



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:17 AM GMT

PDB ID : 3A6P
Title : Crystal structure of Exportin-5:RanGTP:pre-miRNA complex
Authors : Okada, C.; Yamashita, E.; Lee, S.J.; Shibata, S.; Katahira, J.; Nakagawa, A.; Yoneda, Y.; Tsukihara, T.
Deposited on : 2009-09-07
Resolution : 2.92 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

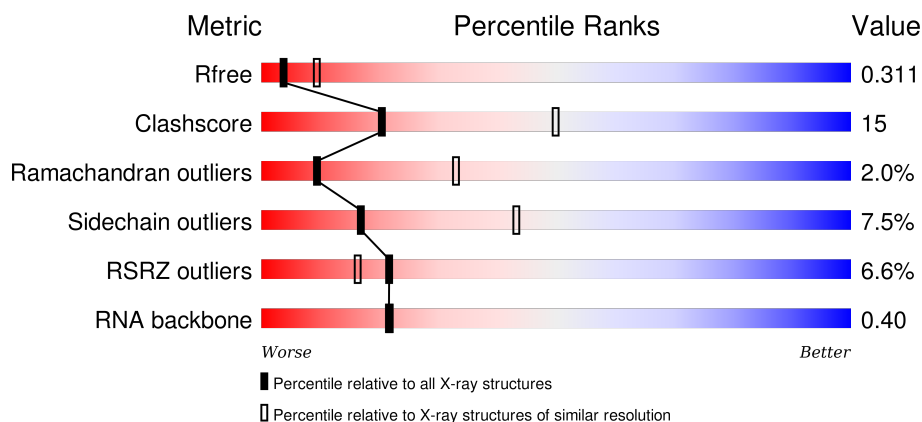
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	1643 (2.94-2.90)
Clashscore	102246	1871 (2.94-2.90)
Ramachandran outliers	100387	1824 (2.94-2.90)
Sidechain outliers	100360	1826 (2.94-2.90)
RSRZ outliers	91569	1650 (2.94-2.90)
RNA backbone	2183	1004 (3.30-2.54)

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	1204	<div> <div>3%</div> <div>58%</div> <div>26%</div> <div>•</div> <div>11%</div> </div>
1	F	1204	<div> <div>8%</div> <div>60%</div> <div>24%</div> <div>5%</div> <div>•</div> <div>11%</div> </div>
2	B	13	<div> <div>100%</div> </div>
2	G	13	<div> <div>92%</div> <div>8%</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	216	
3	H	216	
4	D	24	
4	I	24	
5	E	24	
5	J	24	

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
6	GTP	C	1177	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 22052 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 Exportin-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1072	Total	C	N	O	S	0	0	0
			8570	5480	1442	1574	74			
1	F	1072	Total	C	N	O	S	0	0	0
			8570	5480	1442	1574	74			

- Molecule 2 is a protein called 13-mer peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	13	Total	C	N	O	0	0	0
			66	39	13	14			
2	G	13	Total	C	N	O	0	0	0
			66	39	13	14			

- Molecule 3 is a protein called GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	170	Total	C	N	O	S	0	0	0
			1386	900	244	238	4			
3	H	170	Total	C	N	O	S	0	0	0
			1386	900	244	238	4			

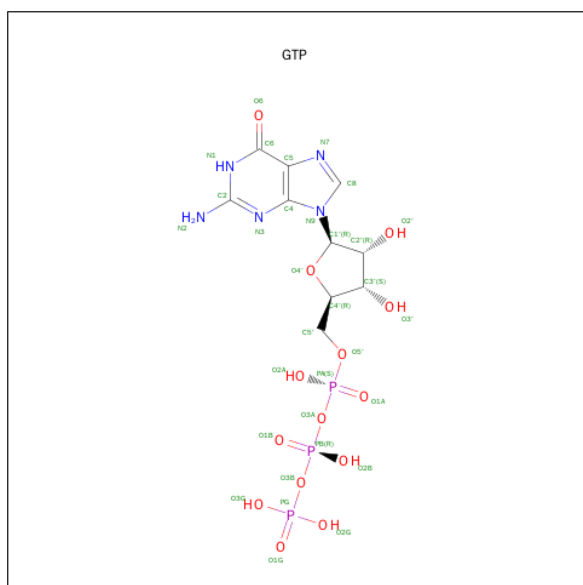
- Molecule 4 is a RNA chain called pre-microRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	22	Total	C	N	O	P	0	0	0
			466	211	88	147	20			
4	I	22	Total	C	N	O	P	0	0	0
			466	211	88	147	20			

- Molecule 5 is a RNA chain called pre-microRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	24	Total	C	N	O	P	0	0	0
			505	226	84	172	23			
5	J	24	Total	C	N	O	P	0	0	0
			505	226	84	172	23			

- Molecule 6 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
6	H	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

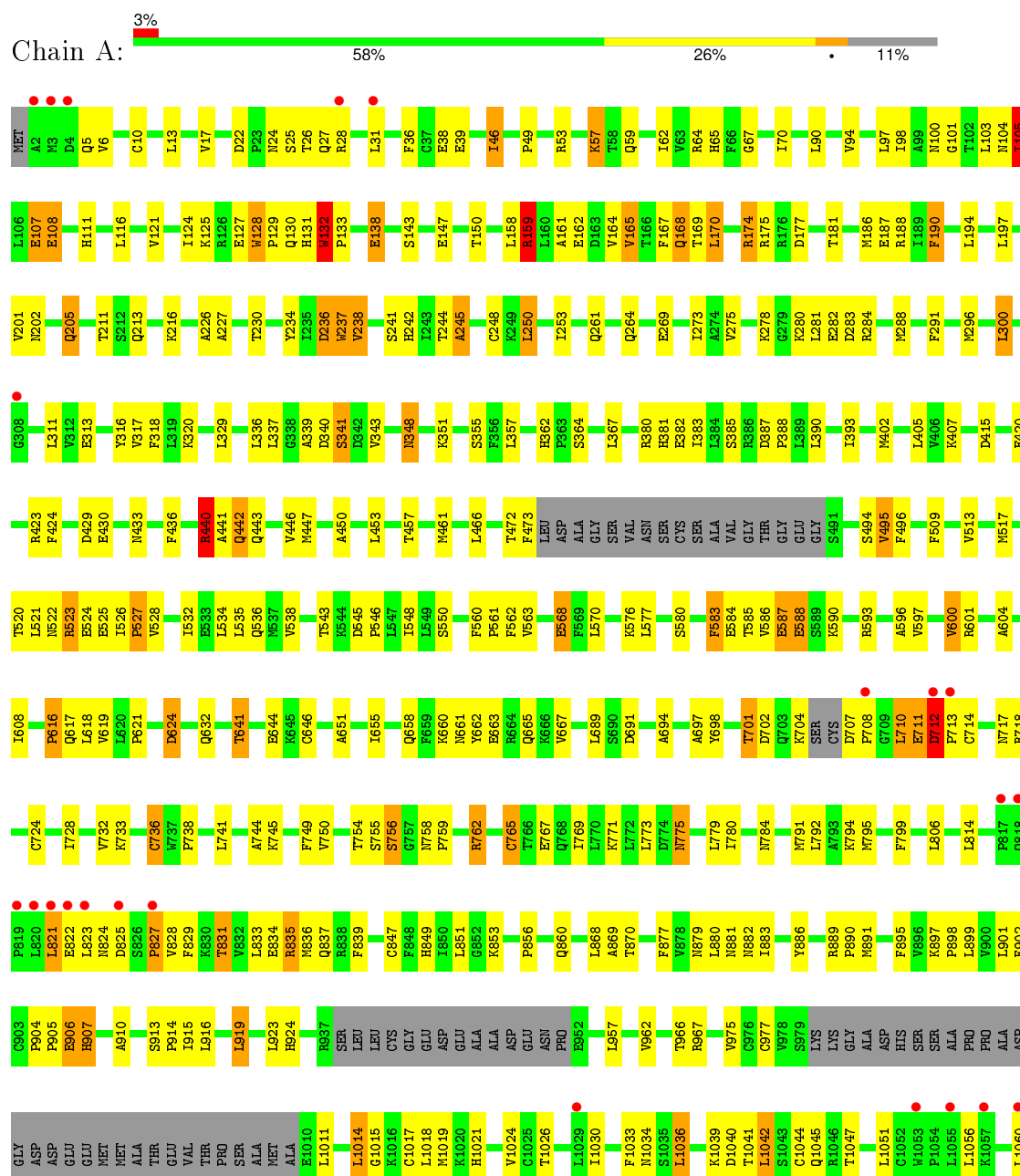
- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

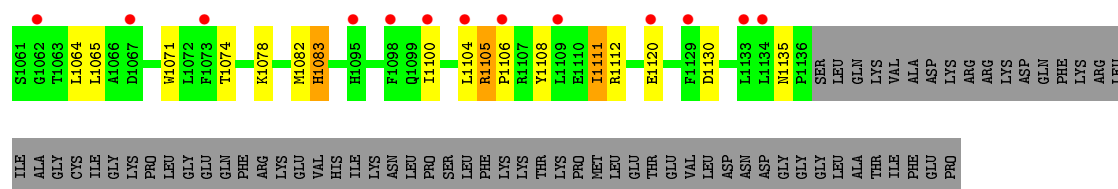
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	1	Total	Mg	0	0
			1	1		
7	C	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

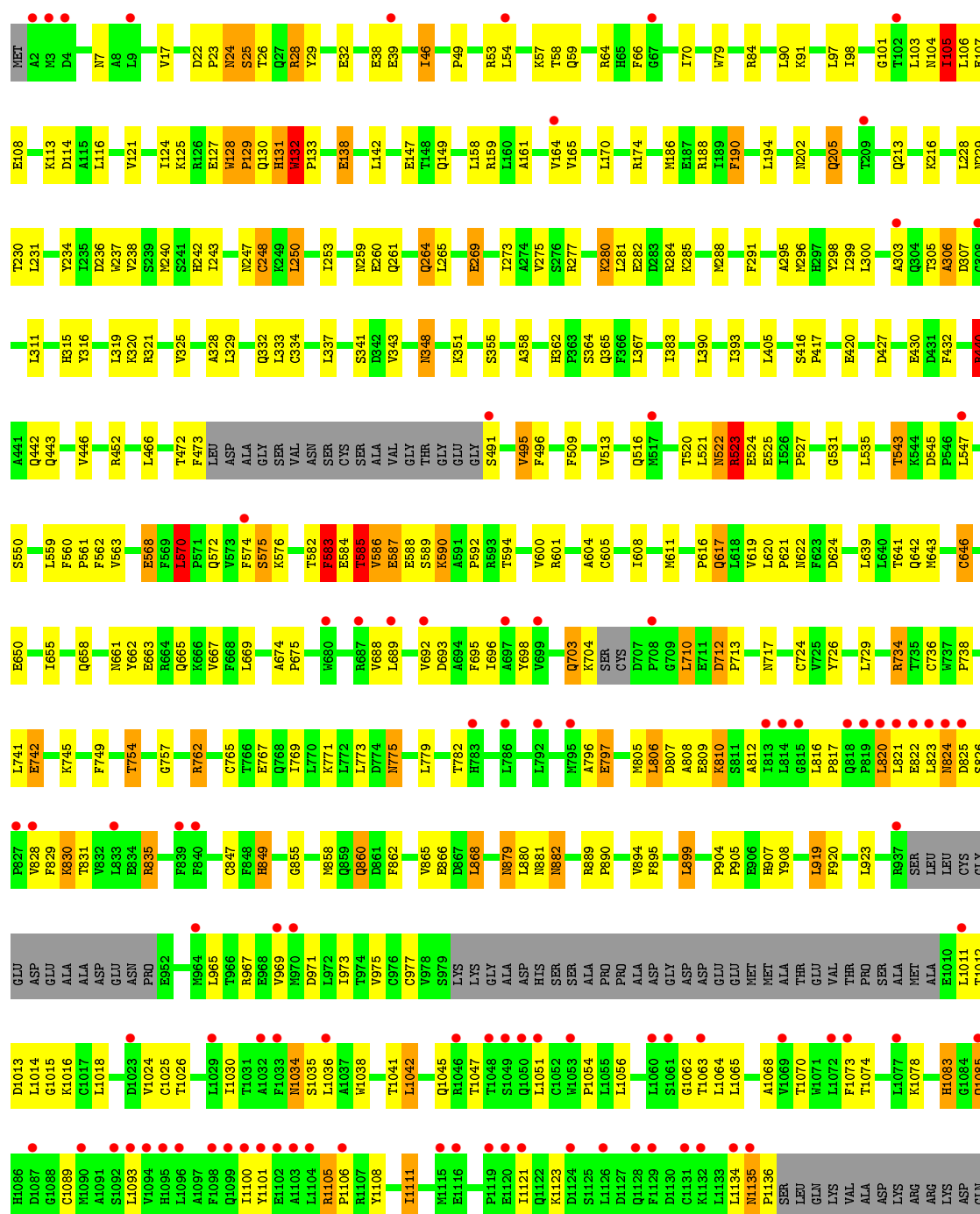
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Exportin-5





Molecule 1: Exportin-5



PHE
LYS
ARG
LEU
ILE
ALA
GLY
CYS
ILE
GLY
LYS
PRO
LEU
GLY
GLN
PHE
ARG
LYS
GLU
VAL
HIS
ILE
LYS
ASN
LEU
PRO
SER
LEU
PHE
LYS
LYS
THR
LYS
PRO
MET
LEU
GLU
THR
GLU
VAL
LEU
ASP
ASN
ASP
GLY
GLY
GLY
LEU
ALA
THR
ILE
PHE
GLU
PRO

- Molecule 2: 13-mer peptide

Chain B:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: 13-mer peptide

Chain G:  92% 8%

X1305
X1315
X1316
X1317

- Molecule 3: GTP-binding nuclear protein Ran

Chain C:  3% 56% 23% 21%

MET
ALA
ALA
GLN
GLY
GLU
P7
Q8
V9
Q10
F11
K12
G19
G22
K23
V27
K28
R29
H30
L31
T32
G33
E34
F35
Y39
V47
I59
K60
Q69
L75
R76
Y80
I81
Q84
C86
V101
P102
R106
R110
V111
C112
I117
V118
L119
K123

V124
D125
K127
F138
H139
R140
K141
K142
N143
L144
Q145
Y146
Y147
D148
I149
S150
S153
N154
Y155
N156
F157
P160
L164
A165
R166
K167
F176
VAL
ALA
MET
PRO
PRO
ALA
LEU
ALA
PRO
GLU
VAL
VAL
MET
ASP
PRO
ALA
LEU
ALA
ALA
GLN
TVR
HIS
ASP
GLU
VAL

ALA
GLN
THR
ALA
LEU
PRO
ASP
GLU
ASP
ASP
ASP
LEU

- Molecule 3: GTP-binding nuclear protein Ran

Chain H:  52% 25% 21%

MET
ALA
ALA
GLY
GLY
P7
Q8
V9
Q10
F11
K12
L13
G17
D18
G19
G22
K23
T24
T25
R29
G33
L43
G44
V45
E46
V47
H48
P49
P58
I59
K60
V63
G68
Q69
L75
R76
Y80
I81
Q82
A83
Q84
C85
V92
V101
P102
R106

R110
V111
I117
V118
L119
N122
K123
V124
D125
I126
K127
K130
V131
K132
H139
R140
K141
L144
Q145
Y146
Y147
D148
I149
S150
S153
N156
P160
L164
F176
VAL
ALA
MET
PRO
PRO
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LEU
ALA
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GLU
VAL
VAL
MET
ASP
PRO
ALA
LEU
ALA
ALA
GLN

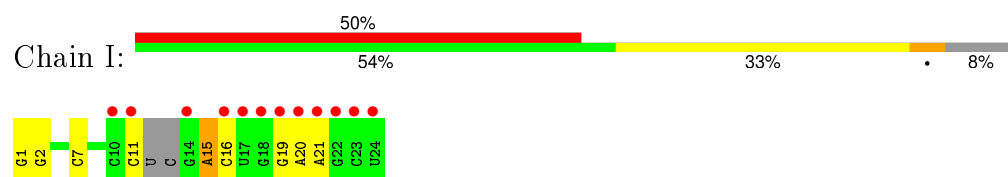
TYR
GLU
HIS
ASP
LEU
GLU
VAL
ALA
GLN
THR
THR
ALA
LEU
PRO
ASP
ASP
ASP
LEU

- Molecule 4: pre-microRNA

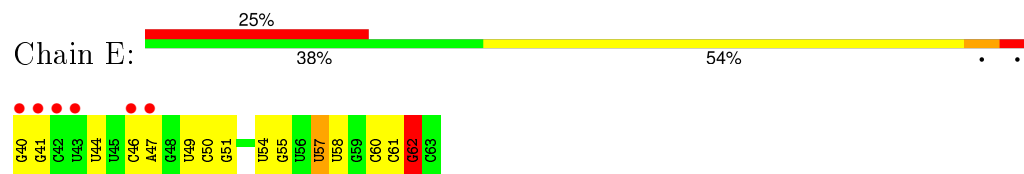
Chain D:  25% 42% 42% 8% 8%

G1
G2
U3
A4
A5
A6
U9
G10
C11
U
C
G14
A15
C16
U17
G18
G19
A20
A21
G22
C23
U24

- Molecule 4: pre-microRNA



- Molecule 5: pre-microRNA



- Molecule 5: pre-microRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.16Å 304.67Å 89.23Å 90.00° 110.79° 90.00°	Depositor
Resolution (Å)	39.84 – 2.92 62.93 – 2.92	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.84-2.92) 98.2 (62.93-2.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.20 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.247 , 0.312 0.245 , 0.311	Depositor DCC
R_{free} test set	3826 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	69.5	Xtriage
Anisotropy	0.745	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 69.9	EDS
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 74910 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	22052	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	1.06	12/8738 (0.1%)	1.00	23/11831 (0.2%)
1	F	0.88	8/8738 (0.1%)	0.86	7/11831 (0.1%)
3	C	0.87	0/1421	0.82	0/1918
3	H	0.84	0/1421	0.83	0/1918
4	D	1.25	3/521 (0.6%)	1.76	12/809 (1.5%)
4	I	1.11	0/521	1.68	9/809 (1.1%)
5	E	1.23	2/562 (0.4%)	1.75	17/874 (1.9%)
5	J	1.06	0/562	1.51	6/874 (0.7%)
All	All	0.98	25/22484 (0.1%)	1.03	74/30864 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	237	TRP	CG-CD2	14.20	1.67	1.43
1	A	237	TRP	CZ3-CH2	13.24	1.61	1.40
1	A	165	VAL	CA-CB	9.13	1.74	1.54
1	A	237	TRP	CG-CD1	-8.79	1.24	1.36
4	D	1	G	N9-C8	-8.53	1.31	1.37

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	1	G	O4'-C1'-N9	11.60	117.48	108.20
1	A	237	TRP	CD1-NE1-CE2	10.62	118.56	109.00
4	I	2	G	C5-C6-O6	-10.20	122.48	128.60
1	A	237	TRP	CG-CD1-NE1	-10.03	100.07	110.10
4	D	1	G	C4-C5-N7	-9.08	107.17	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	583	PHE	Peptide

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	8570	0	8664	292	0
1	F	8570	0	8664	267	0
2	B	66	0	15	0	0
2	G	66	0	15	1	0
3	C	1386	0	1408	34	0
3	H	1386	0	1408	40	0
4	D	466	0	242	1	0
4	I	466	0	242	0	0
5	E	505	0	258	5	0
5	J	505	0	258	6	0
6	C	32	0	12	9	0
6	H	32	0	12	7	0
7	C	1	0	0	0	0
7	H	1	0	0	0	0
All	All	22052	0	21198	630	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 15.

The worst 5 of 630 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:105:ILE:CG1	1:A:105:ILE:CD1	1.78	1.57
1:A:543:THR:HG22	1:A:545:ASP:H	1.17	1.09
1:F:495:VAL:O	1:F:496:PHE:CD1	2.15	0.99
1:A:168:GLN:HB2	1:A:175:ARG:HD2	1.41	0.99
1:A:545:ASP:OD2	1:A:548:ILE:HG12	1.63	0.99

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	1062/1204 (88%)	965 (91%)	73 (7%)	24 (2%)	8	29
1	F	1062/1204 (88%)	948 (89%)	92 (9%)	22 (2%)	9	32
3	C	168/216 (78%)	154 (92%)	11 (6%)	3 (2%)	11	36
3	H	168/216 (78%)	152 (90%)	15 (9%)	1 (1%)	30	66
All	All	2460/2840 (87%)	2219 (90%)	191 (8%)	50 (2%)	9	33

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	GLU
1	A	211	THR
1	A	245	ALA
1	A	340	ASP
1	A	712	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	967/1073 (90%)	895 (93%)	72 (7%)	17	44
1	F	967/1073 (90%)	885 (92%)	82 (8%)	13	36
3	C	150/185 (81%)	143 (95%)	7 (5%)	32	68
3	H	150/185 (81%)	144 (96%)	6 (4%)	38	73
All	All	2234/2516 (89%)	2067 (92%)	167 (8%)	17	43

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	84	GLN
1	F	188	ARG
1	F	1041	THR
3	C	141	LYS
1	F	39	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1058	GLN
1	F	149	GLN
1	F	935	ASN
3	C	30	HIS
3	C	173	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	20/24 (83%)	7 (35%)	0
4	I	20/24 (83%)	6 (30%)	0
5	E	23/24 (95%)	4 (17%)	0
5	J	23/24 (95%)	3 (13%)	0
All	All	86/96 (89%)	20 (23%)	0

5 of 20 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	6	A

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Mol	Chain	Res	Type
4	D	11	C
4	D	15	A
4	D	16	C
4	D	19	G

There are no RNA pucker outliers to report.

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
6	GTP	C	1177	7	25,34,34	1.11	2 (8%)	34,54,54	2.09	10 (29%)
6	GTP	H	1177	7	25,34,34	0.95	1 (4%)	34,54,54	2.42	12 (35%)

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
6	GTP	C	1177	7	-	0/18/38/38	0/3/3/3
6	GTP	H	1177	7	-	0/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	1177	GTP	C6-N1	2.08	1.37	1.33
6	C	1177	GTP	C2-N1	2.66	1.40	1.35
6	C	1177	GTP	C6-N1	3.76	1.40	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	1177	GTP	O3A-PA-O5'	-5.89	87.31	102.94
6	H	1177	GTP	C2'-C1'-N9	-5.26	106.26	114.29
6	C	1177	GTP	PB-O3B-PG	-5.12	115.51	132.67
6	C	1177	GTP	N3-C2-N1	-4.80	120.13	127.44
6	H	1177	GTP	N3-C2-N1	-4.49	120.61	127.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1177	GTP	9	0
6	H	1177	GTP	7	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	1072/1204 (89%)	0.20	36 (3%) 49 42	32, 76, 127, 156	0
1	F	1072/1204 (89%)	0.48	95 (8%) 12 8	59, 94, 143, 162	0
2	B	0/13	-	-	-	-
2	G	0/13	-	-	-	-
3	C	170/216 (78%)	0.38	7 (4%) 41 35	59, 90, 115, 127	0
3	H	170/216 (78%)	0.25	1 (0%) 90 89	64, 88, 111, 122	0
4	D	22/24 (91%)	1.06	6 (27%) 1 0	62, 126, 220, 227	0
4	I	22/24 (91%)	2.08	12 (54%) 0 0	71, 191, 259, 263	0
5	E	24/24 (100%)	1.06	6 (25%) 1 0	78, 118, 205, 210	0
5	J	24/24 (100%)	2.06	6 (25%) 1 0	121, 170, 256, 271	0
All	All	2576/2962 (86%)	0.38	169 (6%) 22 16	32, 86, 141, 271	0

The worst 5 of 169 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	J	40	G	13.4
1	F	819	PRO	8.8
1	F	4	ASP	8.8
1	F	823	LEU	7.7
1	F	820	LEU	6.8

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
7	MG	H	1178	1/1	0.96	0.23	-0.05	74,74,74,74	0
6	GTP	H	1177	32/32	0.94	0.18	-0.61	92,100,112,115	0
6	GTP	C	1177	32/32	0.93	0.17	-0.88	96,101,105,106	0
7	MG	C	1178	1/1	0.99	0.16	-2.89	85,85,85,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.