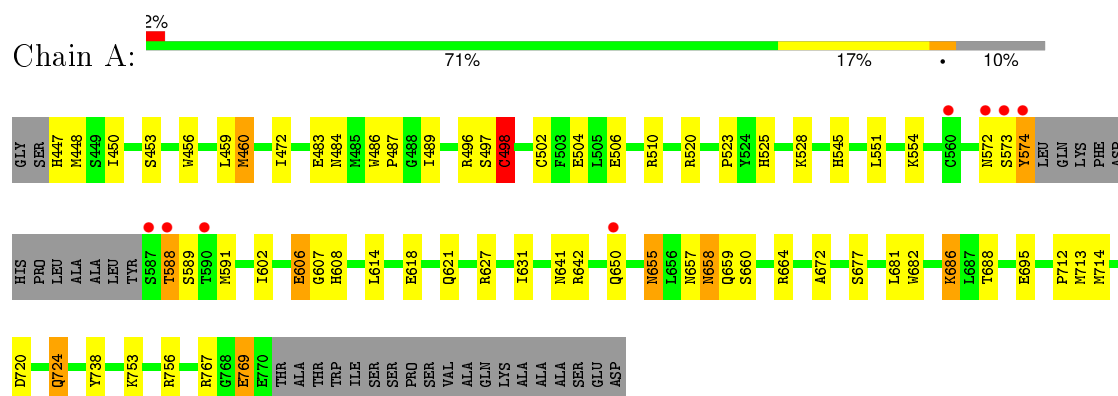| Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	32	25	5	2	0	0

- Molecule 5 is water.

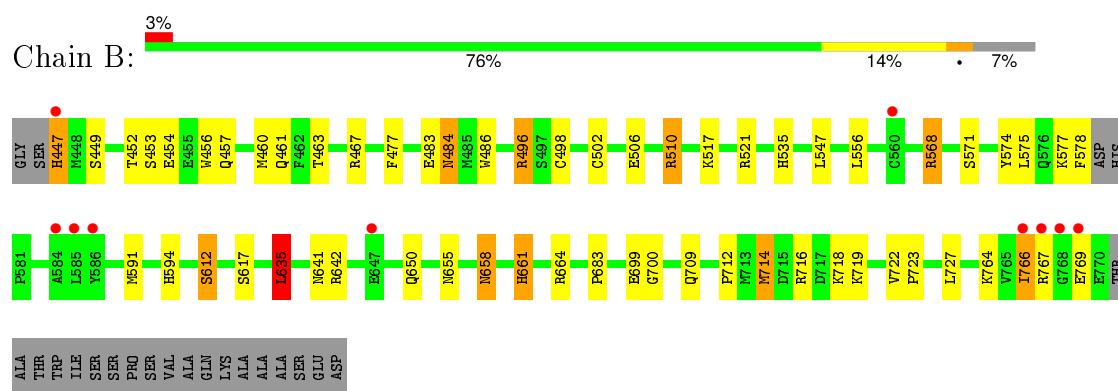| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	109	Total 109	O 109	0	0
5	B	119	Total 119	O 119	0	0

3 Residue-property plots (i)

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 and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

• Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.45Å 82.11Å 159.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.57 – 2.03 32.47 – 2.03	Depositor EDS
% Data completeness (in resolution range)	89.2 (79.57-2.03) 89.2 (32.47-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.62 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.205 , 0.260 0.206 , 0.260	Depositor DCC
R_{free} test set	1959 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	32.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.31$	Xtriage
Outliers	0 of 38756 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5404	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, 490, 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	0.82	0/2589	0.86	0/3502
1	B	0.78	0/2674	0.84	2/3617 (0.1%)
All	All	0.80	0/5263	0.85	2/7119 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	635	LEU	CB-CG-CD2	5.89	121.02	111.00
1	B	510	ARG	NE-CZ-NH1	5.33	122.96	120.30

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	2529	0	2487	47	0
1	B	2611	0	2577	43	0
2	A	1	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	32	0	23	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	109	0	0	4	0
5	B	119	0	0	4	0
All	All	5404	0	5087	87	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 8.

All (87) 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:606:GLU:HG3	1:A:607:GLY:H	1.09	1.11
1:A:606:GLU:CG	1:A:607:GLY:H	1.76	0.97
1:B:655:ASN:H	1:B:661:HIS:HD2	1.14	0.95
1:B:764:LYS:HG3	1:B:767:ARG:NH2	1.83	0.91
1:A:502:CYS:SG	1:A:554:LYS:HD3	2.14	0.87
1:A:641:ASN:HD22	1:A:664:ARG:HH11	1.20	0.87
1:A:606:GLU:HG3	1:A:607:GLY:N	1.92	0.85
1:A:658:ASN:HD22	1:A:658:ASN:C	1.81	0.83
1:B:453:SER:HB3	1:B:457:GLN:NE2	1.97	0.79
1:B:716:ARG:O	1:B:719:LYS:HG2	1.83	0.77
1:B:453:SER:HB3	1:B:457:GLN:HE22	1.50	0.76
1:B:498:CYS:HB3	1:B:502:CYS:SG	2.26	0.76
1:A:606:GLU:CG	1:A:607:GLY:N	2.46	0.71
1:B:764:LYS:HG3	1:B:767:ARG:HH21	1.56	0.69
1:A:448:MET:HE2	1:A:602:ILE:HG13	1.75	0.68
1:B:655:ASN:H	1:B:661:HIS:CD2	2.06	0.67
1:B:655:ASN:N	1:B:661:HIS:HD2	1.91	0.66
1:A:525:HIS:NE2	5:A:921:HOH:O	2.29	0.65
1:B:498:CYS:CB	1:B:502:CYS:SG	2.85	0.64
1:A:447:HIS:HB2	5:A:959:HOH:O	1.97	0.64
1:A:572:ASN:OD1	1:A:591:MET:HB2	2.00	0.62
1:B:452:THR:HB	1:B:454:GLU:OE2	2.00	0.62
1:A:655:ASN:HD21	1:A:657:ASN:HB2	1.64	0.61
1:A:756:ARG:HH22	1:B:484:ASN:ND2	1.98	0.61
1:A:483:GLU:HA	1:A:486:TRP:CE2	2.38	0.59
1:A:523:PRO:HD2	1:A:695:GLU:HG3	1.84	0.59
1:B:483:GLU:HA	1:B:486:TRP:CE2	2.38	0.59
1:B:506:GLU:HG2	1:B:510:ARG:NH2	2.17	0.58
1:A:658:ASN:ND2	1:A:658:ASN:C	2.55	0.58
1:B:641:ASN:HD22	1:B:664:ARG:HH11	1.52	0.58
1:A:456:TRP:CZ3	1:A:506:GLU:HG3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:447:HIS:HA	5:B:954:HOH:O	2.04	0.57
1:B:722:VAL:HB	1:B:723:PRO:HD3	1.86	0.57
1:A:528:LYS:HE2	5:A:983:HOH:O	2.05	0.55
1:B:449:SER:HB3	1:B:517:LYS:HD3	1.88	0.55
1:B:658:ASN:HD22	1:B:658:ASN:C	2.12	0.53
1:B:452:THR:OG1	1:B:454:GLU:HG2	2.10	0.52
1:A:545:HIS:CD2	1:A:545:HIS:H	2.28	0.52
1:A:655:ASN:C	1:A:655:ASN:HD22	2.13	0.51
1:B:712:PRO:HB3	1:B:718:LYS:HD2	1.93	0.50
1:A:627:ARG:O	1:A:631:ILE:HG12	2.11	0.50
1:A:658:ASN:HD22	1:A:659:GLN:N	2.09	0.50
1:A:756:ARG:HH22	1:B:484:ASN:HD21	1.59	0.50
1:A:588:THR:O	1:A:589:SER:C	2.49	0.50
1:A:641:ASN:ND2	1:A:664:ARG:HH11	1.99	0.49
1:A:724:GLN:HG3	1:B:683:PRO:HG3	1.94	0.49
1:A:448:MET:CE	1:A:602:ILE:HG13	2.42	0.49
1:B:727:LEU:HG	1:B:727:LEU:O	2.13	0.48
1:A:658:ASN:ND2	1:A:660:SER:H	2.11	0.48
1:A:655:ASN:ND2	1:A:657:ASN:H	2.11	0.48
1:A:614:LEU:HB3	1:A:618:GLU:HB2	1.96	0.48
1:A:472:ILE:HD11	1:A:489:ILE:HG23	1.96	0.47
1:B:496:ARG:HA	1:B:496:ARG:HD2	1.74	0.47
1:B:506:GLU:CD	1:B:510:ARG:HH22	2.17	0.47
1:B:506:GLU:CG	1:B:510:ARG:NH2	2.77	0.46
1:B:709:GLN:OE1	1:B:709:GLN:HA	2.16	0.46
1:B:568:ARG:HH11	1:B:568:ARG:HG2	1.81	0.46
1:A:641:ASN:HD22	1:A:664:ARG:NH1	2.00	0.45
1:B:635:LEU:HB2	5:B:943:HOH:O	2.17	0.45
1:A:510:ARG:HD2	1:A:607:GLY:O	2.17	0.44
1:B:454:GLU:H	1:B:454:GLU:CD	2.21	0.44
1:A:460:MET:HB3	1:A:460:MET:HE3	1.80	0.44
1:B:456:TRP:HZ3	1:B:460:MET:SD	2.41	0.43
1:A:767:ARG:NH1	1:A:769:GLU:OE2	2.52	0.43
1:B:577:LYS:HB3	1:B:578:PHE:CD2	2.53	0.43
1:B:766:ILE:HG13	1:B:767:ARG:N	2.33	0.43
1:B:461:GLN:NE2	5:B:999:HOH:O	2.51	0.43
1:A:672:ALA:HB1	1:A:738:TYR:CE1	2.53	0.43
1:B:574:TYR:HB2	1:B:699:GLU:OE2	2.19	0.42
1:B:700:GLY:HA3	1:B:714:MET:O	2.20	0.42
1:B:591:MET:O	1:B:594:HIS:HB3	2.19	0.42
1:B:571:SER:O	1:B:575:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:CYS:SG	1:A:554:LYS:CD	2.98	0.42
1:A:459:LEU:HD13	1:A:487:PRO:HB2	2.02	0.42
1:B:556:LEU:HD23	1:B:556:LEU:HA	1.76	0.42
1:B:641:ASN:HD22	1:B:664:ARG:NH1	2.17	0.42
1:A:682:TRP:NE1	1:A:686:LYS:HE2	2.35	0.41
1:A:655:ASN:ND2	1:A:657:ASN:HB2	2.34	0.41
1:A:520:ARG:HD3	5:A:901:HOH:O	2.19	0.41
1:B:447:HIS:CD2	5:B:903:HOH:O	2.73	0.41
1:A:655:ASN:HD22	1:A:657:ASN:H	1.69	0.41
1:A:574:TYR:CD1	1:A:574:TYR:C	2.94	0.41
1:B:477:PHE:HB3	1:B:535:HIS:CE1	2.56	0.40
1:A:510:ARG:HG2	1:A:608:HIS:CE1	2.56	0.40
1:A:497:SER:O	1:A:498:CYS:SG	2.76	0.40
1:A:588:THR:HB	1:A:589:SER:H	1.71	0.40
1:A:677:SER:CB	1:A:688:THR:HG21	2.52	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	308/345 (89%)	295 (96%)	11 (4%)	2 (1%)	30	21
1	B	318/345 (92%)	309 (97%)	8 (2%)	1 (0%)	46	40
All	All	626/690 (91%)	604 (96%)	19 (3%)	3 (0%)	34	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	GLU
1	B	612	SER
1	A	498	CYS

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	283/308 (92%)	258 (91%)	25 (9%)	12	7
1	B	291/308 (94%)	273 (94%)	18 (6%)	23	16
All	All	574/616 (93%)	531 (92%)	43 (8%)	17	10

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	450	ILE
1	A	453	SER
1	A	460	MET
1	A	484	ASN
1	A	496	ARG
1	A	498	CYS
1	A	504	GLU
1	A	551	LEU
1	A	573	SER
1	A	574	TYR
1	A	588	THR
1	A	621	GLN
1	A	642	ARG
1	A	650	GLN
1	A	655	ASN
1	A	658	ASN
1	A	681	LEU
1	A	686	LYS
1	A	712	PRO
1	A	713	MET
1	A	714	MET
1	A	720	ASP
1	A	724	GLN
1	A	753	LYS
1	A	769	GLU
1	B	447	HIS
1	B	463	THR

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Mol	Chain	Res	Type
1	B	467	ARG
1	B	484	ASN
1	B	496	ARG
1	B	521	ARG
1	B	547	LEU
1	B	568	ARG
1	B	612	SER
1	B	617	SER
1	B	635	LEU
1	B	642	ARG
1	B	650	GLN
1	B	658	ASN
1	B	661	HIS
1	B	714	MET
1	B	766	ILE
1	B	769	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	545	HIS
1	A	594	HIS
1	A	641	ASN
1	A	650	GLN
1	A	655	ASN
1	A	658	ASN
1	A	690	ASN
1	A	709	GLN
1	B	457	GLN
1	B	476	HIS
1	B	484	ASN
1	B	641	ASN
1	B	655	ASN
1	B	658	ASN
1	B	661	HIS
1	B	690	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	490	A	803	-	31,36,36	1.50	7 (22%)	34,52,52	1.62	9 (26%)

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
4	490	A	803	-	-	0/11/13/13	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	803	490	C3-C8	-3.81	1.43	1.49
4	A	803	490	C11-C12	-2.71	1.33	1.38
4	A	803	490	C22-C27	-2.54	1.39	1.43
4	A	803	490	N6-N5	-2.27	1.35	1.37
4	A	803	490	C9-C8	-2.21	1.34	1.39
4	A	803	490	C12-C8	2.21	1.44	1.39
4	A	803	490	C9-N13	3.17	1.37	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	803	490	C2-N6-N5	-3.77	101.37	104.55
4	A	803	490	C1-C2-C3	-3.03	126.11	129.51
4	A	803	490	C12-C11-C10	-3.02	115.12	120.00
4	A	803	490	C25-C22-C27	-2.27	114.84	117.64
4	A	803	490	C24-C23-C26	-2.26	114.50	119.28
4	A	803	490	C1-O15-C16	-2.14	112.05	117.58
4	A	803	490	C4-N5-N6	2.12	116.22	112.10
4	A	803	490	C25-C22-C18	2.24	123.52	118.90
4	A	803	490	C11-C12-C8	3.01	125.74	121.42

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	312/345 (90%)	-0.15	8 (2%)	59	61	20, 34, 59, 98	0
1	B	322/345 (93%)	-0.07	10 (3%)	52	54	19, 35, 61, 106	0
All	All	634/690 (91%)	-0.11	18 (2%)	56	58	19, 34, 60, 106	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	587	SER	9.2
1	A	588	THR	4.6
1	B	585	LEU	4.3
1	B	769	GLU	4.2
1	A	574	TYR	3.8
1	B	447	HIS	3.7
1	B	584	ALA	3.6
1	A	590	THR	3.2
1	A	572	ASN	3.0
1	B	767	ARG	2.7
1	B	560	CYS	2.6
1	B	766	ILE	2.4
1	A	573	SER	2.3
1	A	650	GLN	2.2
1	B	768	GLY	2.2
1	B	586	TYR	2.1
1	B	647	GLU	2.0
1	A	560	CYS	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	MG	B	802	1/1	0.99	0.16	0.46	23,23,23,23	0
4	490	A	803	32/32	0.95	0.09	-0.10	27,31,40,41	0
3	MG	A	802	1/1	0.98	0.08	-1.03	24,24,24,24	0
2	ZN	A	801	1/1	0.99	0.08	-1.25	31,31,31,31	0
2	ZN	B	801	1/1	1.00	0.12	-1.53	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.