



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:03 am GMT

PDB ID : 2IEZ
Title : Crystal Structure of mouse Rab27b bound to GDP in monoclinic space group
Authors : Chavas, L.M.G.; Torii, S.; Kamikubo, H.; Kawasaki, M.; Ihara, K.; Kato, R.; Kataoka, M.; Izumi, T.; Wakatsuki, S.
Deposited on : 2006-09-19
Resolution : 2.80 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

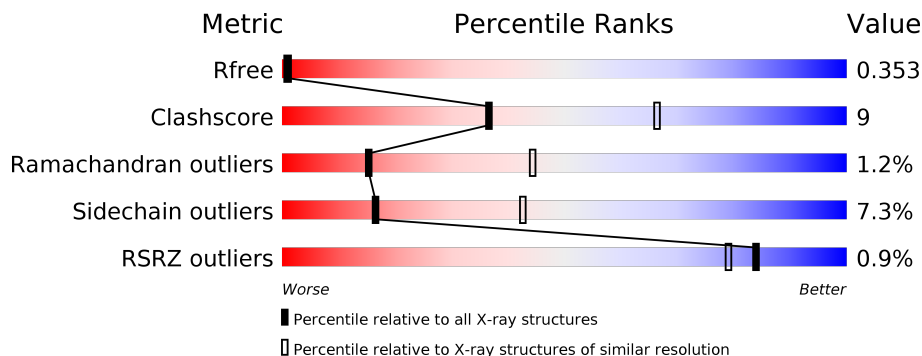
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	220	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>20%</div> <div>•</div> <div>19%</div> </div> </div>
1	B	220	<div> <div></div> <div> <div>59%</div> <div>19%</div> <div>22%</div> </div> </div>
1	H	220	<div> <div></div> <div> <div>60%</div> <div>15%</div> <div>•</div> <div>23%</div> </div> </div>
1	I	220	<div> <div></div> <div> <div>59%</div> <div>19%</div> <div>•</div> <div>21%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5754 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 Ras-related protein Rab-27B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1448	926	244	271	7			
1	B	171	Total	C	N	O	S	0	0	0
			1388	884	235	262	7			
1	H	169	Total	C	N	O	S	0	0	0
			1372	875	234	256	7			
1	I	173	Total	C	N	O	S	0	0	0
			1392	888	232	265	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q99P58
A	0	SER	-	EXPRESSION TAG	UNP Q99P58
A	78	LEU	GLN	ENGINEERED MUTATION	UNP Q99P58
B	-1	GLY	-	EXPRESSION TAG	UNP Q99P58
B	0	SER	-	EXPRESSION TAG	UNP Q99P58
B	78	LEU	GLN	ENGINEERED MUTATION	UNP Q99P58
H	-1	GLY	-	EXPRESSION TAG	UNP Q99P58
H	0	SER	-	EXPRESSION TAG	UNP Q99P58
H	78	LEU	GLN	ENGINEERED MUTATION	UNP Q99P58
I	-1	GLY	-	EXPRESSION TAG	UNP Q99P58
I	0	SER	-	EXPRESSION TAG	UNP Q99P58
I	78	LEU	GLN	ENGINEERED MUTATION	UNP Q99P58

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	I	1	Total Ca 1 1	0	0

- # GDP
-
- The image displays the chemical structure of Guanosine Diphosphate (GDP). It consists of a guanine base (a purine ring system with an amino group at C2) linked to a ribose sugar via a glycosidic bond at C1. The ribose sugar is further linked to two phosphate groups (P1 and P2) via phosphodiester bonds. The structure is labeled with atom names and numbers, and the phosphate groups are shown in pink.
- Nc1ncnc2c1ncn2[C@@H]3O[C@H](COP(=O)(O)OP(=O)(O)O)[C@@H](O)[C@H]3O

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	14	Total O 14 14	0	0
4	B	10	Total O 10 10	0	0
4	H	9	Total O 9 9	0	0

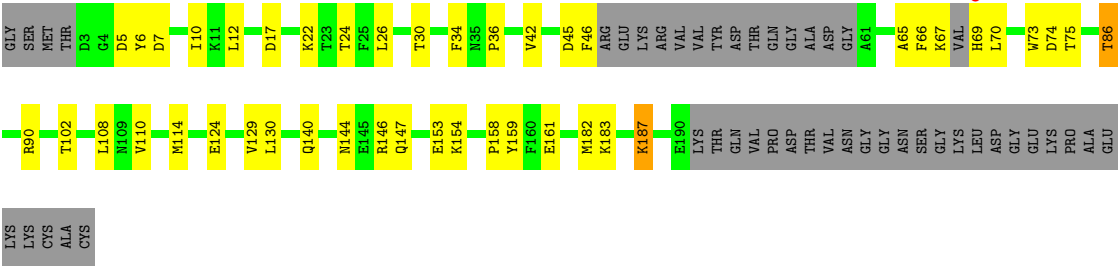
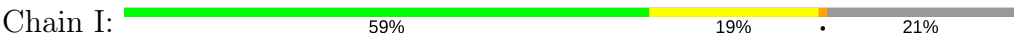
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	5	Total	O	0	0
			5	5		

- Molecule 1: Ras-related protein Rab-27B





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	170.50Å 63.35Å 80.84Å 90.00° 98.45° 90.00°	Depositor
Resolution (Å)	35.60 – 2.80 35.64 – 2.71	Depositor EDS
% Data completeness (in resolution range)	87.4 (35.60-2.80) 85.3 (35.64-2.71)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.262 , 0.363 0.258 , 0.353	Depositor DCC
R_{free} test set	952 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.612	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5754	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: GDP, CA

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	0.42	0/1475	0.54	0/1987
1	B	0.53	1/1413 (0.1%)	0.59	0/1905
1	H	0.42	0/1397	0.57	1/1882 (0.1%)
1	I	0.47	0/1417	0.64	0/1908
All	All	0.46	1/5702 (0.0%)	0.59	1/7682 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	115	SER	CB-OG	7.60	1.52	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	72	LEU	CA-CB-CG	5.38	127.67	115.30

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	1448	0	1432	44	0
1	B	1388	0	1367	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1372	0	1359	24	0
1	I	1392	0	1363	26	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
3	A	28	0	12	2	0
3	B	28	0	12	1	0
3	H	28	0	12	1	0
3	I	28	0	12	0	0
4	A	14	0	0	0	0
4	B	10	0	0	0	0
4	H	9	0	0	0	0
4	I	5	0	0	0	0
All	All	5754	0	5569	102	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 9.

All (102) 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:B:169:ASN:O	1:B:173:SER:HB2	1.85	0.77
1:H:50:ARG:HH12	1:I:6:TYR:HB3	1.49	0.77
1:A:184:ARG:HH11	1:A:184:ARG:HG3	1.51	0.75
1:B:111:ARG:HG3	1:B:151:LEU:HD13	1.69	0.73
1:A:95:PHE:HB2	1:A:128:ILE:HG12	1.72	0.71
1:I:144:ASN:HD22	1:I:147:GLN:H	1.37	0.71
1:B:86:THR:HG22	1:B:90:ARG:NH1	2.05	0.71
1:H:146:ARG:O	1:H:150:GLU:HG2	1.90	0.71
1:I:182:MET:HA	1:I:182:MET:HE2	1.74	0.69
1:B:16:GLY:O	1:B:22:LYS:NZ	2.15	0.68
1:H:150:GLU:HB3	1:H:154:LYS:HE3	1.78	0.66
1:A:178:LEU:CD2	1:B:70:LEU:HD21	2.26	0.65
1:A:10:ILE:HD12	1:B:68:VAL:HG11	1.77	0.65
1:A:134:LYS:HG2	3:A:2001:GDP:C6	2.32	0.64
1:A:14:ALA:HA	1:A:96:LEU:HB2	1.81	0.63
1:A:48:GLU:OE2	1:A:69:HIS:ND1	2.29	0.63
1:A:178:LEU:HD21	1:B:70:LEU:HD21	1.80	0.63
1:A:13:LEU:HD23	1:B:73:TRP:HB2	1.81	0.61
1:A:100:ASP:HB3	1:A:103:SER:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:LEU:HD21	1:A:177:LEU:CD1	2.31	0.60
1:I:10:ILE:HD11	1:I:182:MET:HE1	1.84	0.59
1:I:144:ASN:HD22	1:I:147:GLN:N	2.01	0.59
1:H:168:GLN:HG2	1:H:169:ASN:HD22	1.68	0.58
1:A:84:LEU:HD11	1:B:43:GLY:HA2	1.84	0.58
1:I:102:THR:HG23	1:I:140:GLN:HB3	1.85	0.58
1:A:98:MET:HB3	1:A:131:ILE:HB	1.86	0.58
1:A:98:MET:HA	1:A:131:ILE:O	2.03	0.58
1:I:110:VAL:O	1:I:114:MET:HG3	2.04	0.57
1:A:96:LEU:CD2	1:A:177:LEU:HD11	2.34	0.57
1:I:129:VAL:HG12	1:I:158:PRO:HG2	1.86	0.57
1:A:88:PHE:HB2	1:B:44:ILE:HG21	1.87	0.56
1:A:44:ILE:HG22	1:A:75:THR:HG22	1.88	0.55
1:H:162:THR:HG22	1:H:169:ASN:HB2	1.89	0.55
1:A:160:PHE:HE1	1:A:176:THR:HG21	1.71	0.54
1:H:168:GLN:HG2	1:H:169:ASN:ND2	2.21	0.54
1:A:7:ASP:HB2	1:B:68:VAL:HA	1.91	0.52
1:I:34:PHE:CZ	1:I:36:PRO:HG3	2.44	0.52
1:B:95:PHE:N	1:B:127:ASP:O	2.43	0.52
1:A:27:TYR:HD2	1:A:28:ARG:HG3	1.74	0.51
1:A:160:PHE:CE1	1:A:176:THR:HG21	2.45	0.51
1:A:111:ARG:HG3	1:A:151:LEU:HD12	1.91	0.51
1:A:96:LEU:HD21	1:A:177:LEU:HD11	1.92	0.51
1:A:97:LEU:HD21	1:A:110:VAL:HG13	1.92	0.51
1:A:20:VAL:HG22	1:A:100:ASP:HB2	1.92	0.50
1:I:26:LEU:O	1:I:30:THR:HB	2.11	0.50
1:A:13:LEU:HD12	1:A:95:PHE:CE2	2.47	0.50
1:A:96:LEU:HD21	1:A:177:LEU:HD12	1.92	0.50
1:H:11:LYS:N	1:H:93:MET:HG2	2.28	0.49
1:A:69:HIS:CD2	1:B:6:TYR:HB3	2.49	0.48
1:A:161:GLU:O	1:A:168:GLN:NE2	2.46	0.48
1:I:183:LYS:O	1:I:187:LYS:HB2	2.13	0.48
1:A:7:ASP:HB2	1:B:68:VAL:N	2.29	0.48
1:B:86:THR:HG22	1:B:90:ARG:HH11	1.77	0.47
1:H:178:LEU:O	1:H:182:MET:HG2	2.14	0.47
1:I:154:LYS:HG2	1:I:154:LYS:O	2.15	0.47
1:H:150:GLU:HB3	1:H:154:LYS:CE	2.44	0.47
1:H:72:LEU:HD12	1:I:12:LEU:HD12	1.97	0.47
1:B:134:LYS:HD3	3:B:1001:GDP:C4	2.50	0.47
1:I:17:ASP:O	1:I:22:LYS:NZ	2.47	0.47
1:A:30:THR:HG21	1:B:47:ARG:HD3	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:134:LYS:HG2	3:H:4001:GDP:C5	2.50	0.46
1:I:144:ASN:HD21	1:I:146:ARG:HB3	1.80	0.46
1:A:12:LEU:HD22	1:A:177:LEU:HD13	1.97	0.46
1:H:44:ILE:HD12	1:H:73:TRP:HZ3	1.81	0.46
1:I:144:ASN:ND2	1:I:147:GLN:H	2.08	0.46
1:B:94:GLY:HA3	1:B:181:ILE:HD11	1.97	0.45
1:I:45:ASP:CG	1:I:74:ASP:HB3	2.36	0.45
1:B:97:LEU:HD21	1:B:110:VAL:HG13	1.98	0.45
1:H:101:LEU:HD23	1:H:143:VAL:HB	1.99	0.45
1:I:159:TYR:OH	1:I:161:GLU:HG2	2.17	0.45
1:A:13:LEU:HD22	1:A:88:PHE:CE2	2.52	0.44
1:H:44:ILE:HD12	1:H:73:TRP:CZ3	2.52	0.44
1:A:48:GLU:HA	1:A:70:LEU:O	2.18	0.44
1:B:44:ILE:HD12	1:B:73:TRP:HZ3	1.83	0.44
1:I:45:ASP:OD2	1:I:74:ASP:HB3	2.16	0.44
1:H:128:ILE:HB	1:H:157:ILE:HG21	1.99	0.44
1:H:13:LEU:HD12	1:H:95:PHE:CE2	2.53	0.44
1:A:73:TRP:HB2	1:B:13:LEU:HD23	1.99	0.43
1:B:22:LYS:O	1:B:26:LEU:HG	2.18	0.43
1:A:172:LYS:O	1:A:176:THR:HB	2.18	0.43
1:A:184:ARG:HG3	1:A:184:ARG:NH1	2.26	0.43
1:I:182:MET:HA	1:I:182:MET:CE	2.47	0.43
1:A:105:GLN:HA	1:A:108:LEU:HB2	2.01	0.43
1:H:11:LYS:N	1:H:92:ALA:HA	2.34	0.43
1:H:36:PRO:HD2	1:I:46:PHE:O	2.18	0.43
1:B:177:LEU:O	1:B:180:LEU:HB2	2.19	0.42
1:B:154:LYS:HE3	1:B:154:LYS:HB2	1.89	0.42
1:I:86:THR:O	1:I:90:ARG:HB3	2.20	0.42
1:A:100:ASP:H	1:A:106:SER:HB3	1.85	0.41
1:H:134:LYS:HB3	1:H:137:LEU:HD12	2.02	0.41
1:H:180:LEU:HD23	1:H:180:LEU:HA	1.93	0.41
1:H:50:ARG:NH1	1:I:6:TYR:HB3	2.26	0.41
1:H:11:LYS:HD3	1:I:73:TRP:NE1	2.35	0.41
1:A:13:LEU:HD12	1:A:95:PHE:HE2	1.84	0.41
1:A:134:LYS:HE2	3:A:2001:GDP:C4	2.56	0.41
1:H:47:ARG:HD2	1:I:30:THR:HG21	2.03	0.40
1:A:100:ASP:H	1:A:106:SER:CB	2.34	0.40
1:A:13:LEU:HD21	1:A:88:PHE:O	2.21	0.40
1:I:10:ILE:HD11	1:I:182:MET:CE	2.51	0.40
1:A:36:PRO:HD2	1:B:46:PHE:O	2.21	0.40
1:H:168:GLN:O	1:H:170:VAL:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ASP:HB3	1:B:103:SER:HB3	2.02	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	174/220 (79%)	161 (92%)	9 (5%)	4 (2%)	7	25
1	B	167/220 (76%)	156 (93%)	10 (6%)	1 (1%)	28	62
1	H	165/220 (75%)	155 (94%)	9 (6%)	1 (1%)	28	62
1	I	167/220 (76%)	152 (91%)	13 (8%)	2 (1%)	15	44
All	All	673/880 (76%)	624 (93%)	41 (6%)	8 (1%)	15	44

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	B	17	ASP
1	I	65	ALA
1	H	169	ASN
1	I	66	PHE
1	A	91	ASP
1	A	189	VAL
1	A	7	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	156/186 (84%)	149 (96%)	7 (4%)	32	66
1	B	150/186 (81%)	141 (94%)	9 (6%)	22	54
1	H	148/186 (80%)	134 (90%)	14 (10%)	10	28
1	I	149/186 (80%)	135 (91%)	14 (9%)	10	29
All	All	603/744 (81%)	559 (93%)	44 (7%)	16	42

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	THR
1	A	78	LEU
1	A	124	GLU
1	A	159	TYR
1	A	179	ASP
1	A	184	ARG
1	A	188	CYS
1	B	9	LEU
1	B	32	ASN
1	B	33	LYS
1	B	40	THR
1	B	80	ARG
1	B	82	ARG
1	B	93	MET
1	B	118	GLN
1	B	141	ARG
1	H	20	VAL
1	H	41	THR
1	H	72	LEU
1	H	82	ARG
1	H	91	ASP
1	H	93	MET
1	H	106	SER
1	H	109	ASN
1	H	116	GLN
1	H	118	GLN
1	H	120	ASN
1	H	130	LEU
1	H	140	GLN
1	H	178	LEU

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Mol	Chain	Res	Type
1	I	5	ASP
1	I	7	ASP
1	I	24	THR
1	I	42	VAL
1	I	67	LYS
1	I	69	HIS
1	I	70	LEU
1	I	75	THR
1	I	86	THR
1	I	108	LEU
1	I	124	GLU
1	I	130	LEU
1	I	153	GLU
1	I	187	LYS

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	35	ASN
1	A	71	GLN
1	A	140	GLN
1	A	168	GLN
1	A	169	ASN
1	B	32	ASN
1	B	35	ASN
1	B	71	GLN
1	B	109	ASN
1	H	71	GLN
1	H	109	ASN
1	H	116	GLN
1	H	169	ASN
1	I	71	GLN
1	I	144	ASN
1	I	168	GLN

5.3.3 RNA ⓘ

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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$
3	GDP	A	2001	2	25,30,30	1.16	2 (8%)	26,47,47	1.92	6 (23%)
3	GDP	B	1001	2	25,30,30	1.15	2 (8%)	26,47,47	2.02	6 (23%)
3	GDP	H	4001	2	25,30,30	1.17	2 (8%)	26,47,47	2.15	7 (26%)
3	GDP	I	3001	2	25,30,30	1.21	2 (8%)	26,47,47	2.03	6 (23%)

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
3	GDP	A	2001	2	-	0/12/32/32	0/3/3/3
3	GDP	B	1001	2	-	0/12/32/32	0/3/3/3
3	GDP	H	4001	2	-	0/12/32/32	0/3/3/3
3	GDP	I	3001	2	-	0/12/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	4001	GDP	C5-C4	2.96	1.47	1.40
3	I	3001	GDP	C5-C4	3.01	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1001	GDP	C5-C4	3.11	1.47	1.40
3	A	2001	GDP	C5-C4	3.18	1.47	1.40
3	B	1001	GDP	C6-C5	3.57	1.48	1.41
3	A	2001	GDP	C6-C5	3.81	1.48	1.41
3	H	4001	GDP	C6-C5	4.25	1.49	1.41
3	I	3001	GDP	C6-C5	4.48	1.49	1.41

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	4001	GDP	C6-C5-C4	-4.65	116.22	120.84
3	B	1001	GDP	C5-C6-N1	-4.16	117.56	123.48
3	I	3001	GDP	C4-C5-N7	-3.96	105.58	109.41
3	A	2001	GDP	C5-C6-N1	-3.94	117.87	123.48
3	I	3001	GDP	C6-C5-C4	-3.84	117.02	120.84
3	B	1001	GDP	C6-C5-C4	-3.82	117.04	120.84
3	A	2001	GDP	C6-C5-C4	-3.47	117.40	120.84
3	H	4001	GDP	C5-C6-N1	-3.41	118.63	123.48
3	B	1001	GDP	N3-C2-N1	-3.39	122.51	127.46
3	H	4001	GDP	N3-C2-N1	-3.33	122.60	127.46
3	I	3001	GDP	C5-C6-N1	-3.27	118.83	123.48
3	H	4001	GDP	C4-C5-N7	-3.20	106.32	109.41
3	A	2001	GDP	N3-C2-N1	-3.03	123.04	127.46
3	I	3001	GDP	N3-C2-N1	-2.97	123.12	127.46
3	A	2001	GDP	C4-C5-N7	-2.82	106.68	109.41
3	B	1001	GDP	C4-C5-N7	-2.52	106.98	109.41
3	H	4001	GDP	C1'-N9-C4	-2.05	123.09	126.64
3	I	3001	GDP	C6-N1-C2	3.72	121.41	116.06
3	H	4001	GDP	C6-N1-C2	4.15	122.03	116.06
3	B	1001	GDP	C2-N3-C4	4.35	120.24	115.16
3	A	2001	GDP	C6-N1-C2	4.36	122.33	116.06
3	B	1001	GDP	C6-N1-C2	4.78	122.93	116.06
3	A	2001	GDP	C2-N3-C4	4.88	120.86	115.16
3	H	4001	GDP	C2-N3-C4	5.12	121.14	115.16
3	I	3001	GDP	C2-N3-C4	5.82	121.96	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2001	GDP	2	0
3	B	1001	GDP	1	0
3	H	4001	GDP	1	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 [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	178/220 (80%)	0.04	4 (2%) 62 52	40, 66, 85, 89	0
1	B	171/220 (77%)	-0.31	0 100 100	32, 42, 56, 67	0
1	H	169/220 (76%)	-0.16	1 (0%) 89 86	44, 65, 78, 82	0
1	I	173/220 (78%)	-0.12	1 (0%) 89 86	32, 50, 78, 82	0
All	All	691/880 (78%)	-0.13	6 (0%) 84 79	32, 55, 80, 89	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	TYR	5.4
1	A	190	GLU	3.8
1	A	150	GLU	2.5
1	H	151	LEU	2.5
1	A	163	SER	2.1
1	I	69	HIS	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	GDP	A	2001	28/28	0.96	0.15	-0.51	42,56,59,59	0
3	GDP	H	4001	28/28	0.93	0.15	-0.65	56,58,59,59	0
3	GDP	I	3001	28/28	0.97	0.14	-0.87	31,32,36,38	0
3	GDP	B	1001	28/28	0.97	0.14	-0.87	31,34,37,37	0
2	CA	H	401	1/1	0.75	0.09	-	47,47,47,47	0
2	CA	A	219	1/1	0.79	0.08	-	44,44,44,44	0
2	CA	I	301	1/1	0.92	0.08	-	52,52,52,52	0
2	CA	B	219	1/1	0.91	0.08	-	27,27,27,27	0

6.5 Other polymers

There are no such residues in this entry.