W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 11:52 PM GMT

|		
PDB ID	:	1YRA
Title	:	PAB0955 crystal structure : a GTPase in GDP bound form from Pyrococcus abyssi
Authors	:	Gras, S.; Carpentier, P.; Armengaud, J.; Housset, D.
Deposited on	:	2005-02-03
Resolution	:	2.30 Å(reported)

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 2.30 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		0.203
Clashscore		18
Ramachandran outliers		1.4%
Sidechain outliers		6.5%
RSRZ outliers		4.0%

Worse　　　　　*Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
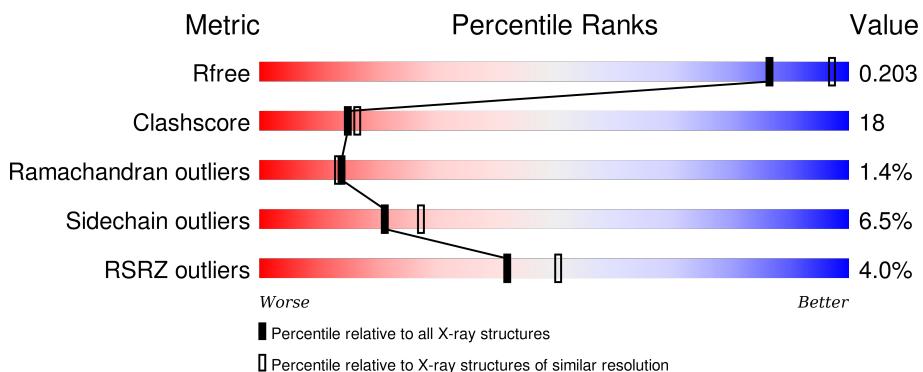
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	262	3%　69%　25%　5% ·
1	B	262	5%　68%　29% ·

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4477 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 ATP(GTP)binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	2	0
			2124	1362	349	397	16			
1	B	261	Total	C	N	O	S	0	2	0
			2128	1364	346	402	16			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	487	MET	-	EXPRESSION TAG	GB 5458856
A	488	ARG	-	EXPRESSION TAG	GB 5458856
A	489	GLY	-	EXPRESSION TAG	GB 5458856
A	490	SER	-	EXPRESSION TAG	GB 5458856
A	491	HIS	-	EXPRESSION TAG	GB 5458856
A	492	HIS	-	EXPRESSION TAG	GB 5458856
A	493	HIS	-	EXPRESSION TAG	GB 5458856
A	494	HIS	-	EXPRESSION TAG	GB 5458856
A	495	HIS	-	EXPRESSION TAG	GB 5458856
A	496	HIS	-	EXPRESSION TAG	GB 5458856
A	497	GLY	-	EXPRESSION TAG	GB 5458856
A	498	MET	-	EXPRESSION TAG	GB 5458856
A	499	ALA	-	EXPRESSION TAG	GB 5458856
A	500	SER	-	EXPRESSION TAG	GB 5458856
B	487	MET	-	EXPRESSION TAG	GB 5458856
B	488	ARG	-	EXPRESSION TAG	GB 5458856
B	489	GLY	-	EXPRESSION TAG	GB 5458856
B	490	SER	-	EXPRESSION TAG	GB 5458856
B	491	HIS	-	EXPRESSION TAG	GB 5458856
B	492	HIS	-	EXPRESSION TAG	GB 5458856
B	493	HIS	-	EXPRESSION TAG	GB 5458856
B	494	HIS	-	EXPRESSION TAG	GB 5458856
B	495	HIS	-	EXPRESSION TAG	GB 5458856
B	496	HIS	-	EXPRESSION TAG	GB 5458856
B	497	GLY	-	EXPRESSION TAG	GB 5458856

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Chain	Residue	Modelled	Actual	Comment	Reference
B	498	MET	-	EXPRESSION TAG	GB 5458856
B	499	ALA	-	EXPRESSION TAG	GB 5458856
B	500	SER	-	EXPRESSION TAG	GB 5458856

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).
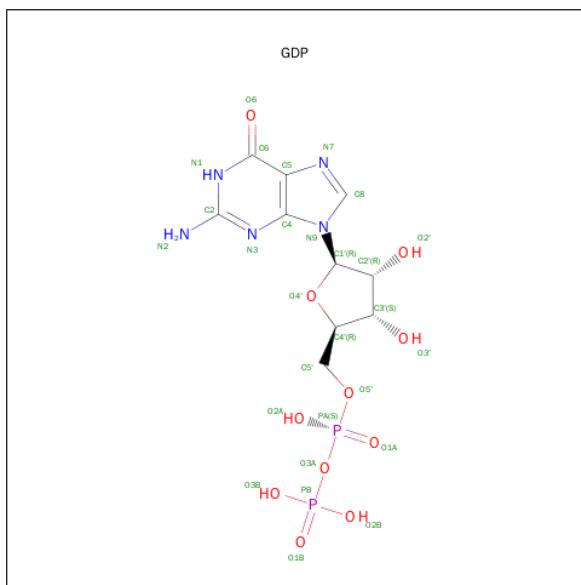
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
2	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		
3	B	80	Total	O	0	0
			80	80		

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: ATP(GTP)binding protein
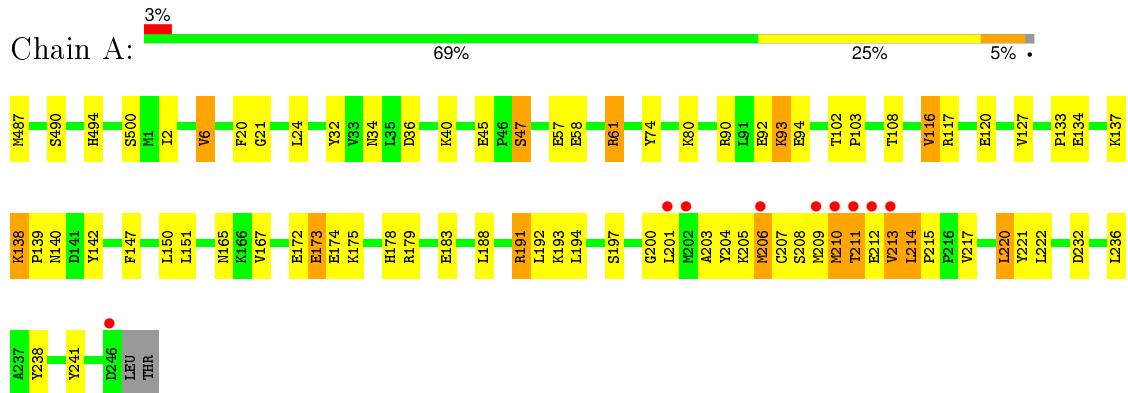
- Molecule 1: ATP(GTP)binding protein
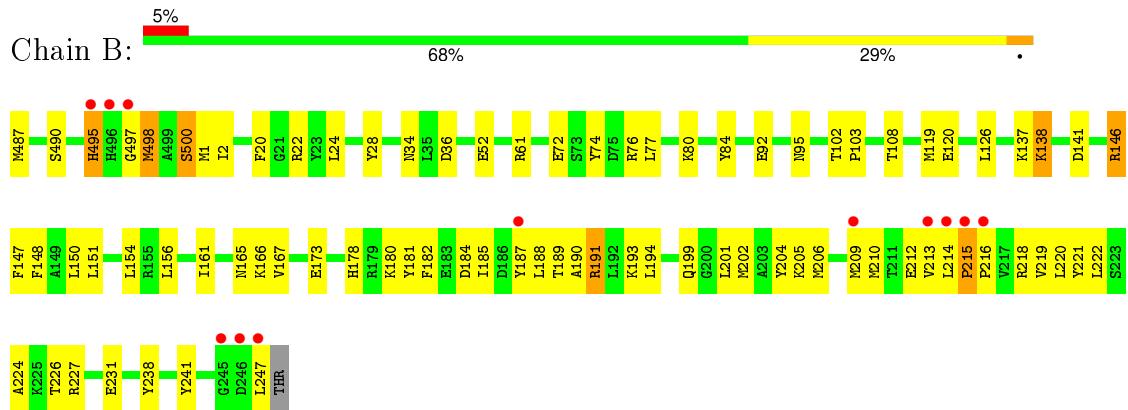
4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.19Å 84.95Å 60.20Å 90.00° 95.07° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30 59.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (15.00-2.30) 97.9 (59.96-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.43 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.190 , 0.264 0.189 , 0.203	Depositor DCC
R_{free} test set	2650 reflections (11.42%)	DCC
Wilson B-factor (Å^2)	31.9	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 44.5	EDS
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 26447 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4477	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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: GDP

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	0.55	0/2181	0.64	0/2946
1	B	0.53	0/2187	0.62	0/2956
All	All	0.54	0/4368	0.63	0/5902

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	2124	0	2092	84	1
1	B	2128	0	2089	75	1
2	A	28	0	12	0	0
2	B	28	0	12	0	0
3	A	89	0	0	9	0
3	B	80	0	0	13	0
All	All	4477	0	4205	150	1

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 18.

All (150) 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:193[A]:LYS:CD	1:A:204:TYR:CZ	2.43	1.00
1:A:214:LEU:N	1:A:215:PRO:HD3	1.78	0.99
1:A:193[A]:LYS:HD2	1:A:204:TYR:CE2	1.99	0.96
1:B:146:ARG:HH11	1:B:146:ARG:HG3	1.27	0.95
1:A:193[A]:LYS:CD	1:A:204:TYR:CE2	2.50	0.93
1:B:146:ARG:NH1	1:B:185:ILE:HD11	1.86	0.91
1:A:220:LEU:HD21	1:A:232:ASP:HB3	1.52	0.90
1:B:487:MET:N	1:B:490:SER:HG	1.72	0.87
1:B:191:ARG:O	3:B:554:HOH:O	1.93	0.87
1:A:193[A]:LYS:HD2	1:A:204:TYR:CZ	2.09	0.87
1:B:500:SER:HB3	1:B:95:ASN:O	1.75	0.86
1:A:214:LEU:H	1:A:215:PRO:HD3	1.34	0.86
1:B:182:PHE:CE2	1:B:219:VAL:HG11	2.15	0.81
1:B:495:HIS:CD2	3:B:573:HOH:O	2.35	0.79
1:A:193[A]:LYS:HD3	1:A:204:TYR:CE2	2.17	0.78
1:B:146:ARG:HG3	1:B:146:ARG:NH1	1.95	0.78
1:A:45:GLU:HG3	3:A:566:HOH:O	1.82	0.77
1:B:500:SER:OG	1:B:92:GLU:HG2	1.85	0.77
1:A:173:GLU:HG3	1:A:174:GLU:H	1.49	0.77
1:A:193[A]:LYS:HD3	1:A:204:TYR:CZ	2.22	0.74
1:B:138:LYS:HE3	3:B:566:HOH:O	1.87	0.74
1:B:146:ARG:NH1	1:B:185:ILE:CD1	2.50	0.74
1:A:138:LYS:NZ	1:A:140:ASN:OD1	2.21	0.74
1:A:213:VAL:O	1:A:214:LEU:HB2	1.85	0.73
1:B:146:ARG:HH11	1:B:185:ILE:HD11	1.53	0.73
1:A:487:MET:HA	3:A:543:HOH:O	1.87	0.72
1:B:202:MET:O	1:B:206:MET:HG3	1.90	0.72
1:B:165:ASN:HD21	1:B:224:ALA:H	1.38	0.71
1:B:495:HIS:HD2	3:B:573:HOH:O	1.71	0.71
1:A:193[A]:LYS:HE3	1:A:204:TYR:CZ	2.25	0.70
1:B:120:GLU:OE1	3:B:553:HOH:O	2.09	0.69
1:A:214:LEU:N	1:A:215:PRO:CD	2.53	0.69
1:A:487:MET:N	1:A:490:SER:HG	1.90	0.69
1:A:34:ASN:HD21	1:A:36:ASP:HB3	1.57	0.69
1:A:209:MET:O	1:A:210:MET:HG2	1.93	0.68
1:A:90[B]:ARG:NH1	1:A:94:GLU:OE2	2.27	0.68
1:B:146:ARG:HH11	1:B:146:ARG:CG	2.08	0.66
1:A:193[A]:LYS:CE	1:A:204:TYR:CZ	2.78	0.66
1:A:116:VAL:O	1:A:120:GLU:HG3	1.95	0.66
1:B:34:ASN:HD21	1:B:36:ASP:HB3	1.62	0.64
1:B:182:PHE:CD2	1:B:219:VAL:HG11	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:ARG:HG2	1:B:61:ARG:HH11	1.62	0.64
1:A:150:LEU:HB3	1:B:206:MET:CE	2.27	0.64
1:A:175:LYS:O	1:A:179:ARG:HG3	1.98	0.62
1:A:487:MET:CA	3:A:543:HOH:O	2.46	0.62
1:B:185:ILE:O	1:B:185:ILE:HG22	2.00	0.62
1:A:179:ARG:HB3	1:A:183:GLU:OE2	2.00	0.62
1:B:146:ARG:HH12	1:B:185:ILE:CG1	2.13	0.61
1:A:151:LEU:CD2	1:B:148:PHE:HD1	2.14	0.61
1:A:172:GLU:HG3	1:A:172:GLU:O	2.00	0.61
1:B:146:ARG:HH12	1:B:185:ILE:HG13	1.66	0.61
1:A:151:LEU:HD21	1:B:148:PHE:HD1	1.67	0.60
1:A:193[A]:LYS:HE3	1:A:204:TYR:CE1	2.38	0.59
1:B:52[A]:GLU:HG2	3:B:545:HOH:O	2.02	0.59
1:A:173:GLU:HG3	1:A:174:GLU:N	2.17	0.59
1:B:214:LEU:HD12	1:B:215:PRO:HD2	1.85	0.59
1:A:209:MET:O	1:A:210:MET:CB	2.51	0.59
1:A:74:TYR:CD2	1:A:108:THR:HG21	2.38	0.58
1:A:36:ASP:OD2	3:A:531:HOH:O	2.16	0.58
1:B:193:LYS:HE2	1:B:204:TYR:OH	2.03	0.58
1:B:182:PHE:CE2	1:B:219:VAL:CG1	2.86	0.58
1:A:494:HIS:HE1	3:A:567:HOH:O	1.86	0.57
1:A:209:MET:O	1:A:210:MET:CG	2.52	0.57
1:A:201:LEU:HB2	3:A:580:HOH:O	2.04	0.56
1:A:150:LEU:HB3	1:B:206:MET:HE3	1.85	0.56
1:A:134:GLU:O	1:A:137:LYS:NZ	2.33	0.56
1:B:226:THR:O	1:B:227:ARG:HB2	2.06	0.55
1:A:206:MET:C	1:A:208:SER:H	2.10	0.55
1:A:500:SER:OG	1:A:92:GLU:HG2	2.06	0.54
1:A:167:VAL:HG22	1:A:222:LEU:O	2.06	0.54
1:A:209:MET:C	1:A:210:MET:HG2	2.28	0.54
1:B:52[A]:GLU:CG	3:B:545:HOH:O	2.53	0.54
1:A:211:THR:HG22	1:A:212:GLU:N	2.22	0.54
1:A:203:ALA:HB2	1:B:154:LEU:HD13	1.90	0.53
1:B:126:LEU:HD11	1:B:161:ILE:HD11	1.91	0.53
1:B:167:VAL:HG11	1:B:221:TYR:HB3	1.91	0.53
1:A:193[A]:LYS:HD2	1:A:204:TYR:CD2	2.43	0.53
1:A:2:ILE:HD11	1:A:92:GLU:HG3	1.91	0.53
1:B:74:TYR:HA	1:B:77:LEU:HB2	1.91	0.53
1:A:90[B]:ARG:NH2	1:A:94:GLU:OE1	2.41	0.52
1:B:1:MET:HG2	3:B:570:HOH:O	2.08	0.52
1:A:139:PRO:HB2	1:A:192:LEU:HD23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:GLU:OE1	1:B:76:ARG:NE	2.33	0.52
1:A:193[A]:LYS:HE3	1:A:204:TYR:OH	2.10	0.51
1:B:137:LYS:HE3	3:B:532:HOH:O	2.09	0.51
1:B:119:MET:HG3	1:B:156:LEU:HD22	1.91	0.51
1:B:247:LEU:HD22	3:B:580:HOH:O	2.11	0.51
1:B:193:LYS:CE	1:B:204:TYR:OH	2.59	0.51
1:A:20:PHE:CE2	1:A:24:LEU:HD11	2.46	0.51
1:A:214:LEU:H	1:A:215:PRO:CD	2.11	0.51
1:A:150:LEU:HB3	1:B:206:MET:HE1	1.92	0.50
1:A:209:MET:O	1:A:209:MET:CG	2.59	0.50
1:B:214:LEU:O	1:B:216:PRO:HD3	2.11	0.50
1:A:93:LYS:HD2	3:A:528:HOH:O	2.11	0.50
1:A:191:ARG:O	1:A:191:ARG:HD2	2.12	0.49
1:B:165:ASN:ND2	1:B:166:LYS:H	2.10	0.49
1:A:133:PRO:HD3	1:A:165:ASN:O	2.13	0.49
1:B:150:LEU:HD22	1:B:210:MET:HG2	1.93	0.49
1:B:61:ARG:NH1	1:B:61:ARG:HG2	2.28	0.49
1:A:102:THR:HB	1:A:103:PRO:HD2	1.95	0.48
1:B:495:HIS:O	1:B:498:MET:HB3	2.14	0.48
1:A:142:TYR:HE1	1:A:178:HIS:HA	1.79	0.47
1:A:21:GLY:HA3	1:A:32:TYR:OH	2.14	0.47
1:B:180:LYS:O	1:B:184:ASP:HB3	2.15	0.47
1:B:102:THR:HB	1:B:103:PRO:HD2	1.97	0.47
1:B:20:PHE:CE2	1:B:24:LEU:HD11	2.49	0.47
1:A:209:MET:O	1:A:210:MET:HB3	2.15	0.46
1:A:6:VAL:HG13	1:A:127:VAL:HG13	1.98	0.45
1:A:213:VAL:O	1:A:214:LEU:CB	2.60	0.45
1:B:189:THR:O	1:B:190:ALA:C	2.54	0.45
1:A:34:ASN:ND2	1:A:36:ASP:H	2.14	0.45
1:B:497:GLY:N	3:B:555:HOH:O	2.44	0.45
1:A:138:LYS:HB2	1:A:139:PRO:HD2	1.99	0.45
1:A:203:ALA:HB2	1:B:154:LEU:CD1	2.47	0.45
1:B:74:TYR:CE2	1:B:108:THR:HG21	2.51	0.44
1:B:219:VAL:HG12	1:B:220:LEU:N	2.33	0.44
1:B:34:ASN:ND2	3:B:528:HOH:O	2.50	0.44
1:A:138:LYS:HZ2	1:A:138:LYS:HB2	1.81	0.44
1:A:47:SER:OG	3:A:552:HOH:O	1.98	0.44
1:A:213:VAL:HG12	1:B:205:LYS:HE3	2.00	0.44
1:B:84:TYR:OH	3:B:545:HOH:O	2.04	0.44
1:B:193:LYS:HE2	1:B:204:TYR:CZ	2.53	0.44
1:A:205:LYS:HE3	1:A:205:LYS:HB2	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:LEU:HD21	1:A:232:ASP:CB	2.36	0.43
1:B:138:LYS:HG3	1:B:141:ASP:OD2	2.18	0.43
1:A:58:GLU:HA	1:A:61:ARG:HG3	1.99	0.43
1:B:147:PHE:O	1:B:150:LEU:HB3	2.18	0.43
1:B:2:ILE:HD11	1:B:92:GLU:HG3	1.99	0.43
1:A:193[A]:LYS:CE	1:A:204:TYR:OH	2.66	0.43
1:B:77:LEU:HA	1:B:77:LEU:HD23	1.79	0.43
1:B:146:ARG:NH1	1:B:185:ILE:CG1	2.78	0.42
1:A:167:VAL:HG11	1:A:221:TYR:HB3	2.00	0.42
1:A:147:PHE:CZ	1:A:209:MET:HB3	2.54	0.42
1:B:34:ASN:ND2	1:B:36:ASP:H	2.16	0.42
1:A:238:TYR:O	1:A:241:TYR:HB3	2.19	0.42
1:B:238:TYR:O	1:B:241:TYR:HB3	2.20	0.42
1:B:231:GLU:N	1:B:231:GLU:OE2	2.34	0.42
1:B:178:HIS:O	1:B:182:PHE:CB	2.68	0.42
1:B:167:VAL:HG22	1:B:222:LEU:O	2.19	0.42
1:A:487:MET:HB3	3:A:543:HOH:O	2.19	0.41
1:A:206:MET:O	1:A:208:SER:N	2.50	0.41
1:A:57:GLU:N	1:A:57:GLU:OE1	2.47	0.41
1:A:197:SER:OG	1:A:200:GLY:N	2.50	0.41
1:B:209:MET:O	1:B:213:VAL:HG23	2.21	0.41
1:A:151:LEU:HD22	1:B:151:LEU:HD22	2.03	0.40
1:A:206:MET:C	1:A:208:SER:N	2.75	0.40
1:A:191:ARG:CG	1:A:191:ARG:HH11	2.35	0.40
1:A:102:THR:HB	1:A:103:PRO:CD	2.51	0.40
1:B:181:TYR:CE1	1:B:187:TYR:HE1	2.39	0.40
1:B:80:LYS:HD2	1:B:80:LYS:HA	1.89	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LYS:NZ	1:B:173:GLU:OE2[1_556]	2.01	0.19

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	260/262 (99%)	247 (95%)	7 (3%)	6 (2%)	8	6
1	B	261/262 (100%)	249 (95%)	11 (4%)	1 (0%)	39	48
All	All	521/524 (99%)	496 (95%)	18 (4%)	7 (1%)	14	15

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	MET
1	A	214	LEU
1	A	213	VAL
1	A	211	THR
1	A	206	MET
1	A	207	CYS
1	B	215	PRO

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	234/234 (100%)	218 (93%)	16 (7%)	20	25
1	B	235/234 (100%)	221 (94%)	14 (6%)	24	31
All	All	469/468 (100%)	439 (94%)	30 (6%)	21	28

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	VAL
1	A	40	LYS
1	A	47	SER
1	A	61	ARG
1	A	80	LYS

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Mol	Chain	Res	Type
1	A	93	LYS
1	A	116	VAL
1	A	117	ARG
1	A	138	LYS
1	A	173	GLU
1	A	188	LEU
1	A	191	ARG
1	A	194	LEU
1	A	217	VAL
1	A	220	LEU
1	A	236	LEU
1	B	495	HIS
1	B	498	MET
1	B	500	SER
1	B	22	ARG
1	B	28	TYR
1	B	138	LYS
1	B	146	ARG
1	B	188	LEU
1	B	191	ARG
1	B	194	LEU
1	B	199	GLN
1	B	201	LEU
1	B	212	GLU
1	B	218	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	121	ASN
1	A	165	ASN
1	B	492	HIS
1	B	34	ASN
1	B	165	ASN
1	B	240	HIS

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)

2 ligands are modelled in this entry.

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	$\#|Z| > 2$
2	GDP	A	401	-	23,30,30	1.19	2 (8%)	30,47,47	1.86	6 (20%)
2	GDP	B	402	-	23,30,30	1.21	3 (13%)	30,47,47	2.12	7 (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
2	GDP	A	401	-	-	0/12/32/32	0/3/3/3
2	GDP	B	402	-	-	0/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	GDP	O4'-C1'	2.08	1.43	1.41
2	A	401	GDP	C5-C4	2.69	1.46	1.40
2	A	401	GDP	C6-C5	3.05	1.47	1.41
2	B	402	GDP	C5-C4	3.28	1.47	1.40
2	B	402	GDP	C6-C5	3.61	1.48	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	GDP	C5-C6-N1	-4.61	117.28	123.59
2	B	402	GDP	C5-C6-N1	-4.46	117.49	123.59
2	B	402	GDP	C2'-C1'-N9	-4.22	107.84	114.29
2	B	402	GDP	PA-O3A-PB	-4.16	118.71	132.67
2	B	402	GDP	C6-C5-C4	-3.46	116.76	120.90
2	A	401	GDP	N3-C2-N1	-3.44	122.20	127.44
2	B	402	GDP	N3-C2-N1	-3.24	122.51	127.44
2	B	402	GDP	C4-C5-N7	-3.19	106.54	109.48
2	A	401	GDP	C4-C5-N7	-3.04	106.69	109.48
2	A	401	GDP	C6-C5-C4	-2.73	117.64	120.90
2	A	401	GDP	PA-O3A-PB	-2.58	124.01	132.67
2	A	401	GDP	C6-N1-C2	5.06	122.97	115.94
2	B	402	GDP	C6-N1-C2	5.23	123.19	115.94

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	260/262 (99%)	0.10	9 (3%)	48	56	14, 31, 59, 79	11 (4%)
1	B	261/262 (99%)	0.06	12 (4%)	36	45	20, 33, 61, 79	14 (5%)
All	All	521/524 (99%)	0.08	21 (4%)	42	51	14, 32, 61, 79	25 (4%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	211	THR	12.6
1	A	212	GLU	5.7
1	B	497	GLY	4.8
1	B	213	VAL	4.3
1	B	496	HIS	3.8
1	B	495	HIS	3.7
1	B	215	PRO	3.6
1	B	246	ASP	3.5
1	B	247	LEU	3.2
1	B	214	LEU	3.2
1	A	246	ASP	3.0
1	A	201	LEU	3.0
1	B	216	PRO	2.9
1	A	210	MET	2.9
1	A	209	MET	2.7
1	B	187	TYR	2.6
1	B	245	GLY	2.6
1	A	206	MET	2.4
1	A	213	VAL	2.4
1	A	202	MET	2.3
1	B	209	MET	2.1

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
2	GDP	B	402	28/28	0.97	0.12	-0.17	28,36,38,38	0
2	GDP	A	401	28/28	0.98	0.10	-1.05	27,32,35,37	0

6.5 Other polymers (i)

There are no such residues in this entry.