



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:51 AM GMT

PDB ID : 3NBZ
Title : Crystal structure of the HIV-1 Rev NES-CRM1-RanGTP nuclear export complex (crystal I)
Authors : Guttler, T.; Madl, T.; Neumann, P.; Deichsel, D.; Corsini, L.; Monecke, T.; Ficner, R.; Sattler, M.; Gorlich, D.
Deposited on : 2010-06-04
Resolution : 2.80 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

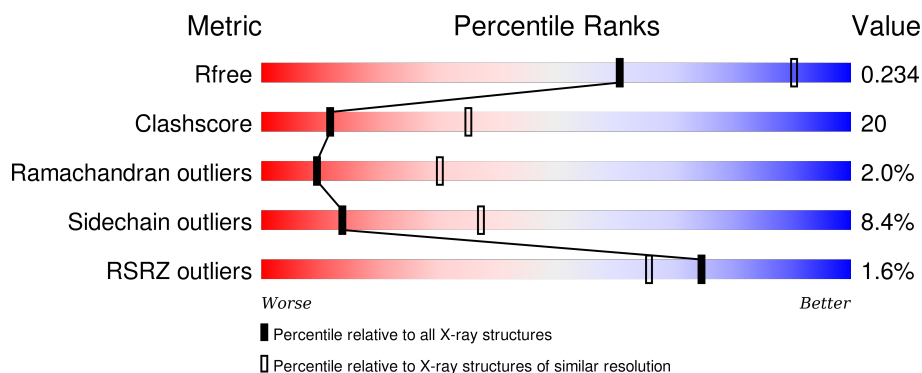
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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	1073	<div> <div>2%</div> <div>58%</div> <div>34%</div> <div>• •</div> </div>
1	D	1073	<div> <div>2%</div> <div>57%</div> <div>35%</div> <div>• •</div> </div>
2	B	362	<div> <div>2%</div> <div>42%</div> <div>33%</div> <div>6%</div> <div>20%</div> </div>
2	E	362	<div> <div>2%</div> <div>45%</div> <div>32%</div> <div>•</div> <div>19%</div> </div>
3	C	176	<div> <div>2%</div> <div>61%</div> <div>31%</div> <div>6%</div> <div>•</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	176	<div><div><div>%</div><div><div></div></div><div>56%</div><div>37%</div><div>5% •</div></div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 25144 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-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1038	Total	C	N	O	S	0	0	0
			8394	5387	1411	1543	53			
1	D	1038	Total	C	N	O	S	0	0	0
			8394	5387	1411	1543	53			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q6P5F9
A	0	SER	-	expression tag	UNP Q6P5F9
D	-1	GLY	-	expression tag	UNP Q6P5F9
D	0	SER	-	expression tag	UNP Q6P5F9

- Molecule 2 is a protein called Snurportin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	291	Total	C	N	O	S	0	0	0
			2339	1491	403	430	15			
2	E	293	Total	C	N	O	S	0	0	0
			2354	1500	405	434	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP O95149
B	0	SER	-	expression tag	UNP O95149
B	1	PRO	-	expression tag	UNP O95149
B	2	VAL	-	expression tag	UNP O95149
B	3	PRO	-	expression tag	UNP O95149
B	4	LEU	-	expression tag	UNP O95149
B	5	GLN	-	expression tag	UNP O95149
B	6	LEU	-	expression tag	UNP O95149

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	7	PRO	-	expression tag	UNP O95149
B	8	PRO	-	expression tag	UNP O95149
B	9	LEU	-	expression tag	UNP O95149
B	10	GLU	-	expression tag	UNP O95149
B	11	ARG	-	expression tag	UNP O95149
B	12	LEU	-	expression tag	UNP O95149
B	13	THR	-	expression tag	UNP O95149
B	14	LEU	-	expression tag	UNP O95149
E	-1	GLY	-	expression tag	UNP O95149
E	0	SER	-	expression tag	UNP O95149
E	1	PRO	-	expression tag	UNP O95149
E	2	VAL	-	expression tag	UNP O95149
E	3	PRO	-	expression tag	UNP O95149
E	4	LEU	-	expression tag	UNP O95149
E	5	GLN	-	expression tag	UNP O95149
E	6	LEU	-	expression tag	UNP O95149
E	7	PRO	-	expression tag	UNP O95149
E	8	PRO	-	expression tag	UNP O95149
E	9	LEU	-	expression tag	UNP O95149
E	10	GLU	-	expression tag	UNP O95149
E	11	ARG	-	expression tag	UNP O95149
E	12	LEU	-	expression tag	UNP O95149
E	13	THR	-	expression tag	UNP O95149
E	14	LEU	-	expression tag	UNP O95149

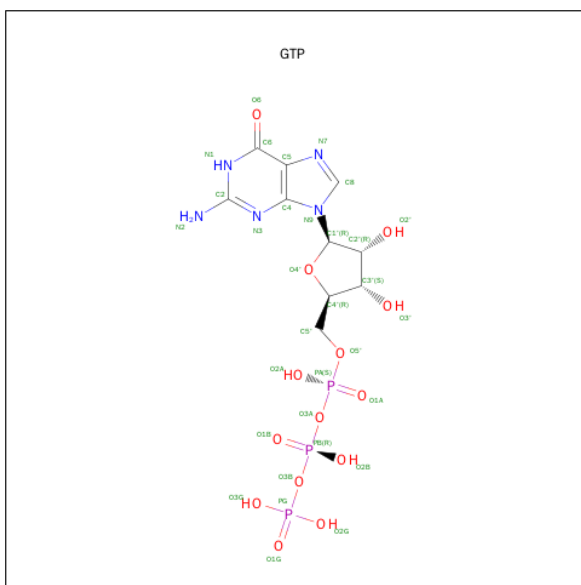
- Molecule 3 is a protein called GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	173	Total	C	N	O	S	0	0	0
			1405	914	246	240	5			
3	F	173	Total	C	N	O	S	0	0	0
			1405	914	246	240	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	69	LEU	GLN	engineered	UNP P62826
F	69	LEU	GLN	engineered	UNP P62826

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	1	Total	Na	0	0
			1	1		
6	C	1	Total	Na	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	237	Total	O	0	0
			237	237		

Continued on next page...

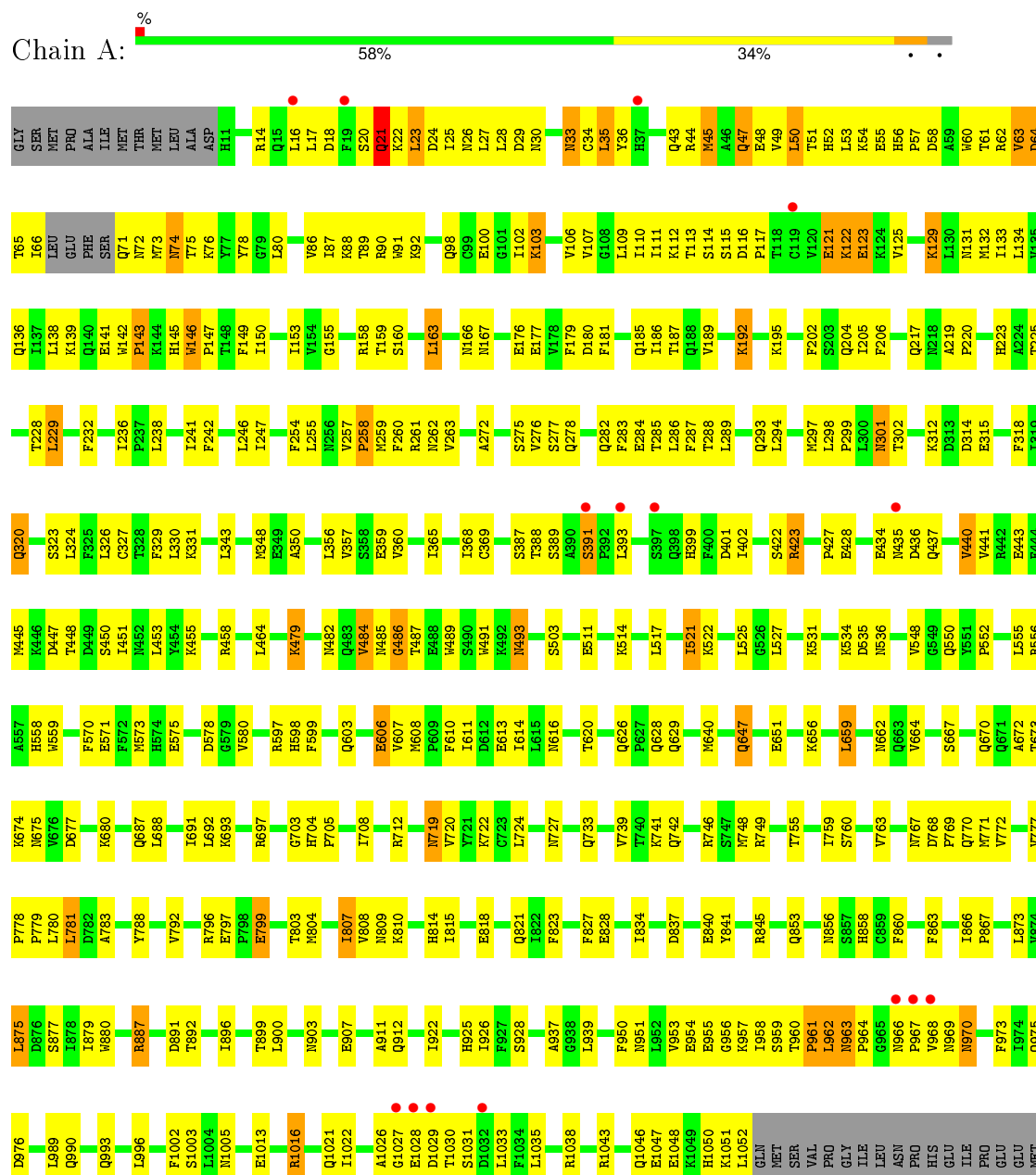
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	94	Total 94	O 94	0	0
7	C	53	Total 53	O 53	0	0
7	D	279	Total 279	O 279	0	0
7	E	71	Total 71	O 71	0	0
7	F	51	Total 51	O 51	0	0

3 Residue-property plots

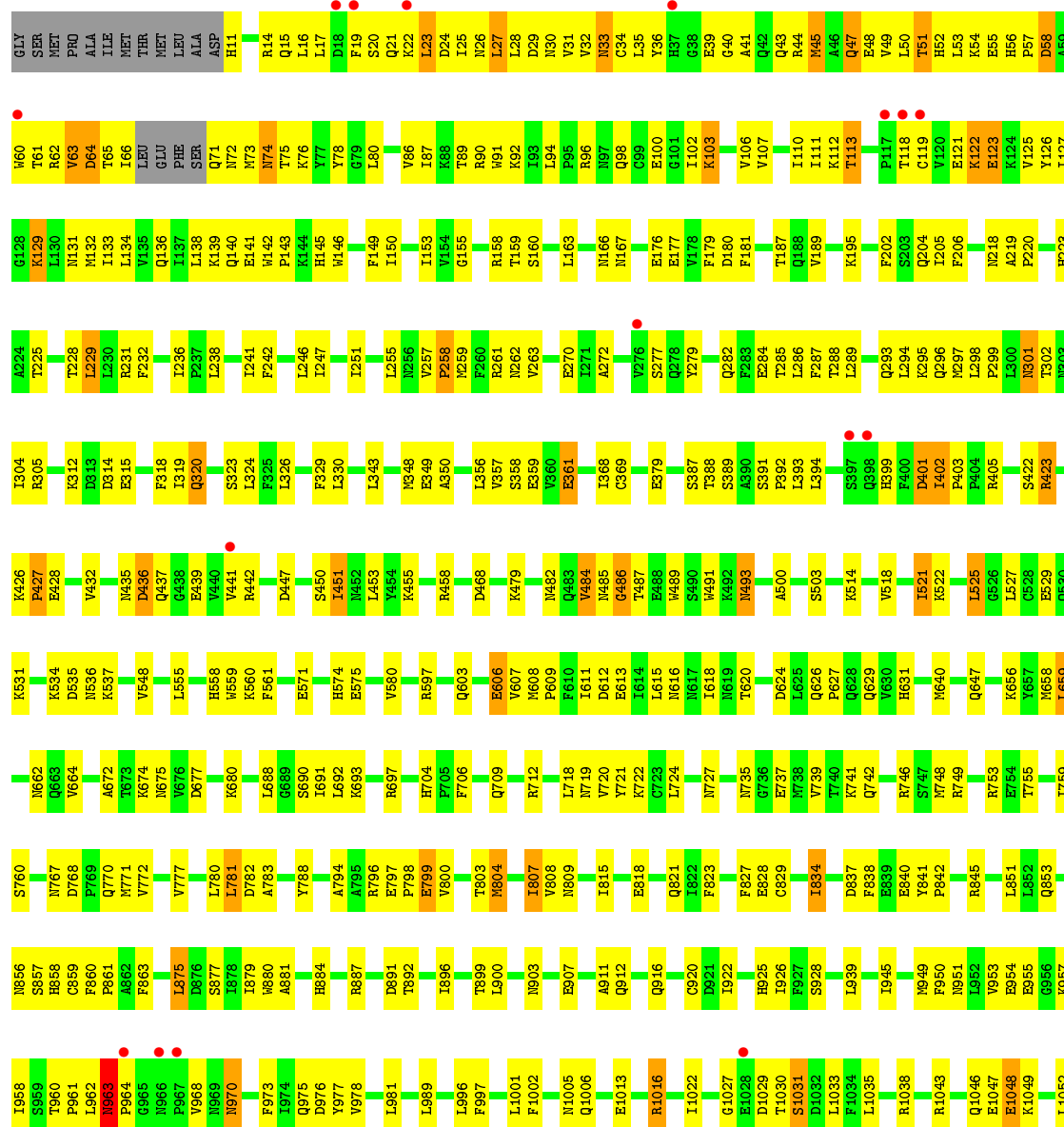
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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-1

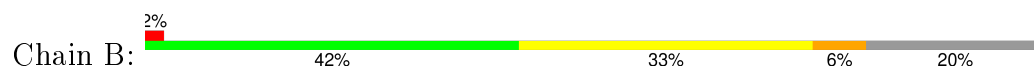


CYS
ASP

• Molecule 1: Exportin-1

GLN
MET
SER
PRO
VAL
GLY
ILE
LEU
ASN
HIS
GLU
PHE
MET
CYS
ASP

• Molecule 2: Snurportin-1



I87	I88	M89	F90	D91	V92	T93	S94	M100	V101	H105	R106	V109	R110	E113	N114	I117	G120	G121	N122	K123	A133	I136	V137	F138	H139	R140	K141	K142	M143	L144	Q145	Y146	Y147	S153	N154	Y155	N156	F157	L164	L174	E175	F176	V177	A178	M179	P180
-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.66Å 224.62Å 164.02Å 90.00° 100.82° 90.00°	Depositor
Resolution (Å)	38.90 – 2.80 38.90 – 2.80	Depositor EDS
% Data completeness (in resolution range)	90.1 (38.90-2.80) 81.4 (38.90-2.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.226 , 0.285 0.224 , 0.234	Depositor DCC
R_{free} test set	5700 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.3	EDS
Estimated twinning fraction	0.119 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	1 of 114007 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	25144	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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: GTP, NA, 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	0.31	0/8566	0.47	0/11604
1	D	0.31	0/8566	0.48	0/11604
2	B	0.34	0/2404	0.53	0/3263
2	E	0.34	0/2419	0.53	0/3283
3	C	0.32	0/1440	0.48	0/1945
3	F	0.32	0/1440	0.49	0/1945
All	All	0.32	0/24835	0.49	0/33644

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	8394	0	8460	325	0
1	D	8394	0	8460	347	0
2	B	2339	0	2295	114	0
2	E	2354	0	2311	110	0
3	C	1405	0	1434	52	0
3	F	1405	0	1434	62	0
4	C	32	0	12	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	32	0	12	2	0
5	C	1	0	0	0	0
5	F	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	237	0	0	17	0
7	B	94	0	0	7	0
7	C	53	0	0	6	0
7	D	279	0	0	22	0
7	E	71	0	0	3	0
7	F	51	0	0	6	0
All	All	25144	0	24418	992	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 20.

The worst 5 of 992 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:E:290:VAL:H	2:E:291:PRO:HD3	1.09	1.10
2:B:52:LYS:HZ3	2:B:264:THR:HA	1.17	1.08
2:E:52:LYS:HZ3	2:E:264:THR:HA	1.18	1.02
1:D:45:MET:HE3	3:F:44:GLY:HA3	1.46	0.98
1:A:131:ASN:HD21	1:A:166:ASN:HD21	1.12	0.95

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	1034/1073 (96%)	931 (90%)	85 (8%)	18 (2%)	11 36

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	1034/1073 (96%)	933 (90%)	83 (8%)	18 (2%)	11	36
2	B	285/362 (79%)	251 (88%)	23 (8%)	11 (4%)	4	12
2	E	287/362 (79%)	249 (87%)	28 (10%)	10 (4%)	4	15
3	C	171/176 (97%)	157 (92%)	13 (8%)	1 (1%)	30	65
3	F	171/176 (97%)	154 (90%)	16 (9%)	1 (1%)	30	65
All	All	2982/3222 (93%)	2675 (90%)	248 (8%)	59 (2%)	9	30

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
1	A	963	ASN
2	B	216	GLU
1	D	123	GLU
1	D	963	ASN

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	942/973 (97%)	869 (92%)	73 (8%)	16	41
1	D	942/973 (97%)	870 (92%)	72 (8%)	16	42
2	B	263/327 (80%)	236 (90%)	27 (10%)	9	26
2	E	265/327 (81%)	244 (92%)	21 (8%)	15	40
3	C	152/154 (99%)	136 (90%)	16 (10%)	8	24
3	F	152/154 (99%)	133 (88%)	19 (12%)	6	17
All	All	2716/2908 (93%)	2488 (92%)	228 (8%)	14	37

5 of 228 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	38	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	74	ASN
3	F	9	VAL
3	C	51	VAL
3	C	156	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	30	HIS
1	D	165	GLN
2	E	200	GLN
3	C	82	GLN
3	C	156	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 6 ligands modelled in this entry, 4 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
4	GTP	C	217	5	25,34,34	0.95	1 (4%)	34,54,54	1.87	8 (23%)
4	GTP	F	217	5	25,34,34	0.92	1 (4%)	34,54,54	1.79	8 (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
4	GTP	C	217	5	-	0/18/38/38	0/3/3/3
4	GTP	F	217	5	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	217	GTP	C6-N1	2.60	1.37	1.33
4	F	217	GTP	C6-N1	2.75	1.38	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	217	GTP	N3-C2-N1	-5.17	119.58	127.44
4	F	217	GTP	PA-O3A-PB	-4.95	118.84	132.73
4	F	217	GTP	N3-C2-N1	-4.71	120.27	127.44
4	C	217	GTP	PB-O3B-PG	-4.61	117.22	132.67
4	C	217	GTP	PA-O3A-PB	-3.25	123.61	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	217	GTP	4	0
4	F	217	GTP	2	0

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 [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	1038/1073 (96%)	-0.20	15 (1%) 78 69	14, 47, 107, 152	0
1	D	1038/1073 (96%)	-0.16	16 (1%) 76 68	14, 47, 103, 176	0
2	B	291/362 (80%)	-0.11	9 (3%) 52 40	15, 44, 116, 167	0
2	E	293/362 (80%)	-0.12	7 (2%) 62 50	15, 45, 123, 167	0
3	C	173/176 (98%)	-0.31	1 (0%) 90 86	21, 39, 79, 132	0
3	F	173/176 (98%)	-0.28	1 (0%) 90 86	20, 39, 79, 106	0
All	All	3006/3222 (93%)	-0.18	49 (1%) 74 66	14, 45, 106, 176	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	966	ASN	6.8
1	A	967	PRO	6.1
2	B	32	LYS	5.9
1	D	1028	GLU	4.9
2	E	360	ASN	4.9

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
5	MG	F	218	1/1	0.95	0.17	0.48	26,26,26,26	0
4	GTP	F	217	32/32	0.97	0.16	-0.10	16,34,50,56	0
6	NA	D	1072	1/1	0.85	0.19	-0.70	52,52,52,52	0
4	GTP	C	217	32/32	0.97	0.15	-0.82	12,29,37,71	0
5	MG	C	218	1/1	0.97	0.13	-0.87	14,14,14,14	0
6	NA	C	1	1/1	0.93	0.20	-	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.