



# wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 04:40 PM GMT

PDB ID : 1K5G  
Title : Crystal structure of Ran-GDP-AlFx-RanBP1-RanGAPcomplex  
Authors : Seewald, M.J.; Koerner, C.; Wittinghofer, A.; Vetter, I.R.  
Deposited on : 2001-10-10  
Resolution : 3.10 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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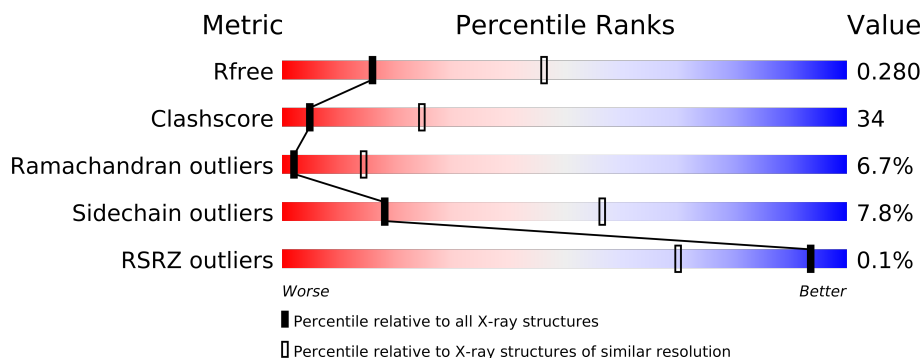
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.10 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))
$R_{free}$	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	216	
1	D	216	
1	G	216	
1	J	216	
2	B	201	
2	E	201	
2	H	201	
2	K	201	
3	C	386	
3	F	386	
3	I	386	
3	L	386	

The following table lists non-polymeric compounds that are outliers for geometric or electron-

density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	MG	A	1251	-	X
4	MG	D	2251	-	X
4	MG	G	3251	-	X
4	MG	J	4251	-	X
6	AF3	D	2252	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22396 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GTP-binding nuclear protein RAN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	D	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	G	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	J	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			

- Molecule 2 is a protein called Ran-specific GTPase-activating protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	E	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	H	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	K	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			

- Molecule 3 is a protein called Ran GTPase activating protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	F	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	I	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	L	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			

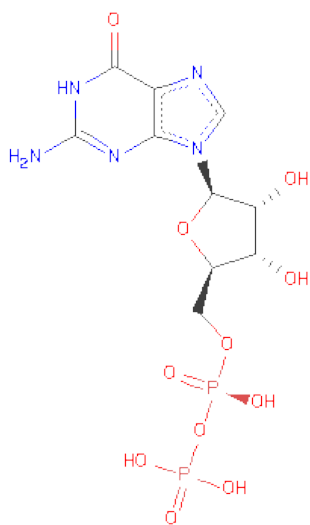
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ALA	SER	SEE REMARK 999	UNP P41391
F	2	ALA	SER	SEE REMARK 999	UNP P41391
I	2	ALA	SER	SEE REMARK 999	UNP P41391
L	2	ALA	SER	SEE REMARK 999	UNP P41391

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Mg 1 1	0	0
4	J	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

- Molecule 5 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



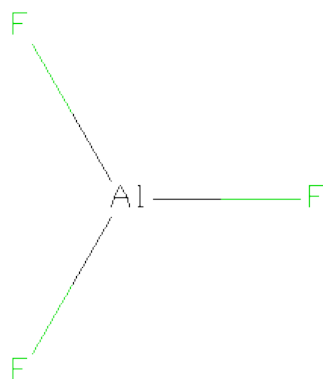
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 28 10 5 11 2	0	0
5	D	1	Total C N O P 28 10 5 11 2	0	0

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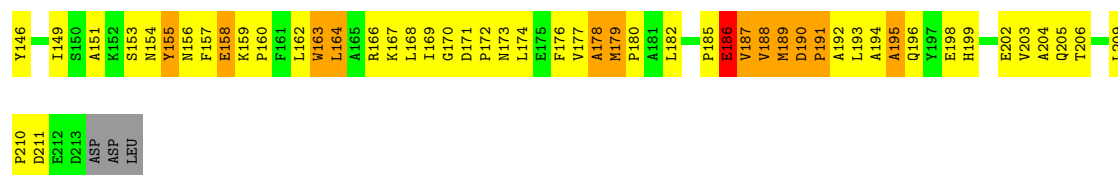
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
5	J	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 6 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula:  $\text{AlF}_3$ ).



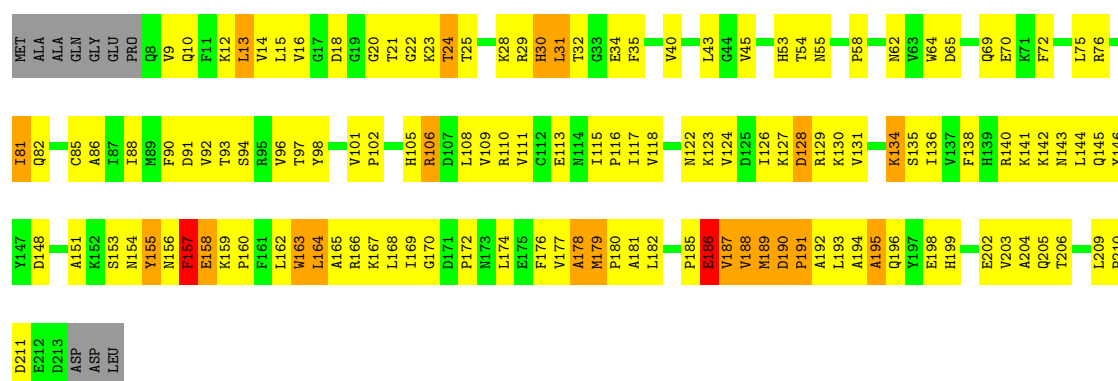
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Al	F	0	0
			4	1	3		
6	D	1	Total	Al	F	0	0
			4	1	3		
6	G	1	Total	Al	F	0	0
			4	1	3		
6	J	1	Total	Al	F	0	0
			4	1	3		





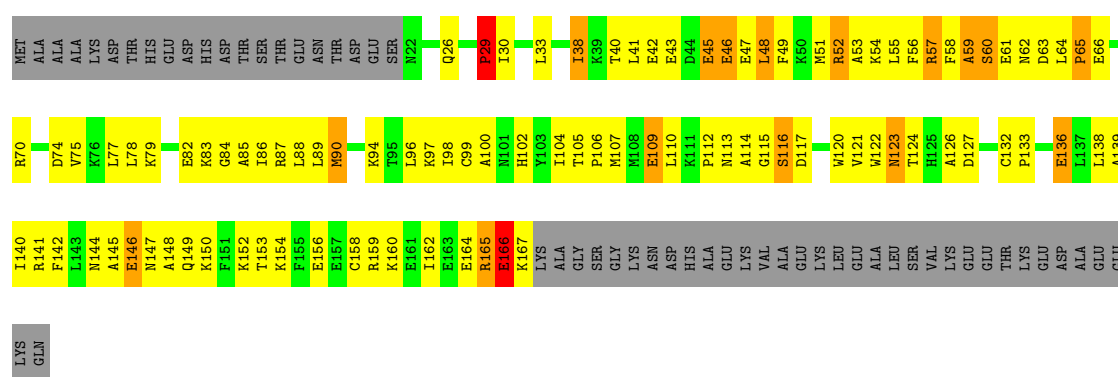
• Molecule 1: GTP-binding nuclear protein RAN

Chain J:



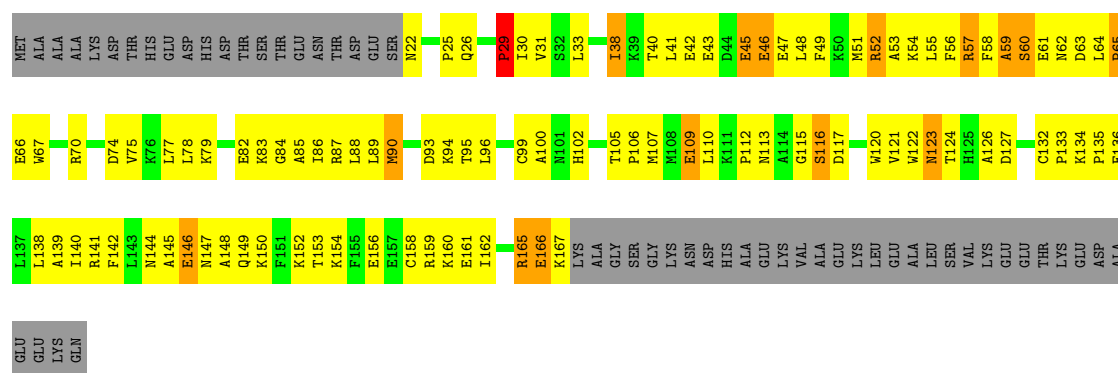
• Molecule 2: Ran-specific GTPase-activating protein

Chain B:



• Molecule 2: Ran-specific GTPase-activating protein

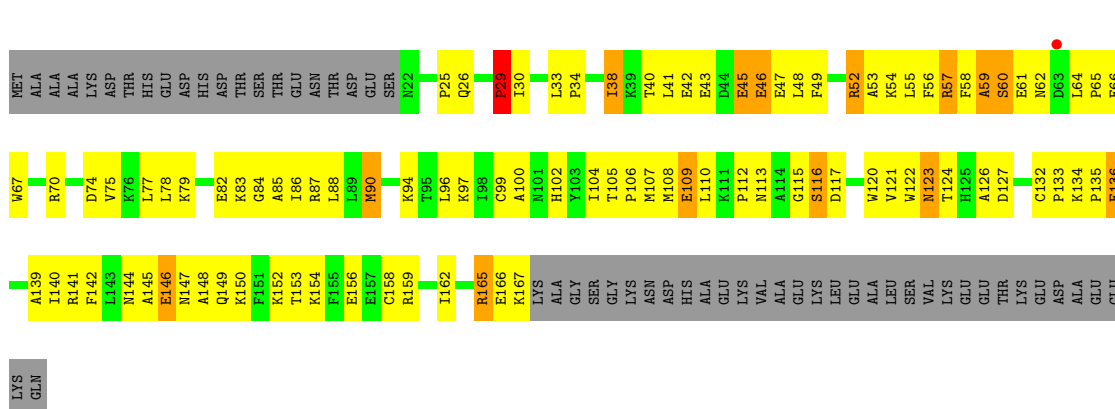
Chain E:





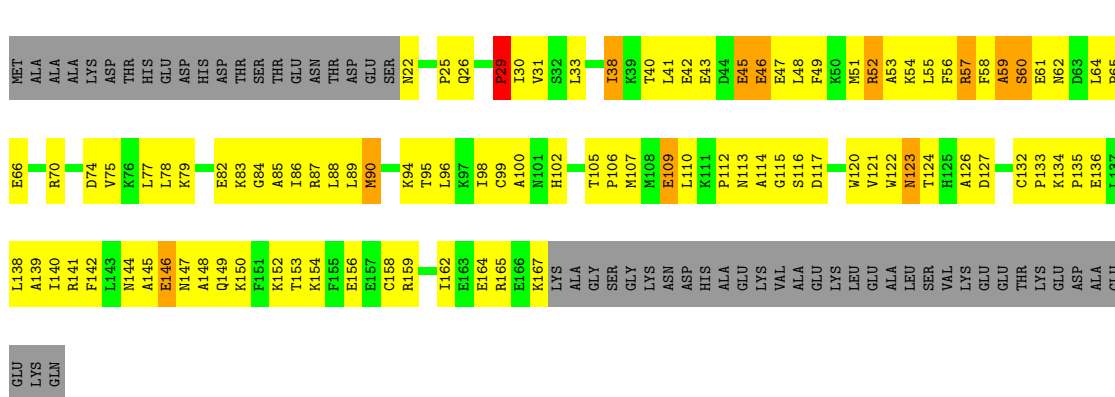
- Molecule 2: Ran-specific GTPase-activating protein

Chain H:



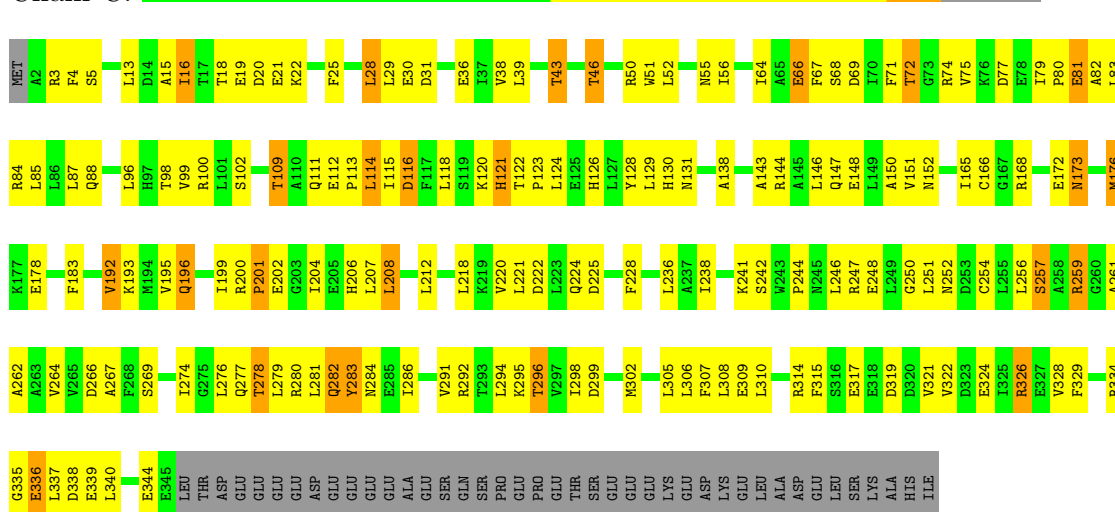
- Molecule 2: Ran-specific GTPase-activating protein

Chain K:



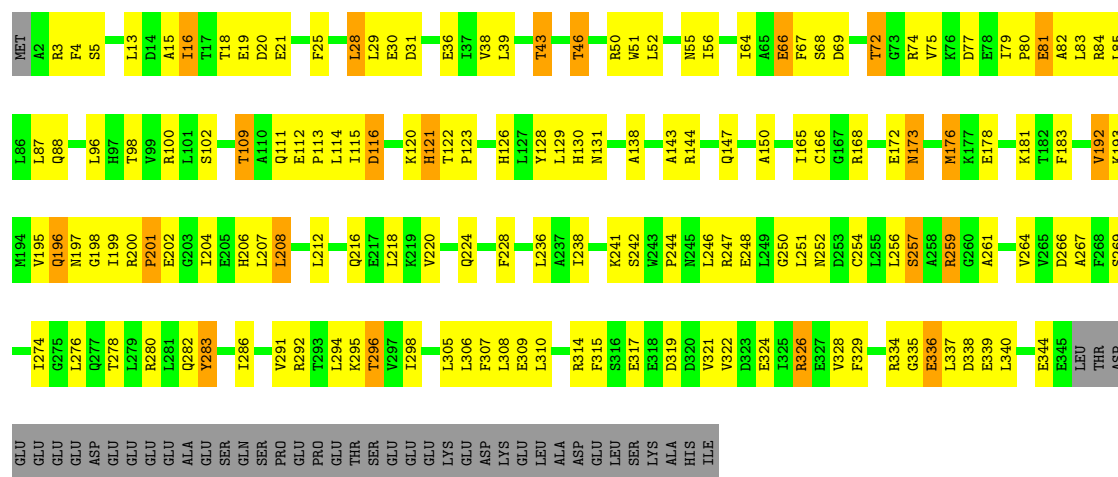
- Molecule 3: Ran GTPase activating protein 1

Chain C:



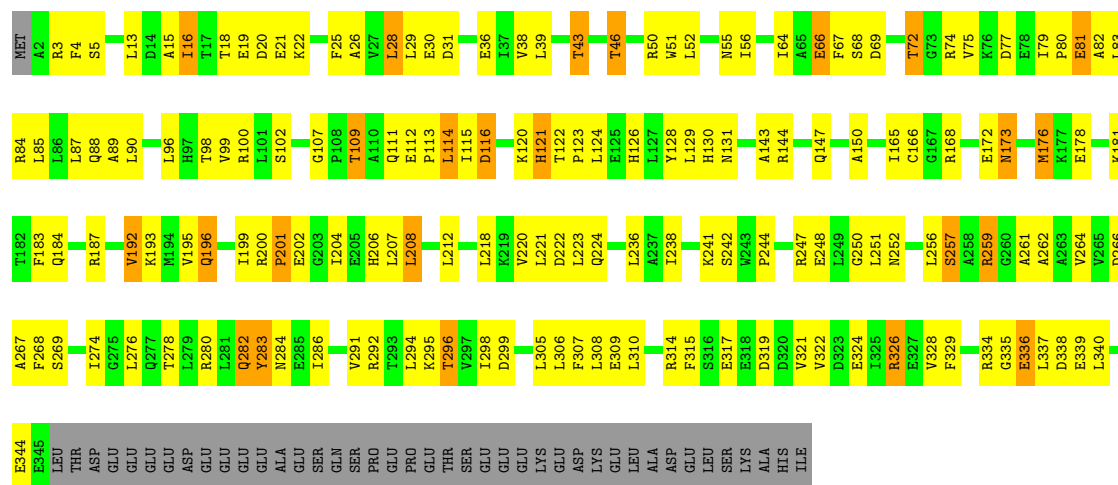
- Molecule 3: Ran GTPase activating protein 1

Chain F:



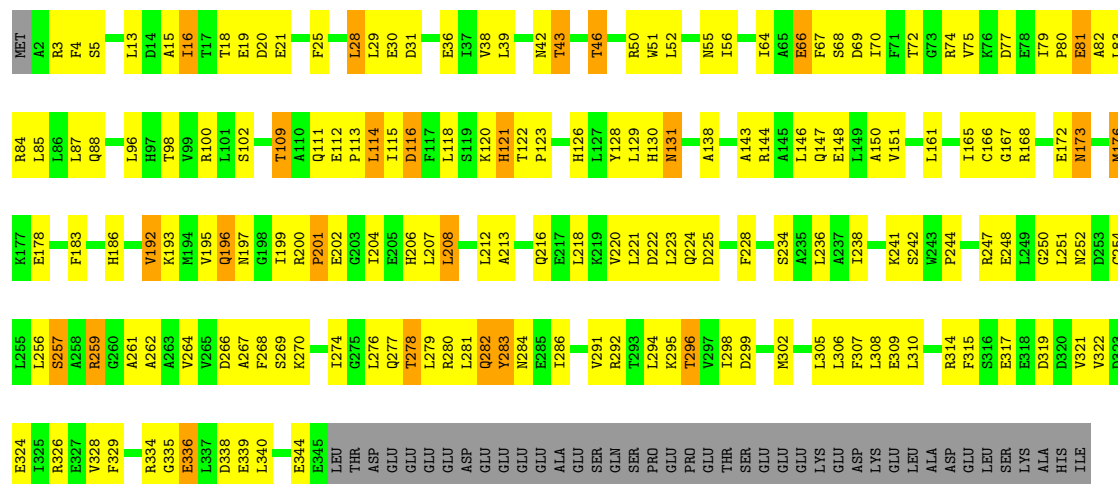
### • Molecule 3: Ran GTPase activating protein 1

Chain I:



### • Molecule 3: Ran GTPase activating protein 1

Chain L:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.93Å 102.57Å 118.85Å 71.67° 79.09° 67.81°	Depositor
Resolution (Å)	31.00 – 3.10 31.22 – 2.88	Depositor EDS
% Data completeness (in resolution range)	96.2 (31.00-3.10) 94.2 (31.22-2.88)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.23 (at 2.90Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.250 , 0.269 0.246 , 0.280	Depositor DCC
$R_{free}$ test set	8869 reflections (11.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	63.8	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 26.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 88616 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	22396	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, AF3

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	0/1693	0.67	0/2296
1	D	0.45	0/1693	0.68	0/2296
1	G	0.43	0/1693	0.67	0/2296
1	J	0.46	0/1693	0.69	0/2296
2	B	0.37	0/1242	0.63	0/1666
2	E	0.36	0/1242	0.62	0/1666
2	H	0.38	0/1242	0.62	0/1666
2	K	0.38	0/1242	0.63	0/1666
3	C	0.41	0/2737	0.68	0/3697
3	F	0.41	0/2737	0.68	0/3697
3	I	0.41	0/2737	0.67	0/3697
3	L	0.42	0/2737	0.69	0/3697
All	All	0.41	0/22688	0.67	0/30636

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1652	0	1660	129	0
1	D	1652	0	1659	141	0
1	G	1652	0	1659	140	0
1	J	1652	0	1660	145	0
2	B	1216	0	1208	117	0
2	E	1216	0	1208	118	0
2	H	1216	0	1208	107	0
2	K	1216	0	1208	110	0
3	C	2698	0	2733	166	0
3	F	2698	0	2733	143	0
3	I	2698	0	2733	162	0
3	L	2698	0	2733	164	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
5	A	28	0	12	5	0
5	D	28	0	12	5	0
5	G	28	0	12	5	0
5	J	28	0	12	4	0
6	A	4	0	0	0	0
6	D	4	0	0	0	0
6	G	4	0	0	0	0
6	J	4	0	0	0	0
All	All	22396	0	22450	1526	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 34.

The worst 5 of 1526 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:I:259:ARG:NH1	3:I:259:ARG:HB3	1.68	1.07
3:F:259:ARG:HB3	3:F:259:ARG:NH1	1.69	1.06
3:L:259:ARG:NH1	3:L:259:ARG:HB3	1.71	1.04
3:C:259:ARG:HB3	3:C:259:ARG:NH1	1.73	1.04
3:I:259:ARG:HH11	3:I:259:ARG:HB3	1.20	1.03

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	204/216 (94%)	156 (76%)	27 (13%)	21 (10%)	1	6
1	D	204/216 (94%)	153 (75%)	29 (14%)	22 (11%)	1	5
1	G	204/216 (94%)	156 (76%)	28 (14%)	20 (10%)	1	6
1	J	204/216 (94%)	154 (76%)	28 (14%)	22 (11%)	1	5
2	B	144/201 (72%)	118 (82%)	14 (10%)	12 (8%)	1	9
2	E	144/201 (72%)	117 (81%)	15 (10%)	12 (8%)	1	9
2	H	144/201 (72%)	119 (83%)	14 (10%)	11 (8%)	2	11
2	K	144/201 (72%)	117 (81%)	18 (12%)	9 (6%)	2	16
3	C	342/386 (89%)	275 (80%)	54 (16%)	13 (4%)	5	30
3	F	342/386 (89%)	280 (82%)	48 (14%)	14 (4%)	4	27
3	I	342/386 (89%)	278 (81%)	50 (15%)	14 (4%)	4	27
3	L	342/386 (89%)	278 (81%)	50 (15%)	14 (4%)	4	27
All	All	2760/3212 (86%)	2201 (80%)	375 (14%)	184 (7%)	2	14

5 of 184 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	106	ARG
1	A	135	SER
1	A	179	MET
1	A	186	GLU

### 5.3.2 Protein sidechains ⓘ

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	178/185 (96%)	164 (92%)	14 (8%)	18	55
1	D	178/185 (96%)	161 (90%)	17 (10%)	12	42
1	G	178/185 (96%)	163 (92%)	15 (8%)	16	52
1	J	178/185 (96%)	161 (90%)	17 (10%)	12	42
2	B	131/176 (74%)	117 (89%)	14 (11%)	10	35
2	E	131/176 (74%)	118 (90%)	13 (10%)	11	39
2	H	131/176 (74%)	117 (89%)	14 (11%)	10	35
2	K	131/176 (74%)	119 (91%)	12 (9%)	13	45
3	C	295/334 (88%)	277 (94%)	18 (6%)	26	67
3	F	295/334 (88%)	277 (94%)	18 (6%)	26	67
3	I	295/334 (88%)	277 (94%)	18 (6%)	26	67
3	L	295/334 (88%)	277 (94%)	18 (6%)	26	67
All	All	2416/2780 (87%)	2228 (92%)	188 (8%)	18	57

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	173	ASN
1	G	155	TYR
3	L	43	THR
3	F	192	VAL
1	G	18	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	224	GLN
2	H	123	ASN
3	L	147	GLN
3	F	252	ASN
1	G	145	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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$
5	GDP	A	1250	4,6	30,30,30	1.59	5 (16%)	44,47,47	3.01	8 (18%)
6	AF3	A	1252	5,4	0,3,3	0.00	-	0,3,3	0.00	-
5	GDP	D	2250	4,6	30,30,30	1.66	7 (23%)	44,47,47	2.80	5 (11%)
6	AF3	D	2252	5,4	0,3,3	0.00	-	0,3,3	0.00	-
5	GDP	G	3250	4,6	30,30,30	1.47	6 (20%)	44,47,47	3.05	7 (15%)
6	AF3	G	3252	5,4	0,3,3	0.00	-	0,3,3	0.00	-
5	GDP	J	4250	4,6	30,30,30	1.62	6 (20%)	44,47,47	2.66	9 (20%)
6	AF3	J	4252	5,4	0,3,3	0.00	-	0,3,3	0.00	-

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
5	GDP	A	1250	4,6	-	0/16/32/32	0/1/3/3
6	AF3	A	1252	5,4	-	0/0/0/0	0/0/0/0
5	GDP	D	2250	4,6	-	0/16/32/32	0/1/3/3
6	AF3	D	2252	5,4	-	0/0/0/0	0/0/0/0
5	GDP	G	3250	4,6	-	0/16/32/32	0/1/3/3
6	AF3	G	3252	5,4	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GDP	J	4250	4,6	-	0/16/32/32	0/1/3/3
6	AF3	J	4252	5,4	-	0/0/0/0	0/0/0/0

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	2250	GDP	C6-C5	4.40	1.48	1.41
5	J	4250	GDP	C6-C5	4.13	1.48	1.41
5	A	1250	GDP	C6-C5	3.63	1.47	1.41
5	G	3250	GDP	C6-C5	3.51	1.47	1.41
5	A	1250	GDP	C2'-C1'	-3.23	1.48	1.53

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	3250	GDP	C6-C5-N7	-17.82	131.74	134.14
5	A	1250	GDP	C6-C5-N7	-17.57	131.77	134.14
5	D	2250	GDP	C6-C5-N7	-15.96	131.99	134.14
5	J	4250	GDP	C6-C5-N7	-14.64	132.17	134.14
5	G	3250	GDP	C8-N9-C4	-3.89	103.93	106.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	206/216 (95%)	-0.34	0 100 100	21, 57, 156, 186	0
1	D	206/216 (95%)	-0.35	1 (0%) 88 39	13, 46, 161, 199	0
1	G	206/216 (95%)	-0.38	0 100 100	14, 50, 159, 198	0
1	J	206/216 (95%)	-0.42	0 100 100	11, 47, 148, 199	0
2	B	146/201 (72%)	-0.21	0 100 100	43, 88, 148, 200	0
2	E	146/201 (72%)	-0.03	0 100 100	43, 100, 162, 195	0
2	H	146/201 (72%)	-0.22	1 (0%) 84 32	32, 80, 158, 187	0
2	K	146/201 (72%)	-0.25	0 100 100	44, 80, 145, 188	0
3	C	344/386 (89%)	-0.47	0 100 100	18, 48, 107, 144	0
3	F	344/386 (89%)	-0.54	0 100 100	11, 47, 93, 143	0
3	I	344/386 (89%)	-0.48	0 100 100	15, 50, 100, 148	0
3	L	344/386 (89%)	-0.52	0 100 100	8, 43, 97, 150	0
All	All	2784/3212 (86%)	-0.40	2 (0%) 93 70	8, 55, 139, 200	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	191	PRO	3.6
2	H	63	ASP	2.3

### 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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	MG	J	4251	1/1	0.36	11.50	33,33,33,33	0
4	MG	D	2251	1/1	0.32	8.49	45,45,45,45	0
4	MG	A	1251	1/1	0.37	7.74	31,31,31,31	0
4	MG	G	3251	1/1	0.38	6.42	44,44,44,44	0
6	AF3	D	2252	4/4	0.28	4.86	57,57,57,57	0
6	AF3	J	4252	4/4	0.24	1.66	57,57,57,57	0
6	AF3	A	1252	4/4	0.24	1.10	57,57,57,57	0
6	AF3	G	3252	4/4	0.20	0.73	57,57,57,57	0
5	GDP	A	1250	28/28	0.15	-0.43	43,43,43,43	0
5	GDP	G	3250	28/28	0.14	-0.51	35,35,35,35	0
5	GDP	J	4250	28/28	0.12	-0.68	29,29,29,29	0
5	GDP	D	2250	28/28	0.13	-0.70	31,31,31,31	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.