



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:52 PM GMT

PDB ID : 1CUL
Title : COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH 2',5'-DIDEOXY-ADENOSINE 3'-TRIPHOSPHATE AND MG
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Deposited on : 1999-08-20
Resolution : 2.40 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

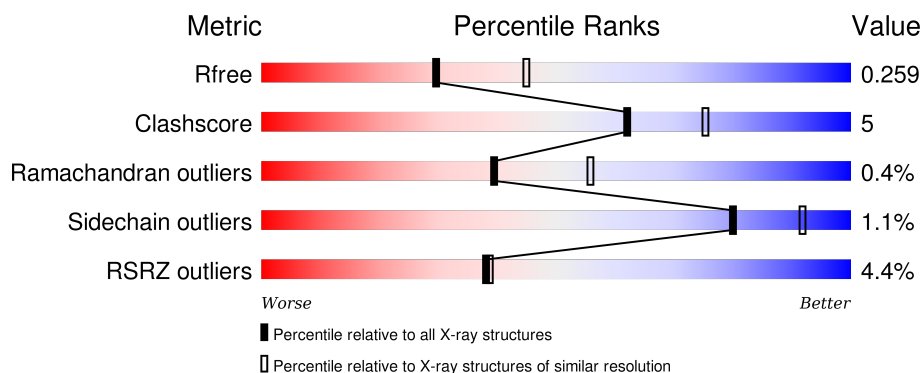
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	217	<div> <div>4%</div> <div>72%</div> <div>14%</div> <div>13%</div> </div>
2	B	208	<div> <div>5%</div> <div>81%</div> <div>11%</div> <div>9%</div> </div>
3	C	380	<div> <div>3%</div> <div>77%</div> <div>9%</div> <div>14%</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
10	MES	B	1083	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 5847 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 TYPE V ADENYLYL CYCLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	189	Total	C	N	O	S	0	0	0
			1476	929	259	271	17			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	476	MET	VAL	engineered	UNP P30803

- Molecule 2 is a protein called TYPE II ADENYLYL CYCLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	190	Total	C	N	O	S	0	0	0
			1480	944	243	283	10			

- Molecule 3 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN G(S).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	328	Total	C	N	O	S	0	0	0
			2684	1702	466	503	13			

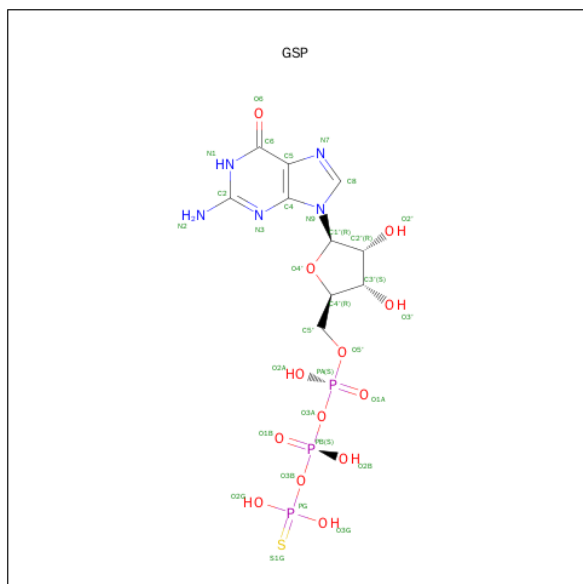
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	C	1	Total	Mg	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

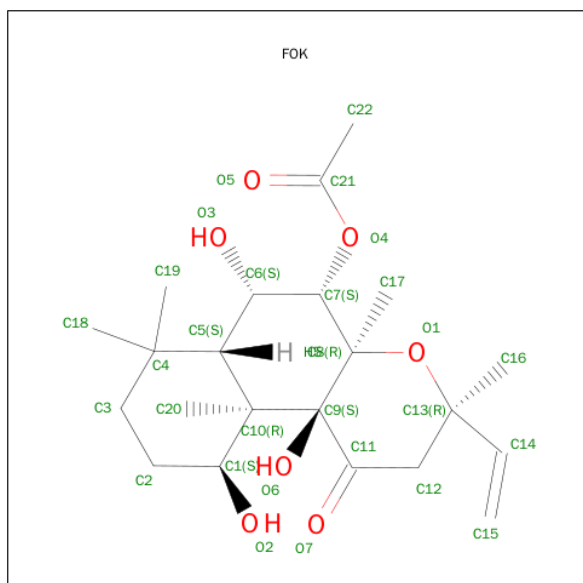
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	2	Total Cl 2 2	0	0

- Molecule 6 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (three-letter code: GSP) (formula: C₁₀H₁₆N₅O₁₃P₃S).



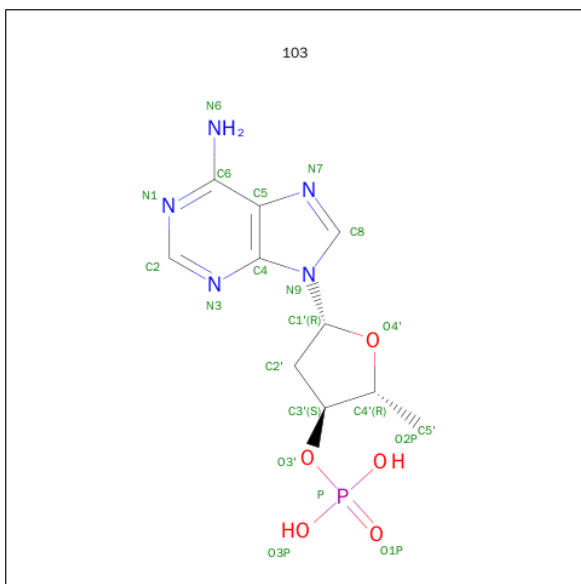
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		

- Molecule 7 is FORSKOLIN (three-letter code: FOK) (formula: C₂₂H₃₄O₇).



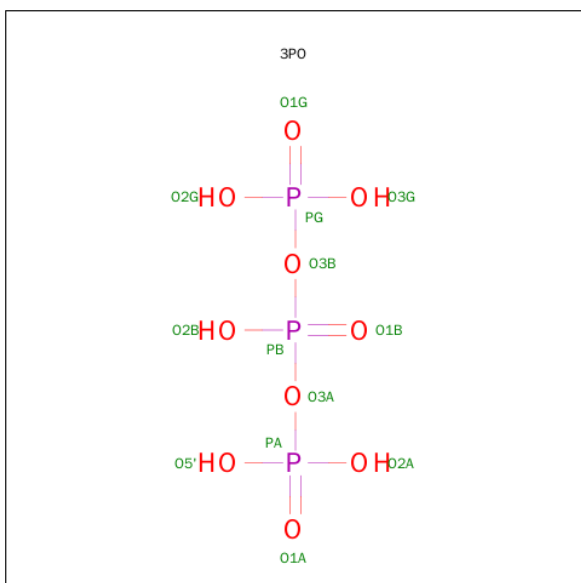
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			29	22	7		

- Molecule 8 is 2',5'-DIDEOXY-ADENOSINE 3'-MONOPHOSPHATE (three-letter code: 103) (formula: $C_{10}H_{14}N_5O_5P$).



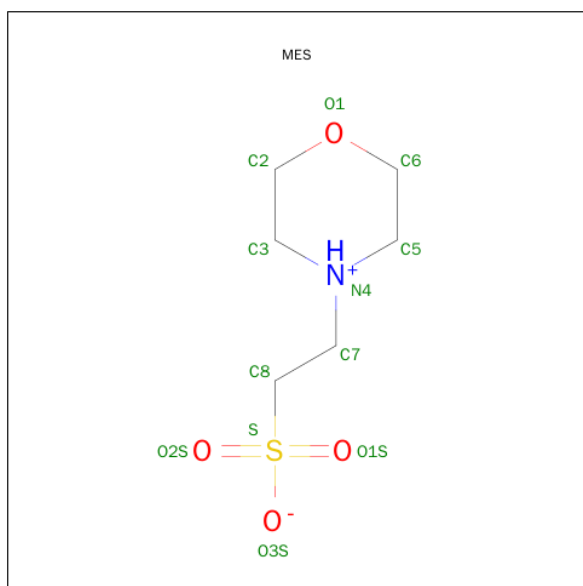
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			21	10	5	5	1		

- Molecule 9 is TRIPHOSPHATE (three-letter code: 3PO) (formula: $H_5O_{10}P_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	O	P	0	0
			13	10	3		

- Molecule 10 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
10	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	14	Total	O	0	0
			14	14		
11	B	33	Total	O	0	0
			33	33		
11	C	36	Total	O	0	0
			36	36		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	118.20 Å 133.60 Å 70.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 37.67 – 2.40	Depositor EDS
% Data completeness (in resolution range)	74.4 (15.00-2.40) 74.3 (37.67-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.39 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.263 0.215 , 0.259	Depositor DCC
R_{free} test set	3364 reflections (10.22%)	DCC
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	1.233	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 33059 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5847	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GSP, MG, CL, MES, 3PO, 103, FOK

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	0.35	0/1504	0.57	0/2027
2	B	0.39	0/1506	0.58	0/2033
3	C	0.38	0/2740	0.58	0/3707
All	All	0.38	0/5750	0.58	0/7767

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	1476	0	1450	22	0
2	B	1480	0	1474	20	0
3	C	2684	0	2633	17	0
4	A	2	0	0	0	0
4	C	1	0	0	0	0
5	C	2	0	0	0	0
6	C	32	0	12	0	0
7	A	29	0	34	4	0
8	B	21	0	12	1	0
9	A	13	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	12	0	13	0	0
10	B	12	0	13	4	0
11	A	14	0	0	0	0
11	B	33	0	0	0	0
11	C	36	0	0	0	0
All	All	5847	0	5641	61	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 5.

All (61) 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:B:1013:GLN:HG3	2:B:1014:LYS:HG2	1.65	0.78
2:B:1055:THR:HG23	2:B:1076:ASN:HB2	1.66	0.78
7:A:1001:FOK:H201	7:A:1001:FOK:H173	1.65	0.78
2:B:1038:LYS:HD2	10:B:1083:MES:H51	1.68	0.73
1:A:382:ILE:HD11	1:A:384:ILE:HD12	1.74	0.69
3:C:87:GLU:HG3	3:C:88:LYS:H	1.57	0.68
3:C:45:LEU:HD23	3:C:245:ILE:HB	1.76	0.67
2:B:1030:MET:HE1	2:B:1040:GLN:HG2	1.79	0.65
9:A:1003:3PO:O5'	8:B:1082:103:H3'	1.97	0.64
2:B:1013:GLN:HG3	2:B:1014:LYS:N	2.14	0.62
2:B:1013:GLN:NE2	2:B:1014:LYS:HE2	2.15	0.60
7:A:1001:FOK:H193	7:A:1001:FOK:H202	1.86	0.57
2:B:1030:MET:CE	2:B:1040:GLN:HG2	2.34	0.56
1:A:422:ARG:O	1:A:426:LEU:HG	2.04	0.56
3:C:277:TRP:NE1	3:C:349:SER:HA	2.21	0.55
1:A:507:TRP:O	1:A:508:SER:HB3	2.06	0.55
2:B:1061:ILE:N	2:B:1061:ILE:HD12	2.22	0.55
3:C:183:ASP:HA	3:C:186:LYS:HE2	1.90	0.54
1:A:508:SER:OG	1:A:511:VAL:HG23	2.07	0.54
1:A:477:THR:HG22	1:A:479:VAL:HG23	1.89	0.54
2:B:1038:LYS:CD	10:B:1083:MES:H51	2.38	0.54
2:B:1013:GLN:HG3	2:B:1014:LYS:H	1.73	0.53
1:A:462:MET:HE2	1:A:466:MET:HG3	1.91	0.51
1:A:456:ALA:O	1:A:460:VAL:HG23	2.10	0.51
1:A:426:LEU:HB2	1:A:462:MET:HE3	1.93	0.51
7:A:1001:FOK:H163	7:A:1001:FOK:H171	1.93	0.51
2:B:1000:ILE:HB	2:B:1041:VAL:HG12	1.91	0.50
2:B:1076:ASN:HA	10:B:1083:MES:H61	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:379:CYS:O	3:C:383:ILE:HG13	2.11	0.50
2:B:915:LEU:O	2:B:919:ILE:HG12	2.14	0.48
3:C:364:THR:HA	3:C:371:ASN:HD21	1.79	0.48
1:A:460:VAL:O	1:A:464:MET:HG2	2.14	0.48
3:C:364:THR:HG22	3:C:375:VAL:HG11	1.95	0.47
3:C:321:PRO:HG2	3:C:324:ALA:HB2	1.96	0.47
1:A:541:GLU:HB3	1:A:565:LEU:HD12	1.97	0.47
1:A:434:ARG:HG3	1:A:442:TYR:CZ	2.50	0.47
1:A:455:HIS:CD2	1:A:456:ALA:N	2.83	0.47
1:A:491:ARG:CZ	2:B:907:GLU:HG2	2.45	0.46
2:B:963:GLU:HB3	2:B:966:TYR:HB2	1.97	0.46
7:A:1001:FOK:H201	7:A:1001:FOK:C17	2.42	0.46
3:C:213:GLN:HG2	3:C:218:ASN:OD1	2.16	0.45
1:A:546:CYS:O	1:A:549:GLU:HG2	2.16	0.45
3:C:166:SER:HA	3:C:169:TYR:CE1	2.51	0.45
3:C:130:TYR:CD2	3:C:149:HIS:HD2	2.35	0.45
2:B:893:PRO:HG2	2:B:1036:LEU:HD21	1.98	0.45
3:C:121:ASN:HB2	3:C:124:ASN:ND2	2.33	0.44
1:A:462:MET:HG3	1:A:466:MET:HE3	1.99	0.44
3:C:266:LEU:HD23	3:C:312:PHE:CE1	2.53	0.43
2:B:904:VAL:HG11	3:C:207:ILE:CG2	2.48	0.43
1:A:393:LEU:HD23	1:A:394:PHE:N	2.32	0.43
1:A:393:LEU:C	1:A:393:LEU:HD23	2.39	0.42
2:B:989:HIS:HD2	3:C:279:ASN:HA	1.85	0.42
1:A:397:ILE:HA	1:A:482:ASN:O	2.19	0.42
2:B:1038:LYS:NZ	10:B:1083:MES:H31	2.35	0.42
1:A:400:PHE:CG	1:A:440:ASP:HB3	2.55	0.41
1:A:391:SER:OG	1:A:455:HIS:HD2	2.03	0.41
1:A:463:GLY:O	1:A:467:ILE:HG13	2.20	0.41
3:C:121:ASN:HB2	3:C:124:ASN:HD22	1.84	0.41
2:B:1036:LEU:HD23	2:B:1036:LEU:HA	1.92	0.41
3:C:107:VAL:CG1	3:C:128:VAL:HG13	2.52	0.40
1:A:479:VAL:HG12	1:A:481:VAL:HG13	2.04	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	187/217 (86%)	180 (96%)	6 (3%)	1 (0%)	34	48
2	B	186/208 (89%)	180 (97%)	6 (3%)	0	100	100
3	C	324/380 (85%)	314 (97%)	8 (2%)	2 (1%)	30	43
All	All	697/805 (87%)	674 (97%)	20 (3%)	3 (0%)	39	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	138	PRO
1	A	508	SER
3	C	354	ASP

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	158/182 (87%)	158 (100%)	0	100	100
2	B	163/180 (91%)	160 (98%)	3 (2%)	66	84
3	C	295/341 (86%)	291 (99%)	4 (1%)	74	88
All	All	616/703 (88%)	609 (99%)	7 (1%)	80	92

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	888	MET
2	B	1050	GLN
2	B	1059	ARG
3	C	261	ASN
3	C	306	SER
3	C	323	ASP
3	C	357	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	455	HIS
1	A	537	ASN
2	B	989	HIS
2	B	1013	GLN
2	B	1050	GLN
2	B	1076	ASN
3	C	97	ASN
3	C	149	HIS
3	C	227	GLN
3	C	362	HIS
3	C	371	ASN
3	C	377	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 11 ligands modelled in this entry, 5 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	$\# Z > 2$
7	FOK	A	1001	-	26,31,31	0.82	0	35,54,54	0.85	1 (2%)
9	3PO	A	1003	8,4	8,12,12	1.26	0	15,20,20	1.19	2 (13%)
10	MES	A	1004	-	11,12,12	1.07	1 (9%)	14,16,16	0.57	0
8	103	B	1082	9,4	19,23,23	0.82	0	19,35,35	0.83	1 (5%)
10	MES	B	1083	-	11,12,12	1.08	1 (9%)	14,16,16	0.57	0
6	GSP	C	395	4	25,34,34	1.15	1 (4%)	31,54,54	2.18	3 (9%)

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
7	FOK	A	1001	-	-	0/7/80/80	0/3/3/3
9	3PO	A	1003	8,4	-	0/12/12/12	0/0/0/0
10	MES	A	1004	-	-	0/6/14/14	0/1/1/1
8	103	B	1082	9,4	-	0/5/21/21	0/3/3/3
10	MES	B	1083	-	-	0/6/14/14	0/1/1/1
6	GSP	C	395	4	-	0/15/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	395	GSP	C6-N1	3.15	1.38	1.33
10	B	1083	MES	C5-N4	3.31	1.56	1.46
10	A	1004	MES	C5-N4	3.43	1.56	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	395	GSP	C5-C6-N1	-8.82	111.54	123.59
6	C	395	GSP	N3-C2-N1	-2.63	123.44	127.44
7	A	1001	FOK	C13-O1-C8	2.28	122.42	120.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1003	3PO	O2G-PG-O1G	2.74	119.39	110.58
9	A	1003	3PO	O2A-PA-O1A	2.80	119.59	110.58
8	B	1082	103	O2P-P-O1P	2.87	119.83	110.58
6	C	395	GSP	C6-N1-C2	6.73	125.28	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1001	FOK	4	0
9	A	1003	3PO	1	0
8	B	1082	103	1	0
10	B	1083	MES	4	0

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	189/217 (87%)	0.37	8 (4%) 40 41	29, 56, 88, 98	0
2	B	190/208 (91%)	0.15	10 (5%) 30 30	23, 39, 73, 100	0
3	C	328/380 (86%)	-0.02	13 (3%) 42 43	24, 45, 70, 97	1 (0%)
All	All	707/805 (87%)	0.13	31 (4%) 38 39	23, 46, 77, 100	1 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	39	ALA	5.1
3	C	86	GLY	5.0
2	B	963	GLU	4.7
3	C	139	ASP	4.2
2	B	878	TYR	4.1
3	C	385	ARG	4.0
1	A	476	MET	3.9
1	A	472	LEU	3.6
3	C	384	GLN	3.3
3	C	322	GLU	3.2
1	A	477	THR	3.1
3	C	189	ASP	3.0
3	C	386	MET	2.9
3	C	355	GLY	2.9
1	A	438	LEU	2.8
2	B	1077	THR	2.8
2	B	964	ARG	2.8
2	B	952	ALA	2.7
3	C	138	PRO	2.7
1	A	475	GLU	2.6
2	B	940	ILE	2.6
3	C	354	ASP	2.6
2	B	965	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
3	C	40	THR	2.5
2	B	889	PHE	2.4
1	A	439	GLY	2.4
1	A	481	VAL	2.4
2	B	966	TYR	2.2
3	C	218	ASN	2.1
1	A	544	PRO	2.1
2	B	939	THR	2.1

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
10	MES	B	1083	12/12	0.83	0.42	4.03	86,88,96,96	4
9	3PO	A	1003	13/13	0.85	0.27	1.61	91,94,99,99	4
8	103	B	1082	21/21	0.97	0.29	1.02	28,34,48,49	4
5	CL	C	397	1/1	0.99	0.20	0.48	34,34,34,34	0
7	FOK	A	1001	29/29	0.94	0.17	-0.01	25,33,40,42	0
10	MES	A	1004	12/12	0.94	0.16	-0.14	67,71,76,76	0
6	GSP	C	395	32/32	0.97	0.14	-0.30	22,30,46,53	0
4	MG	C	396	1/1	0.98	0.04	-3.40	38,38,38,38	0
4	MG	A	1006	1/1	0.97	0.08	-5.12	50,50,50,50	0
5	CL	C	398	1/1	0.94	0.07	-	40,40,40,40	1
4	MG	A	1007	1/1	0.97	0.39	-	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.