



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:41 am BST

PDB ID : 3WXM  
Title : Crystal structure of archaeal Pelota and GTP-bound EF1 alpha complex  
Authors : Kobayashi, K.; Ishitani, R.; Nureki, O.  
Deposited on : 2014-08-04  
Resolution : 2.30 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

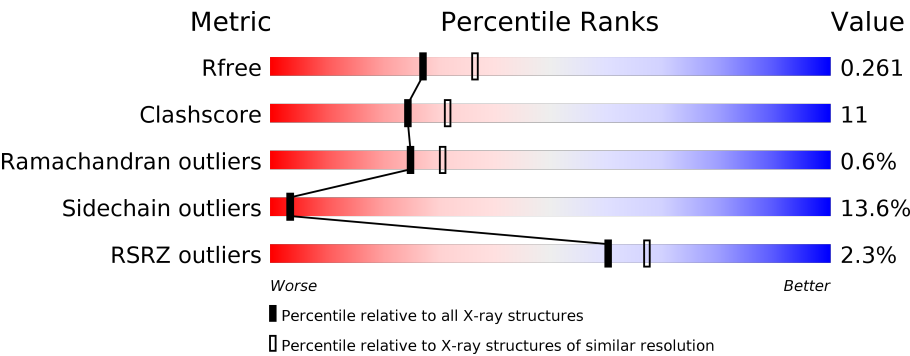
# 1 Overall quality at a glance i

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	447	<div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>68%25%••</div></div>
1	C	447	<div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>74%17%5%•</div></div>
1	E	447	<div><div>2%</div><div><div></div><div></div><div></div><div></div></div><div>70%23%••</div></div>
1	G	447	<div><div>5%</div><div><div></div><div></div><div></div><div></div></div><div>69%23%5%•</div></div>
2	B	376	<div><div>2%</div><div><div></div><div></div><div></div><div></div></div><div>63%26%6%•5%</div></div>
2	D	376	<div><div>2%</div><div><div></div><div></div><div></div><div></div></div><div>63%25%7%5%</div></div>

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Mol	Chain	Length	Quality of chain
2	F	376	<div><div>2%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>61%</div><div>27%</div><div>6%</div><div>6%</div></div>
2	H	376	<div><div>3%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>63%</div><div>25%</div><div>6%</div><div>5%</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 25701 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 Elongation factor 1-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	0	0
			3340	2143	580	604	13			
1	C	431	Total	C	N	O	S	0	0	0
			3354	2152	582	607	13			
1	E	430	Total	C	N	O	S	0	1	0
			3347	2148	581	605	13			
1	G	432	Total	C	N	O	S	0	0	0
			3338	2142	579	604	13			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q9YAV0
A	-1	SER	-	EXPRESSION TAG	UNP Q9YAV0
A	0	HIS	-	EXPRESSION TAG	UNP Q9YAV0
A	438	LEU	-	EXPRESSION TAG	UNP Q9YAV0
A	439	ALA	-	EXPRESSION TAG	UNP Q9YAV0
A	440	ARG	-	EXPRESSION TAG	UNP Q9YAV0
A	441	GLY	-	EXPRESSION TAG	UNP Q9YAV0
A	442	SER	-	EXPRESSION TAG	UNP Q9YAV0
A	443	GLY	-	EXPRESSION TAG	UNP Q9YAV0
A	444	CYS	-	EXPRESSION TAG	UNP Q9YAV0
C	-2	GLY	-	EXPRESSION TAG	UNP Q9YAV0
C	-1	SER	-	EXPRESSION TAG	UNP Q9YAV0
C	0	HIS	-	EXPRESSION TAG	UNP Q9YAV0
C	438	LEU	-	EXPRESSION TAG	UNP Q9YAV0
C	439	ALA	-	EXPRESSION TAG	UNP Q9YAV0
C	440	ARG	-	EXPRESSION TAG	UNP Q9YAV0
C	441	GLY	-	EXPRESSION TAG	UNP Q9YAV0
C	442	SER	-	EXPRESSION TAG	UNP Q9YAV0
C	443	GLY	-	EXPRESSION TAG	UNP Q9YAV0
C	444	CYS	-	EXPRESSION TAG	UNP Q9YAV0
E	-2	GLY	-	EXPRESSION TAG	UNP Q9YAV0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	EXPRESSION TAG	UNP Q9YAV0
E	0	HIS	-	EXPRESSION TAG	UNP Q9YAV0
E	438	LEU	-	EXPRESSION TAG	UNP Q9YAV0
E	439	ALA	-	EXPRESSION TAG	UNP Q9YAV0
E	440	ARG	-	EXPRESSION TAG	UNP Q9YAV0
E	441	GLY	-	EXPRESSION TAG	UNP Q9YAV0
E	442	SER	-	EXPRESSION TAG	UNP Q9YAV0
E	443	GLY	-	EXPRESSION TAG	UNP Q9YAV0
E	444	CYS	-	EXPRESSION TAG	UNP Q9YAV0
G	-2	GLY	-	EXPRESSION TAG	UNP Q9YAV0
G	-1	SER	-	EXPRESSION TAG	UNP Q9YAV0
G	0	HIS	-	EXPRESSION TAG	UNP Q9YAV0
G	438	LEU	-	EXPRESSION TAG	UNP Q9YAV0
G	439	ALA	-	EXPRESSION TAG	UNP Q9YAV0
G	440	ARG	-	EXPRESSION TAG	UNP Q9YAV0
G	441	GLY	-	EXPRESSION TAG	UNP Q9YAV0
G	442	SER	-	EXPRESSION TAG	UNP Q9YAV0
G	443	GLY	-	EXPRESSION TAG	UNP Q9YAV0
G	444	CYS	-	EXPRESSION TAG	UNP Q9YAV0

- Molecule 2 is a protein called Protein pelota homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	357	Total	C	N	O	S	0	0	0
			2722	1699	508	508	7			
2	D	357	Total	C	N	O	S	0	0	0
			2727	1701	509	510	7			
2	F	355	Total	C	N	O	S	0	0	0
			2692	1685	502	498	7			
2	H	356	Total	C	N	O	S	0	0	0
			2700	1685	506	502	7			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	EXPRESSION TAG	UNP Q9YAZ5
B	-18	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
B	-17	SER	-	EXPRESSION TAG	UNP Q9YAZ5
B	-16	SER	-	EXPRESSION TAG	UNP Q9YAZ5
B	-15	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
B	-14	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
B	-13	HIS	-	EXPRESSION TAG	UNP Q9YAZ5

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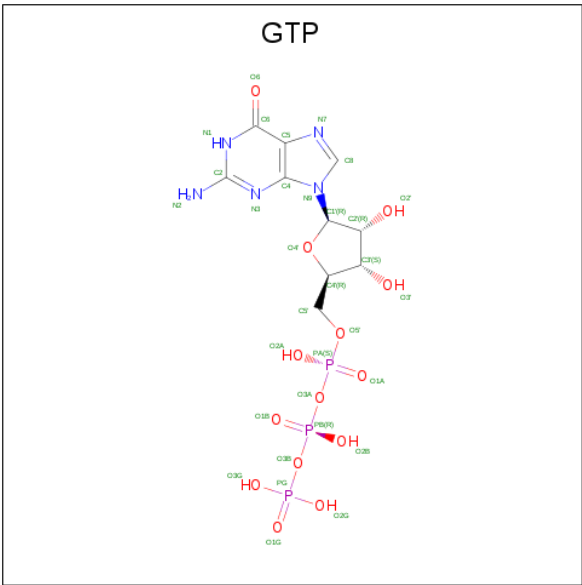
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
B	-11	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
B	-10	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
B	-9	SER	-	EXPRESSION TAG	UNP Q9YAZ5
B	-8	SER	-	EXPRESSION TAG	UNP Q9YAZ5
B	-7	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
B	-6	LEU	-	EXPRESSION TAG	UNP Q9YAZ5
B	-5	VAL	-	EXPRESSION TAG	UNP Q9YAZ5
B	-4	PRO	-	EXPRESSION TAG	UNP Q9YAZ5
B	-3	ARG	-	EXPRESSION TAG	UNP Q9YAZ5
B	-2	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
B	-1	SER	-	EXPRESSION TAG	UNP Q9YAZ5
B	0	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-19	MET	-	EXPRESSION TAG	UNP Q9YAZ5
D	-18	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
D	-17	SER	-	EXPRESSION TAG	UNP Q9YAZ5
D	-16	SER	-	EXPRESSION TAG	UNP Q9YAZ5
D	-15	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-14	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-13	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-12	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-11	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-10	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
D	-9	SER	-	EXPRESSION TAG	UNP Q9YAZ5
D	-8	SER	-	EXPRESSION TAG	UNP Q9YAZ5
D	-7	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
D	-6	LEU	-	EXPRESSION TAG	UNP Q9YAZ5
D	-5	VAL	-	EXPRESSION TAG	UNP Q9YAZ5
D	-4	PRO	-	EXPRESSION TAG	UNP Q9YAZ5
D	-3	ARG	-	EXPRESSION TAG	UNP Q9YAZ5
D	-2	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
D	-1	SER	-	EXPRESSION TAG	UNP Q9YAZ5
D	0	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-19	MET	-	EXPRESSION TAG	UNP Q9YAZ5
F	-18	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
F	-17	SER	-	EXPRESSION TAG	UNP Q9YAZ5
F	-16	SER	-	EXPRESSION TAG	UNP Q9YAZ5
F	-15	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-14	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-13	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-12	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-11	HIS	-	EXPRESSION TAG	UNP Q9YAZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-10	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
F	-9	SER	-	EXPRESSION TAG	UNP Q9YAZ5
F	-8	SER	-	EXPRESSION TAG	UNP Q9YAZ5
F	-7	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
F	-6	LEU	-	EXPRESSION TAG	UNP Q9YAZ5
F	-5	VAL	-	EXPRESSION TAG	UNP Q9YAZ5
F	-4	PRO	-	EXPRESSION TAG	UNP Q9YAZ5
F	-3	ARG	-	EXPRESSION TAG	UNP Q9YAZ5
F	-2	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
F	-1	SER	-	EXPRESSION TAG	UNP Q9YAZ5
F	0	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-19	MET	-	EXPRESSION TAG	UNP Q9YAZ5
H	-18	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
H	-17	SER	-	EXPRESSION TAG	UNP Q9YAZ5
H	-16	SER	-	EXPRESSION TAG	UNP Q9YAZ5
H	-15	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-14	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-13	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-12	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-11	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-10	HIS	-	EXPRESSION TAG	UNP Q9YAZ5
H	-9	SER	-	EXPRESSION TAG	UNP Q9YAZ5
H	-8	SER	-	EXPRESSION TAG	UNP Q9YAZ5
H	-7	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
H	-6	LEU	-	EXPRESSION TAG	UNP Q9YAZ5
H	-5	VAL	-	EXPRESSION TAG	UNP Q9YAZ5
H	-4	PRO	-	EXPRESSION TAG	UNP Q9YAZ5
H	-3	ARG	-	EXPRESSION TAG	UNP Q9YAZ5
H	-2	GLY	-	EXPRESSION TAG	UNP Q9YAZ5
H	-1	SER	-	EXPRESSION TAG	UNP Q9YAZ5
H	0	HIS	-	EXPRESSION TAG	UNP Q9YAZ5

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
3	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
3	E	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
3	G	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	222	Total	O	0	0
			222	222		

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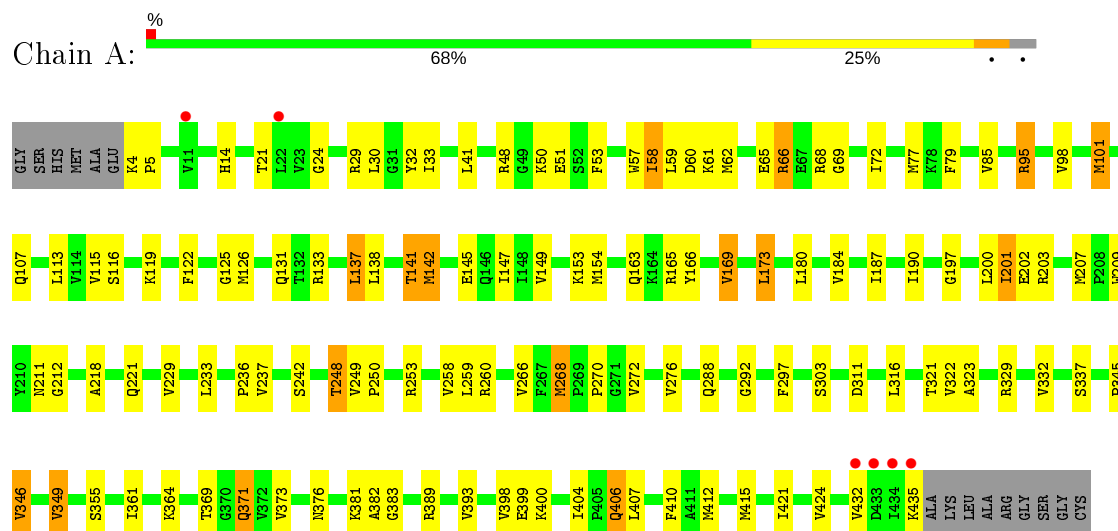
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	160	Total 160	O 160	0	0
5	C	192	Total 192	O 192	0	0
5	D	177	Total 177	O 177	0	0
5	E	178	Total 178	O 178	0	0
5	F	145	Total 145	O 145	0	0
5	G	124	Total 124	O 124	0	0
5	H	151	Total 151	O 151	0	0

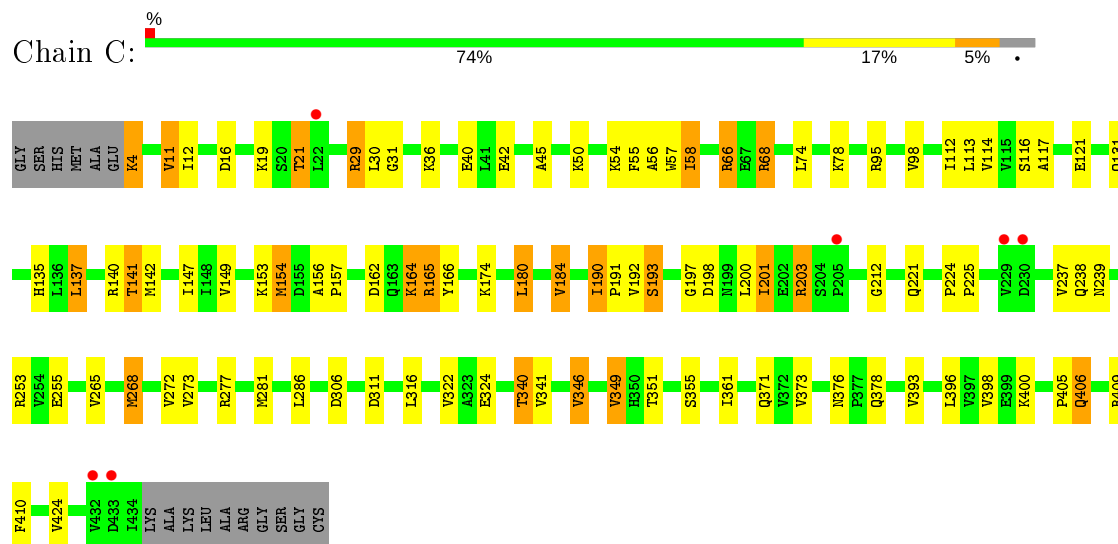
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Elongation factor 1-alpha

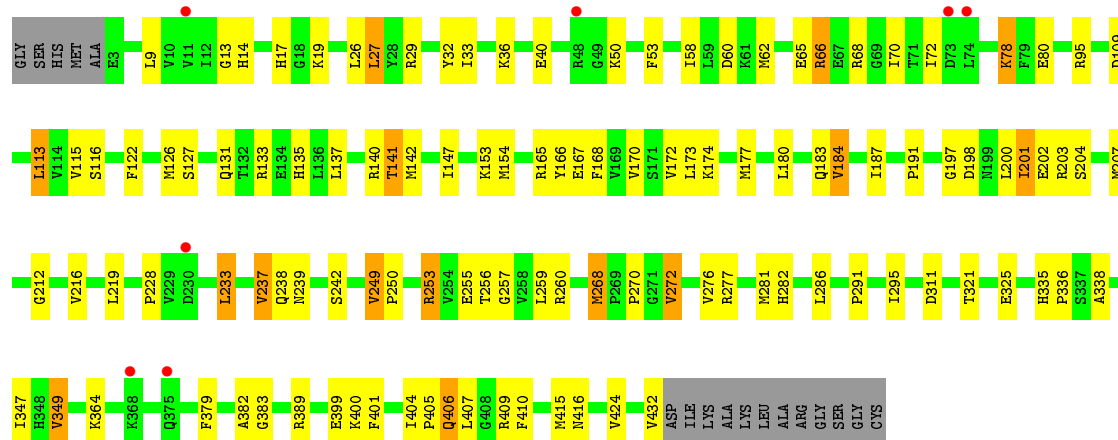


#### • Molecule 1: Elongation factor 1-alpha

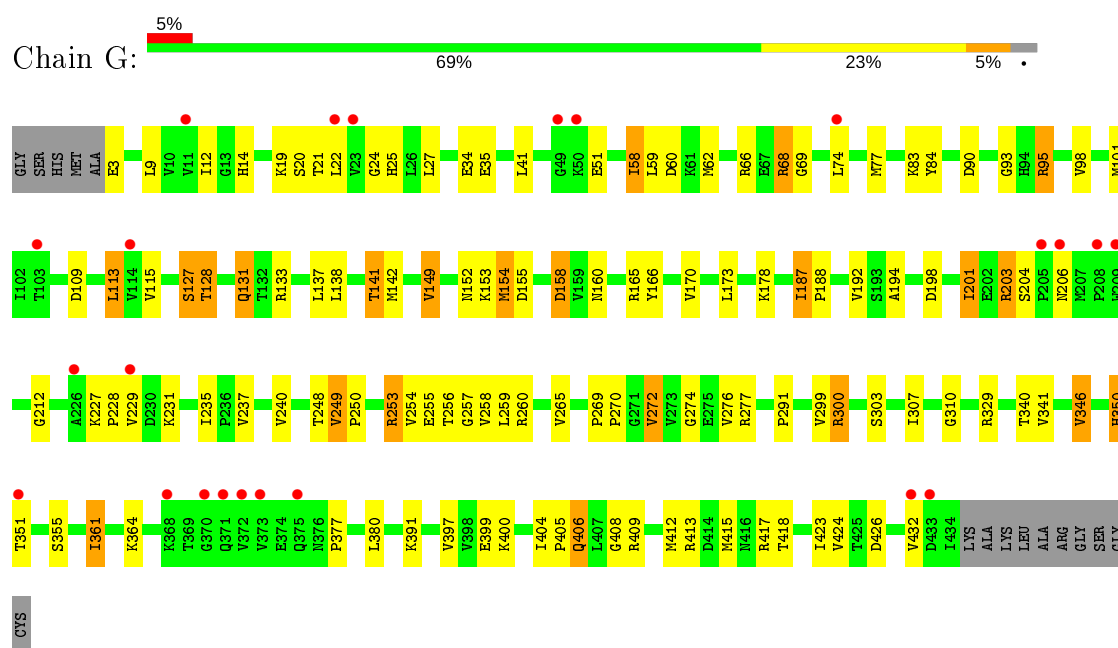


#### • Molecule 1: Elongation factor 1-alpha

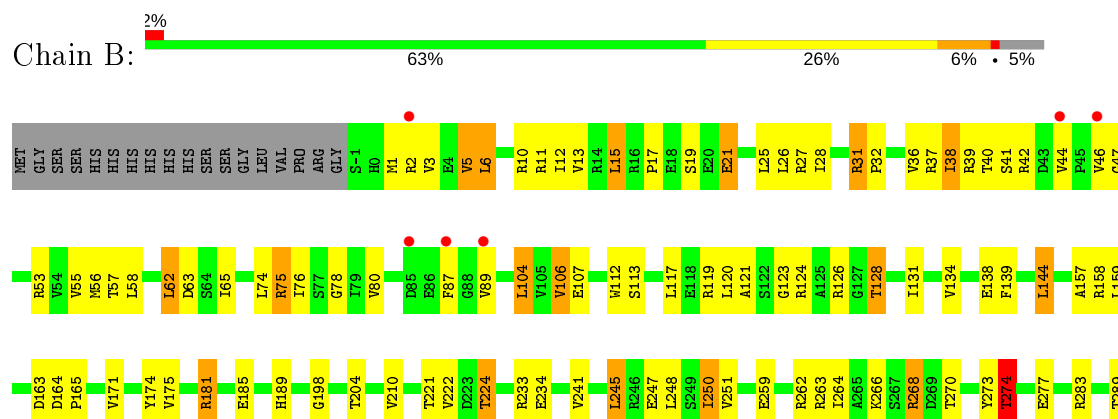




• Molecule 1: Elongation factor 1-alpha

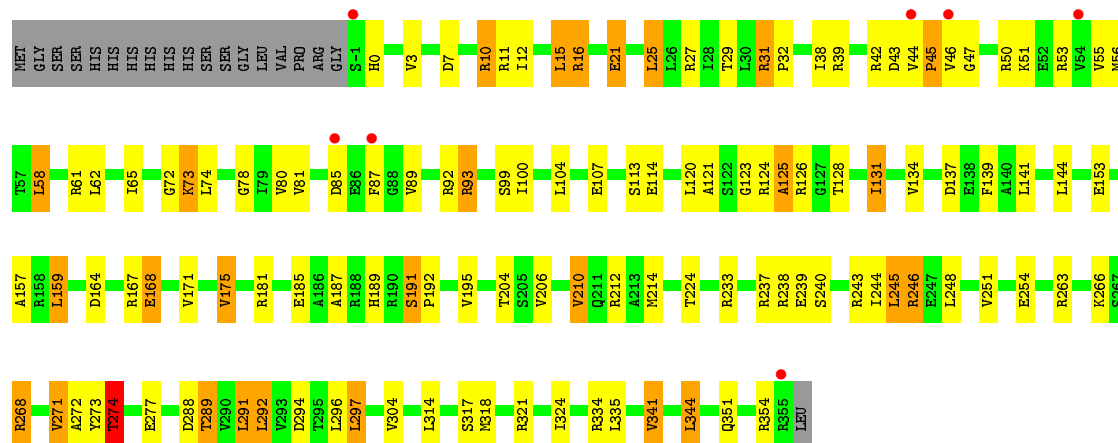


• Molecule 2: Protein pelota homolog

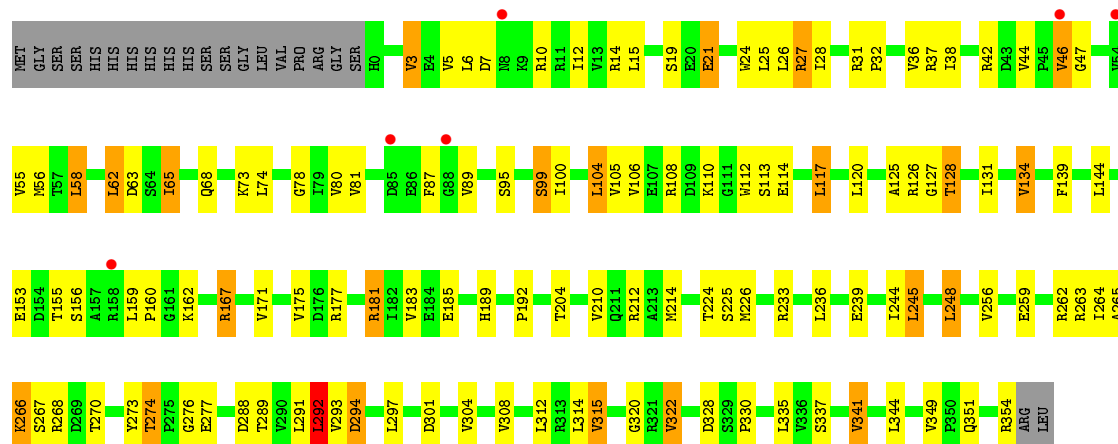




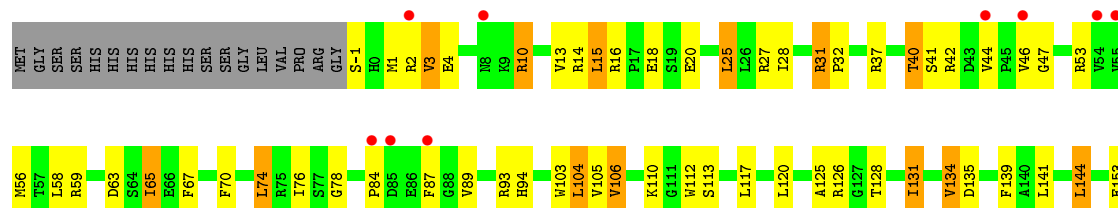
• Molecule 2: Protein pelota homolog



• Molecule 2: Protein pelota homolog



• Molecule 2: Protein pelota homolog





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.93Å 158.94Å 427.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.43 – 2.30 32.43 – 2.19	Depositor EDS
% Data completeness (in resolution range)	96.8 (32.43-2.30) 95.0 (32.43-2.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.63 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.3_1479)	Depositor
R, $R_{free}$	0.198 , 0.261 0.202 , 0.261	Depositor DCC
$R_{free}$ test set	12339 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	25701	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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

### 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	0.46	0/3414	0.62	0/4631
1	C	0.44	0/3428	0.62	0/4645
1	E	0.43	0/3424	0.61	0/4640
1	G	0.40	0/3412	0.57	0/4629
2	B	0.47	0/2758	0.67	3/3732 (0.1%)
2	D	0.46	0/2763	0.68	2/3738 (0.1%)
2	F	0.43	0/2728	0.63	2/3692 (0.1%)
2	H	0.42	0/2735	0.63	3/3702 (0.1%)
All	All	0.44	0/24662	0.63	10/33409 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	H	292	LEU	CA-CB-CG	7.05	131.52	115.30
2	B	292	LEU	CA-CB-CG	6.63	130.55	115.30
2	D	15	LEU	CA-CB-CG	6.36	129.92	115.30
2	F	104	LEU	CA-CB-CG	5.88	128.83	115.30
2	B	104	LEU	CA-CB-CG	5.84	128.74	115.30
2	F	292	LEU	CA-CB-CG	5.60	128.17	115.30
2	B	15	LEU	CA-CB-CG	5.48	127.91	115.30
2	H	104	LEU	CA-CB-CG	5.43	127.78	115.30
2	D	144	LEU	CA-CB-CG	5.34	127.59	115.30
2	H	144	LEU	CA-CB-CG	5.25	127.38	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-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 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	3340	0	3372	77	0
1	C	3354	0	3409	53	0
1	E	3347	0	3397	68	0
1	G	3338	0	3366	75	0
2	B	2722	0	2790	66	0
2	D	2727	0	2799	68	0
2	F	2692	0	2769	68	0
2	H	2700	0	2766	66	0
3	A	32	0	12	3	0
3	C	32	0	12	0	0
3	E	32	0	12	1	0
3	G	32	0	12	6	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	222	0	0	8	0
5	B	160	0	0	5	0
5	C	192	0	0	6	0
5	D	177	0	0	9	0
5	E	178	0	0	6	0
5	F	145	0	0	9	0
5	G	124	0	0	6	0
5	H	151	0	0	4	0
All	All	25701	0	24716	533	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 11.

All (533) 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:H:65:ILE:HG22	2:H:76:ILE:HG22	1.54	0.90
1:E:13:GLY:H	1:E:135:HIS:HD2	1.19	0.90
2:F:63:ASP:HB2	2:F:78:GLY:HA2	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:149:VAL:HG12	1:G:187:ILE:HD11	1.54	0.88
1:A:62:MET:HE3	1:A:72:ILE:HB	1.56	0.85
2:D:134:VAL:HG12	2:D:139:PHE:HD1	1.44	0.82
1:A:349:VAL:HG13	1:A:410:PHE:HB3	1.61	0.82
2:D:292:LEU:HB3	2:D:341:VAL:HG13	1.63	0.81
2:H:313:ARG:NE	5:H:547:HOH:O	2.15	0.78
1:C:117:ALA:O	1:C:165:ARG:NH1	2.16	0.77
2:D:27:ARG:NH1	2:D:294:ASP:OD2	2.17	0.77
1:G:21:THR:HG21	3:G:501:GTP:H8	1.50	0.77
2:F:181:ARG:NH2	2:F:185:GLU:OE1	2.19	0.76
2:D:31:ARG:HG3	2:D:32:PRO:HD2	1.67	0.75
1:A:126:MET:O	1:A:133:ARG:NH1	2.19	0.75
1:G:227:LYS:NZ	1:G:291:PRO:O	2.18	0.74
1:E:140:ARG:NH2	1:E:180:LEU:O	2.20	0.73
2:H:273:TYR:O	2:H:274:THR:HB	1.88	0.73
2:B:157:ALA:O	2:B:159:LEU:N	2.21	0.73
1:E:126:MET:O	1:E:133:ARG:NH1	2.20	0.73
1:C:16:ASP:OD1	5:C:605:HOH:O	2.07	0.72
2:H:42:ARG:NH2	2:H:93:ARG:O	2.23	0.72
1:G:21:THR:HG21	3:G:501:GTP:C8	2.25	0.71
2:F:259:GLU:OE2	2:F:262:ARG:NH1	2.24	0.71
1:E:113:LEU:HB2	1:E:147:ILE:HD11	1.72	0.71
1:C:68:ARG:O	5:C:771:HOH:O	2.07	0.71
1:E:203:ARG:NH1	1:E:212:GLY:O	2.23	0.71
1:A:381:LYS:NZ	5:A:740:HOH:O	2.25	0.70
1:C:378:GLN:NE2	5:C:663:HOH:O	2.25	0.70
2:D:42:ARG:NH2	2:D:93:ARG:O	2.26	0.69
2:B:75:ARG:HH22	1:E:277:ARG:HH11	1.40	0.69
2:F:10:ARG:NH1	5:F:446:HOH:O	2.25	0.69
1:A:119:LYS:O	5:A:626:HOH:O	2.11	0.68
2:B:233:ARG:NH1	5:B:539:HOH:O	2.24	0.68
1:G:361:ILE:HD11	1:G:377:PRO:HG2	1.76	0.68
2:D:134:VAL:HG12	2:D:139:PHE:CD1	2.28	0.68
2:H:16:ARG:HD2	2:H:103:TRP:CE2	2.29	0.67
2:H:292:LEU:HD12	2:H:324:ILE:HG12	1.76	0.67
2:B:28:ILE:O	2:B:31:ARG:NH1	2.26	0.67
1:C:238:GLN:HA	1:C:351:THR:HG21	1.77	0.67
2:B:75:ARG:NH2	1:E:277:ARG:HH11	1.92	0.66
1:A:253:ARG:HE	1:A:292:GLY:HA2	1.60	0.66
1:E:14:HIS:HB3	1:E:17:HIS:CE1	2.30	0.66
2:D:351:GLN:HA	2:D:354:ARG:HD2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:THR:HG21	1:A:303:SER:HA	1.76	0.66
2:B:321:ARG:NH1	5:B:442:HOH:O	2.28	0.65
2:F:21:GLU:HG3	2:F:125:ALA:HA	1.78	0.65
2:F:27:ARG:HA	2:F:65:ILE:HD11	1.78	0.65
1:C:137:LEU:O	1:C:141:THR:HG22	1.96	0.65
2:D:39:ARG:NH1	5:D:554:HOH:O	2.30	0.65
2:B:134:VAL:HG22	2:B:139:PHE:HD1	1.61	0.65
2:B:273:TYR:O	2:B:274:THR:HB	1.95	0.65
1:G:364:LYS:HB2	1:G:377:PRO:HG3	1.77	0.65
2:H:297:LEU:HD21	2:H:324:ILE:HD13	1.77	0.65
1:C:340:THR:HG22	2:D:334:ARG:HH21	1.63	0.64
2:D:212:ARG:NH2	5:D:519:HOH:O	2.29	0.64
1:C:174:LYS:HG3	1:C:184:VAL:HG11	1.79	0.64
1:E:259:LEU:HD11	1:E:276:VAL:HG21	1.78	0.64
2:H:10:ARG:NH1	5:H:424:HOH:O	2.31	0.64
2:D:16:ARG:NH2	5:D:496:HOH:O	2.30	0.64
2:H:63:ASP:HB2	2:H:78:GLY:HA2	1.80	0.63
2:F:42:ARG:NH1	5:F:452:HOH:O	2.32	0.63
1:C:21:THR:HG22	1:C:55:PHE:HB2	1.81	0.63
2:F:315:VAL:HG23	2:F:320:GLY:HA3	1.80	0.63
1:E:238:GLN:NE2	5:E:638:HOH:O	2.30	0.63
1:G:41:LEU:HD13	1:G:58:ILE:HG22	1.81	0.63
2:H:234:GLU:OE1	2:H:238:ARG:NH1	2.31	0.62
1:C:349:VAL:HG13	1:C:410:PHE:HB3	1.79	0.62
2:D:288:ASP:OD1	2:D:289:THR:HG22	1.99	0.62
1:A:60:ASP:O	1:A:66:ARG:NH2	2.33	0.62
1:G:20:SER:OG	1:G:90:ASP:OD2	2.16	0.62
2:H:27:ARG:NH1	2:H:294:ASP:OD2	2.32	0.62
1:E:399:GLU:HG2	1:E:404:ILE:HD12	1.80	0.62
1:C:42:GLU:HA	1:C:54:LYS:HD2	1.82	0.62
1:E:27:LEU:HB3	1:E:33:ILE:HD13	1.81	0.61
2:D:244:ILE:HG22	2:D:245:LEU:HD13	1.83	0.61
2:F:3:VAL:HB	2:F:15:LEU:HD23	1.82	0.61
2:F:292:LEU:HD23	2:F:341:VAL:HG13	1.81	0.61
2:H:37:ARG:NH2	5:H:539:HOH:O	2.32	0.61
1:A:346:VAL:HA	1:A:355:SER:HA	1.83	0.61
1:E:184:VAL:HA	1:E:187:ILE:HD12	1.82	0.61
1:G:12:ILE:HG13	1:G:113:LEU:HD23	1.83	0.61
1:G:240:VAL:HG21	1:G:307:ILE:HG13	1.81	0.61
2:B:274:THR:HG22	2:B:277:GLU:H	1.64	0.61
1:E:389:ARG:NH1	5:E:683:HOH:O	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:266:LYS:NZ	5:B:519:HOH:O	2.34	0.61
1:E:13:GLY:H	1:E:135:HIS:CD2	2.09	0.61
1:G:203:ARG:NH1	1:G:212:GLY:O	2.33	0.61
1:G:127:SER:OG	1:G:128:THR:N	2.31	0.60
1:C:29:ARG:HG2	1:C:201:ILE:HD12	1.84	0.60
2:F:273:TYR:O	2:F:274:THR:HB	2.00	0.60
2:H:106:VAL:HG22	2:H:112:TRP:HZ2	1.65	0.60
1:E:349:VAL:HG13	1:E:410:PHE:HB3	1.84	0.60
1:E:257:GLY:O	1:E:291:PRO:HD3	2.01	0.60
2:F:268:ARG:O	5:F:422:HOH:O	2.16	0.60
1:A:41:LEU:HD13	1:A:58:ILE:HG22	1.84	0.59
2:D:164:ASP:HB3	2:D:167:ARG:HB2	1.84	0.59
2:F:259:GLU:HA	2:F:262:ARG:NH1	2.17	0.59
1:A:21:THR:HG23	3:A:501:GTP:O2A	2.02	0.59
2:B:297:LEU:HD21	2:B:324:ILE:HD13	1.85	0.59
1:G:115:VAL:HG21	1:G:173:LEU:HD11	1.84	0.59
1:C:29:ARG:HH21	1:C:197:GLY:HA3	1.68	0.59
2:D:237:ARG:HG3	2:D:254:GLU:HG2	1.84	0.59
1:G:141:THR:O	1:G:409:ARG:HD3	2.01	0.59
1:E:325:GLU:OE1	1:E:389:ARG:NH1	2.35	0.58
2:B:13:VAL:HG23	2:B:112:TRP:CD1	2.39	0.58
1:C:55:PHE:O	1:C:58:ILE:HG12	2.02	0.58
1:A:163:GLN:HB2	1:A:209:TRP:CE2	2.38	0.58
2:B:106:VAL:HG22	2:B:112:TRP:HZ2	1.68	0.58
1:A:400:LYS:HA	1:A:424:VAL:HG22	1.86	0.58
2:D:10:ARG:NH1	2:D:114:GLU:OE2	2.33	0.58
1:A:137:LEU:O	1:A:141:THR:HG23	2.04	0.58
1:A:50:LYS:HB3	1:A:53:PHE:CD2	2.38	0.58
2:H:181:ARG:NH2	2:H:185:GLU:OE2	2.36	0.58
2:B:38:ILE:HD11	2:B:76:ILE:HD11	1.85	0.57
2:F:244:ILE:HG22	2:F:245:LEU:HD13	1.84	0.57
2:H:112:TRP:HB3	2:H:117:LEU:HD11	1.86	0.57
2:B:36:VAL:HG12	2:B:106:VAL:HB	1.87	0.57
2:F:14:ARG:HB2	2:F:105:VAL:HG22	1.85	0.57
2:F:351:GLN:HA	2:F:354:ARG:HG3	1.86	0.57
1:G:166:TYR:O	1:G:170:VAL:HG23	2.04	0.57
1:C:57:TRP:CD2	1:C:66:ARG:HD2	2.39	0.57
1:E:78:LYS:HD3	1:E:282:HIS:HB3	1.86	0.57
2:B:44:VAL:HG21	2:B:87:PHE:CD1	2.39	0.57
1:E:109:ASP:OD1	1:E:253:ARG:NH2	2.38	0.56
2:H:134:VAL:HG13	2:H:139:PHE:HD1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:237:VAL:HG13	1:C:311:ASP:O	2.05	0.56
1:E:116:SER:O	1:E:122:PHE:HB2	2.05	0.56
1:E:62:MET:HE3	1:E:72:ILE:HB	1.85	0.56
1:A:237:VAL:HG13	1:A:311:ASP:O	2.06	0.56
2:D:3:VAL:HG11	2:D:121:ALA:HB2	1.88	0.56
1:E:270:PRO:HB2	1:E:272:VAL:HG13	1.88	0.56
2:D:56:MET:HE1	2:D:89:VAL:HG21	1.88	0.56
2:F:265:ALA:C	2:F:267:SER:H	2.08	0.56
1:A:389:ARG:HD2	5:A:627:HOH:O	2.06	0.55
1:G:158:ASP:N	1:G:158:ASP:OD1	2.29	0.55
2:D:72:GLY:O	2:D:73:LYS:HD2	2.06	0.55
2:F:274:THR:HG22	2:F:276:GLY:H	1.70	0.55
1:G:257:GLY:O	1:G:291:PRO:HD3	2.06	0.55
1:G:198:ASP:OD1	1:G:204:SER:OG	2.17	0.55
1:G:269:PRO:HD3	1:G:397:VAL:HG23	1.89	0.55
1:A:201:ILE:H	1:A:201:ILE:HD13	1.71	0.55
2:B:28:ILE:HD12	2:B:324:ILE:HD12	1.88	0.55
2:D:27:ARG:HG2	2:D:27:ARG:HH11	1.72	0.55
2:H:20:GLU:OE2	2:H:70:PHE:N	2.35	0.55
1:C:273:VAL:HG13	1:C:316:LEU:HD11	1.89	0.54
1:A:260:ARG:NH1	1:A:288:GLN:OE1	2.40	0.54
2:B:351:GLN:HA	2:B:354:ARG:HD2	1.87	0.54
1:G:98:VAL:HG21	1:G:413:ARG:NH2	2.21	0.54
1:G:60:ASP:O	1:G:66:ARG:NH2	2.41	0.54
2:H:13:VAL:HG23	2:H:112:TRP:CD1	2.43	0.54
2:D:296:LEU:CD1	2:D:341:VAL:HG22	2.37	0.54
1:G:400:LYS:HE2	1:G:426:ASP:HA	1.90	0.54
1:A:101:MET:HE1	1:A:138:LEU:HD13	1.89	0.54
2:B:181:ARG:NH2	2:B:185:GLU:OE2	2.40	0.54
2:D:297:LEU:HD21	2:D:324:ILE:HD13	1.88	0.54
1:E:154:MET:HG2	1:E:207:MET:SD	2.47	0.54
1:E:281:MET:HB2	1:E:295:ILE:HG22	1.89	0.54
2:D:128:THR:HG21	2:D:189:HIS:HB3	1.90	0.54
1:C:40:GLU:OE1	5:C:655:HOH:O	2.18	0.53
2:F:10:ARG:HH11	2:F:10:ARG:HG3	1.73	0.53
1:G:399:GLU:HG2	1:G:404:ILE:HD12	1.90	0.53
2:B:144:LEU:HD11	2:B:250:ILE:HG21	1.90	0.53
2:F:171:VAL:O	2:F:175:VAL:HG13	2.09	0.53
2:F:28:ILE:O	2:F:31:ARG:NH1	2.40	0.53
1:E:13:GLY:N	1:E:135:HIS:HD2	1.97	0.53
2:F:128:THR:HG21	2:F:189:HIS:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:292:LEU:HD23	2:B:341:VAL:HG13	1.90	0.53
1:A:57:TRP:CE2	1:A:66:ARG:HD2	2.44	0.53
2:B:27:ARG:NH1	2:B:294:ASP:OD2	2.42	0.53
2:H:67:PHE:HB2	2:H:74:LEU:HD23	1.91	0.53
1:A:141:THR:HG21	1:A:421:ILE:HG21	1.89	0.53
1:G:153:LYS:HA	3:G:501:GTP:C6	2.44	0.53
2:F:155:THR:HG22	2:F:156:SER:O	2.09	0.52
1:A:399:GLU:HG2	1:A:404:ILE:HD12	1.92	0.52
2:D:246:ARG:NH1	5:D:543:HOH:O	2.29	0.52
2:H:244:ILE:HG22	2:H:245:LEU:HD13	1.92	0.52
1:E:50:LYS:HB3	1:E:53:PHE:CD1	2.44	0.52
2:D:92:ARG:NH2	5:D:401:HOH:O	2.41	0.52
2:D:273:TYR:O	2:D:274:THR:HB	2.10	0.52
2:B:1:MET:HG3	2:B:17:PRO:HA	1.92	0.52
1:G:361:ILE:HD12	1:G:380:LEU:HD11	1.91	0.52
2:D:237:ARG:NE	5:D:440:HOH:O	2.43	0.52
1:G:68:ARG:H	1:G:69:GLY:HA2	1.74	0.52
2:B:134:VAL:HG22	2:B:139:PHE:CD1	2.45	0.52
2:D:44:VAL:HG21	2:D:87:PHE:CD1	2.44	0.52
2:F:134:VAL:HG13	2:F:139:PHE:HD1	1.75	0.52
1:E:131:GLN:NE2	5:E:674:HOH:O	2.42	0.52
1:A:406:GLN:NE2	5:A:650:HOH:O	2.41	0.51
1:A:57:TRP:CD2	1:A:66:ARG:HD2	2.45	0.51
1:E:400:LYS:HA	1:E:424:VAL:HG22	1.92	0.51
1:A:169:VAL:HG23	1:A:173:LEU:HD22	1.91	0.51
2:B:31:ARG:HG3	2:B:32:PRO:HD2	1.92	0.51
1:C:400:LYS:HA	1:C:424:VAL:HG22	1.91	0.51
2:D:171:VAL:O	2:D:175:VAL:HG13	2.10	0.51
1:C:346:VAL:HA	1:C:355:SER:HA	1.92	0.51
1:C:57:TRP:CE2	1:C:66:ARG:HD2	2.45	0.51
2:D:56:MET:HE3	2:D:58:LEU:HD22	1.93	0.51
2:F:212:ARG:NH2	5:F:443:HOH:O	2.35	0.51
2:F:128:THR:O	2:F:192:PRO:HD2	2.11	0.51
2:H:158:ARG:N	5:H:472:HOH:O	2.33	0.51
2:F:301:ASP:HB3	2:F:304:VAL:HG13	1.91	0.51
1:G:400:LYS:HA	1:G:424:VAL:HG22	1.93	0.51
2:H:277:GLU:OE2	2:H:351:GLN:NE2	2.36	0.51
2:H:131:ILE:HD11	2:H:144:LEU:HG	1.92	0.51
1:A:270:PRO:HB2	1:A:272:VAL:HG13	1.93	0.50
2:D:277:GLU:OE2	2:D:354:ARG:HD3	2.11	0.50
1:E:255:GLU:HB3	1:E:406:GLN:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:229:VAL:HG23	1:G:258:VAL:HG23	1.92	0.50
2:D:168:GLU:O	2:D:171:VAL:HG22	2.11	0.50
1:A:323:ALA:HB2	1:A:398:VAL:HG22	1.93	0.50
1:A:116:SER:O	1:A:122:PHE:HB2	2.11	0.50
1:E:173:LEU:O	1:E:177:MET:HG3	2.12	0.50
1:E:281:MET:HB3	1:E:286:LEU:HD11	1.94	0.50
1:E:347:ILE:HG22	1:E:349:VAL:HG22	1.92	0.50
2:H:222:VAL:HG11	2:H:241:VAL:HG23	1.92	0.50
2:B:301:ASP:HB3	2:B:304:VAL:HG22	1.94	0.50
2:H:302:ASP:N	2:H:302:ASP:OD1	2.36	0.50
2:B:56:MET:HE2	2:B:58:LEU:HD21	1.94	0.50
1:E:170:VAL:O	1:E:174:LYS:HB2	2.12	0.50
2:H:185:GLU:OE1	2:H:188:ARG:NE	2.45	0.50
2:H:311:ALA:O	2:H:315:VAL:HG12	2.12	0.50
1:E:201:ILE:HG12	1:E:202:GLU:HG3	1.94	0.50
2:F:274:THR:HG22	2:F:276:GLY:N	2.26	0.50
1:G:340:THR:HG22	1:G:341:VAL:O	2.12	0.50
1:C:197:GLY:HA2	1:C:200:LEU:HD22	1.93	0.49
1:E:268:MET:HE3	1:E:268:MET:HA	1.94	0.49
1:G:153:LYS:HG2	3:G:501:GTP:C5	2.47	0.49
1:G:187:ILE:HD12	1:G:188:PRO:HD2	1.93	0.49
1:C:340:THR:HG22	2:D:334:ARG:NH2	2.27	0.49
2:F:288:ASP:OD2	2:F:289:THR:HG23	2.12	0.49
1:C:11:VAL:HG13	1:C:112:ILE:HB	1.93	0.49
2:H:1:MET:O	2:H:3:VAL:HG12	2.13	0.49
1:C:19:LYS:HA	1:C:114:VAL:HG21	1.95	0.49
1:C:340:THR:HG23	1:C:341:VAL:O	2.13	0.49
1:C:405:PRO:O	1:C:409:ARG:HG2	2.13	0.49
2:F:5:VAL:HG12	2:F:7:ASP:H	1.76	0.49
2:F:56:MET:HG3	2:F:58:LEU:HD21	1.95	0.49
1:G:270:PRO:HB2	1:G:272:VAL:HG13	1.95	0.49
2:H:126:ARG:NH2	2:H:247:GLU:OE2	2.46	0.49
2:D:46:VAL:HA	2:D:47:GLY:HA2	1.61	0.49
1:E:141:THR:O	1:E:409:ARG:HD3	2.13	0.49
2:B:171:VAL:O	2:B:175:VAL:HG13	2.13	0.49
2:B:19:SER:OG	2:B:21:GLU:HG2	2.11	0.48
1:C:4:LYS:N	5:C:784:HOH:O	2.45	0.48
2:D:43:ASP:OD1	2:D:53:ARG:HD3	2.13	0.48
1:G:228:PRO:HG2	1:G:256:THR:HG22	1.95	0.48
2:B:157:ALA:HB2	2:B:174:TYR:CZ	2.49	0.48
2:B:62:LEU:HA	2:B:62:LEU:HD12	1.72	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:83:LYS:HD2	1:G:84:TYR:CE2	2.48	0.48
2:H:310:GLU:OE1	2:H:313:ARG:NE	2.46	0.48
2:B:250:ILE:HD11	2:B:326:PRO:HD2	1.94	0.48
1:A:369:THR:OG1	1:A:371:GLN:NE2	2.42	0.48
1:G:14:HIS:ND1	1:G:131:GLN:HG2	2.29	0.48
1:A:107:GLN:O	1:A:253:ARG:HD3	2.14	0.48
2:B:204:THR:HG22	2:B:221:THR:HG21	1.95	0.48
1:G:255:GLU:HB3	1:G:406:GLN:HG3	1.94	0.48
1:A:51:GLU:O	5:A:739:HOH:O	2.20	0.48
2:F:293:VAL:HG23	2:F:335:LEU:HD12	1.95	0.48
1:C:116:SER:OG	1:C:121:GLU:OE1	2.20	0.48
1:A:229:VAL:HG13	1:A:258:VAL:HG23	1.96	0.47
1:A:33:ILE:HG12	1:A:58:ILE:HD12	1.94	0.47
1:A:21:THR:HG22	5:A:787:HOH:O	2.12	0.47
1:A:266:VAL:HB	1:A:316:LEU:HD22	1.95	0.47
1:A:24:GLY:HA2	1:A:58:ILE:HD11	1.95	0.47
2:B:27:ARG:HH11	2:B:27:ARG:HG2	1.79	0.47
2:D:181:ARG:NH2	2:D:185:GLU:OE2	2.48	0.47
2:F:113:SER:O	2:F:117:LEU:HD22	2.14	0.47
1:C:166:TYR:CD1	1:C:191:PRO:HB3	2.49	0.47
1:C:31:GLY:HA2	5:C:782:HOH:O	2.12	0.47
1:G:346:VAL:HA	1:G:355:SER:HA	1.97	0.47
1:E:29:ARG:NH2	1:E:197:GLY:HA3	2.29	0.47
1:G:405:PRO:HD2	5:G:695:HOH:O	2.14	0.47
1:A:65:GLU:O	1:A:69:GLY:HA2	2.15	0.47
1:E:115:VAL:HG21	1:E:173:LEU:HD11	1.96	0.47
1:E:249:VAL:HA	1:E:250:PRO:HD2	1.70	0.47
1:G:259:LEU:HD11	1:G:276:VAL:HG21	1.96	0.47
2:H:31:ARG:HG3	2:H:32:PRO:HD2	1.97	0.47
1:C:396:LEU:HG	1:C:398:VAL:HG13	1.96	0.47
1:E:116:SER:OG	1:E:153:LYS:HD2	2.14	0.47
2:H:65:ILE:HG13	2:H:298:HIS:CE1	2.50	0.47
1:A:321:THR:OG1	1:A:399:GLU:OE2	2.24	0.47
1:C:154:MET:HB2	1:C:192:VAL:O	2.15	0.47
2:D:157:ALA:HB1	2:D:159:LEU:HD22	1.97	0.47
2:B:17:PRO:HG3	2:B:26:LEU:HD11	1.95	0.47
1:C:21:THR:HG23	1:C:56:ALA:HB2	1.97	0.47
1:E:233:LEU:HA	1:E:256:THR:O	2.15	0.47
1:G:310:GLY:HA2	1:G:351:THR:HG23	1.95	0.47
2:H:44:VAL:HG21	2:H:87:PHE:HB3	1.96	0.47
2:H:84:PRO:HB2	2:H:87:PHE:HD2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:128:THR:HG21	2:B:189:HIS:HB3	1.97	0.46
2:B:333:GLU:O	2:B:336:VAL:HG13	2.15	0.46
1:C:255:GLU:OE1	1:C:406:GLN:HG3	2.15	0.46
2:D:289:THR:HG23	2:D:344:LEU:HD23	1.98	0.46
1:E:321:THR:OG1	1:E:399:GLU:OE2	2.23	0.46
2:F:15:LEU:HD13	2:F:26:LEU:HD21	1.97	0.46
2:H:14:ARG:HB2	2:H:105:VAL:HG22	1.97	0.46
2:H:250:ILE:HD11	2:H:326:PRO:HD2	1.96	0.46
1:A:250:PRO:HD2	1:A:297:PHE:O	2.14	0.46
2:B:112:TRP:HB3	2:B:117:LEU:CD1	2.45	0.46
2:F:31:ARG:HG3	2:F:32:PRO:HD2	1.96	0.46
1:G:201:ILE:H	1:G:201:ILE:HD13	1.81	0.46
1:G:350:HIS:CG	1:G:351:THR:H	2.30	0.46
1:A:329:ARG:HD3	5:A:799:HOH:O	2.15	0.46
1:G:248:THR:HG21	1:G:303:SER:HA	1.96	0.46
2:H:128:THR:HG21	2:H:189:HIS:HB3	1.98	0.46
2:H:46:VAL:HG12	2:H:47:GLY:H	1.81	0.46
2:B:159:LEU:HD21	2:B:171:VAL:HG12	1.97	0.46
2:F:183:VAL:HG13	2:F:214:MET:SD	2.56	0.46
2:F:19:SER:OG	2:F:21:GLU:HG2	2.15	0.46
1:G:277:ARG:HD2	1:G:300:ARG:HB2	1.96	0.46
2:H:296:LEU:CD1	2:H:341:VAL:HG22	2.46	0.46
1:A:29:ARG:HH11	1:A:201:ILE:HD11	1.80	0.46
2:D:80:VAL:HG21	2:D:89:VAL:HG12	1.97	0.46
1:E:33:ILE:HG12	1:E:58:ILE:HD13	1.98	0.46
1:G:260:ARG:NE	5:G:628:HOH:O	2.49	0.46
2:H:56:MET:HE1	2:H:58:LEU:HD21	1.98	0.46
1:A:253:ARG:NE	1:A:292:GLY:HA2	2.28	0.46
1:A:371:GLN:H	1:A:371:GLN:HG3	1.12	0.46
2:D:100:ILE:HG12	5:D:455:HOH:O	2.14	0.46
1:C:116:SER:OG	1:C:153:LYS:HD2	2.16	0.46
1:E:168:PHE:O	1:E:172:VAL:HG23	2.16	0.46
2:F:108:ARG:HB2	2:F:112:TRP:CE2	2.51	0.46
1:G:3:GLU:N	5:G:674:HOH:O	2.49	0.46
1:G:95:ARG:NH2	1:G:417:ARG:HD3	2.31	0.46
1:A:268:MET:HG3	1:A:322:VAL:CG2	2.46	0.45
2:B:80:VAL:HG11	2:B:89:VAL:HG23	1.97	0.45
1:A:142:MET:HE1	1:A:410:PHE:HA	1.98	0.45
1:G:231:LYS:NZ	5:G:695:HOH:O	2.48	0.45
2:H:112:TRP:HB3	2:H:117:LEU:CD1	2.47	0.45
2:F:177:ARG:NH2	5:F:436:HOH:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:37:ARG:NH2	5:F:450:HOH:O	2.49	0.45
1:G:24:GLY:HA2	1:G:58:ILE:HD11	1.98	0.45
1:A:361:ILE:O	1:A:376:ASN:HA	2.17	0.45
1:E:253:ARG:NH1	5:E:677:HOH:O	2.44	0.45
1:G:340:THR:HG21	2:H:338:PHE:HE2	1.82	0.45
1:A:153:LYS:HG2	3:A:501:GTP:C5	2.52	0.45
1:C:162:ASP:OD2	1:C:164:LYS:HB3	2.17	0.45
1:C:36:LYS:O	1:C:40:GLU:HG3	2.16	0.45
1:E:382:ALA:HA	1:E:383:GLY:HA2	1.76	0.45
2:H:274:THR:HG22	2:H:277:GLU:H	1.82	0.45
2:B:263:ARG:HD3	2:B:270:THR:OG1	2.17	0.45
1:E:60:ASP:O	1:E:66:ARG:HD3	2.16	0.45
1:G:101:MET:HE1	1:G:138:LEU:HD13	1.99	0.45
1:G:361:ILE:CD1	1:G:377:PRO:HG2	2.44	0.45
1:A:153:LYS:HG2	3:A:501:GTP:C6	2.52	0.45
2:D:268:ARG:HB2	2:D:268:ARG:CZ	2.46	0.45
2:D:274:THR:HG22	2:D:277:GLU:H	1.82	0.45
1:E:335:HIS:HA	1:E:336:PRO:HD3	1.87	0.45
2:F:21:GLU:OE2	5:F:487:HOH:O	2.21	0.45
1:A:201:ILE:HG12	1:A:202:GLU:N	2.31	0.45
1:A:382:ALA:HA	1:A:383:GLY:HA2	1.77	0.45
1:C:361:ILE:O	1:C:376:ASN:HA	2.16	0.45
1:A:197:GLY:HA2	1:A:200:LEU:HD22	1.99	0.44
1:A:259:LEU:HD11	1:A:276:VAL:HG21	1.97	0.44
1:A:95:ARG:O	1:A:98:VAL:HG13	2.17	0.44
2:F:128:THR:N	5:F:434:HOH:O	2.49	0.44
2:F:245:LEU:HG	2:F:248:LEU:HD22	1.97	0.44
2:H:131:ILE:HG23	2:H:195:VAL:HB	1.98	0.44
2:D:153:GLU:OE1	2:D:181:ARG:NH1	2.51	0.44
1:E:416:ASN:HB2	2:F:225:SER:HB3	1.99	0.44
2:F:159:LEU:HA	2:F:160:PRO:HD3	1.87	0.44
2:F:7:ASP:HB2	2:F:12:ILE:HB	2.00	0.44
1:A:14:HIS:ND1	1:A:125:GLY:HA2	2.33	0.44
1:A:163:GLN:HB2	1:A:209:TRP:CD2	2.52	0.44
2:D:21:GLU:HG3	2:D:125:ALA:HA	1.99	0.44
2:D:238:ARG:HD3	2:D:238:ARG:HA	1.87	0.44
1:G:253:ARG:HD3	1:G:254:VAL:O	2.17	0.44
2:H:141:LEU:HB3	2:H:153:GLU:HB3	1.99	0.44
2:H:37:ARG:HG3	2:H:59:ARG:HG2	1.98	0.44
1:C:180:LEU:HD12	1:C:180:LEU:HA	1.81	0.44
2:D:128:THR:HG22	2:D:191:SER:OG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:203:ARG:HE	1:G:203:ARG:HB3	1.34	0.44
2:B:262:ARG:NH1	5:B:451:HOH:O	2.51	0.44
2:F:304:VAL:O	2:F:308:VAL:HG23	2.18	0.44
1:A:154:MET:HG2	1:A:207:MET:SD	2.58	0.44
2:B:126:ARG:NH1	2:B:247:GLU:OE2	2.51	0.44
2:D:206:VAL:O	2:D:210:VAL:HG13	2.17	0.44
2:F:44:VAL:HG21	2:F:87:PHE:CD1	2.53	0.44
1:A:209:TRP:NE1	5:A:775:HOH:O	2.23	0.44
2:F:46:VAL:HA	2:F:47:GLY:HA2	1.54	0.44
1:G:178:LYS:HD2	1:G:178:LYS:HA	1.71	0.44
1:A:268:MET:HG3	1:A:322:VAL:HG23	2.00	0.43
1:E:140:ARG:NH1	5:E:759:HOH:O	2.50	0.43
1:C:141:THR:O	1:C:409:ARG:HD3	2.18	0.43
2:D:121:ALA:C	2:D:123:GLY:H	2.22	0.43
2:F:21:GLU:CG	2:F:125:ALA:HA	2.44	0.43
2:F:80:VAL:HG11	2:F:89:VAL:HG23	2.00	0.43
1:G:12:ILE:C	1:G:19:LYS:HD3	2.38	0.43
2:H:263:ARG:HD3	2:H:270:THR:OG1	2.18	0.43
2:B:264:ILE:HD13	2:B:268:ARG:HD3	2.00	0.43
2:B:3:VAL:HG11	2:B:121:ALA:HB2	1.99	0.43
1:A:62:MET:HB2	1:A:65:GLU:CG	2.49	0.43
2:D:12:ILE:HD13	2:D:107:GLU:HB2	2.00	0.43
1:A:32:TYR:CE2	1:A:79:PHE:HB2	2.53	0.43
2:D:139:PHE:CE2	2:D:153:GLU:HG2	2.53	0.43
2:F:108:ARG:HD3	2:F:110:LYS:HE2	2.01	0.43
1:G:248:THR:HG22	5:G:655:HOH:O	2.18	0.43
2:H:25:LEU:HD12	2:H:25:LEU:HA	1.82	0.43
1:C:190:ILE:H	1:C:190:ILE:HG12	1.44	0.43
2:D:139:PHE:HE2	2:D:153:GLU:HG2	1.84	0.43
2:D:29:THR:HG21	2:D:120:LEU:HD13	1.99	0.43
1:A:190:ILE:HD11	1:A:218:ALA:HB2	2.01	0.43
1:G:155:ASP:OD1	3:G:501:GTP:N1	2.44	0.43
1:C:272:VAL:HG11	1:C:306:ASP:HB3	2.01	0.43
2:D:25:LEU:HD12	2:D:25:LEU:HA	1.82	0.43
1:A:58:ILE:HG21	1:A:58:ILE:HD13	1.73	0.43
1:A:332:VAL:O	1:A:383:GLY:HA2	2.18	0.43
2:B:245:LEU:HB3	2:B:251:VAL:HG21	1.99	0.43
2:D:291:LEU:HD13	2:D:335:LEU:HD11	2.00	0.43
1:E:166:TYR:CE1	1:E:191:PRO:HG3	2.54	0.43
1:E:198:ASP:OD2	1:E:204:SER:OG	2.35	0.43
2:H:128:THR:OG1	2:H:144:LEU:O	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:ARG:O	2:B:126:ARG:N	2.46	0.42
1:A:14:HIS:HA	1:A:131:GLN:HB2	2.01	0.42
2:D:124:ARG:O	2:D:126:ARG:N	2.51	0.42
1:E:173:LEU:HB3	1:E:177:MET:CE	2.49	0.42
1:G:109:ASP:OD1	1:G:253:ARG:NH2	2.52	0.42
1:G:274:GLY:HA3	1:G:299:VAL:HG12	2.01	0.42
2:H:46:VAL:HG12	2:H:47:GLY:N	2.34	0.42
2:B:75:ARG:HD3	2:B:75:ARG:C	2.39	0.42
1:C:201:ILE:HD13	1:C:201:ILE:H	1.84	0.42
1:C:45:ALA:HB1	1:C:50:LYS:O	2.19	0.42
5:G:673:HOH:O	2:H:135:ASP:HB2	2.19	0.42
2:H:314:LEU:O	2:H:318:MET:HG3	2.19	0.42
1:C:193:SER:HB3	1:C:198:ASP:HB2	2.00	0.42
2:D:243:ARG:NH2	5:D:543:HOH:O	2.52	0.42
2:F:19:SER:HA	2:F:100:ILE:HD13	2.02	0.42
2:F:27:ARG:NH1	2:F:294:ASP:OD2	2.48	0.42
2:F:277:GLU:OE2	2:F:351:GLN:NE2	2.51	0.42
2:D:131:ILE:HG23	2:D:195:VAL:HB	2.02	0.42
2:D:58:LEU:HD23	2:D:58:LEU:N	2.35	0.42
1:E:228:PRO:HB2	1:E:256:THR:HG22	2.02	0.42
2:F:36:VAL:HG12	2:F:106:VAL:HB	2.00	0.42
1:G:153:LYS:HA	3:G:501:GTP:N1	2.35	0.42
1:G:423:ILE:HG13	1:G:423:ILE:O	2.20	0.42
1:G:98:VAL:HG21	1:G:413:ARG:CZ	2.50	0.42
1:G:413:ARG:HG2	1:G:418:THR:HA	2.01	0.42
2:H:13:VAL:HG12	2:H:15:LEU:HD22	2.02	0.42
2:H:15:LEU:N	2:H:15:LEU:HD23	2.35	0.42
2:H:197:ALA:HB2	2:H:222:VAL:HG23	2.01	0.42
2:H:25:LEU:HD12	2:H:28:ILE:HD11	2.01	0.42
1:A:415:MET:SD	2:B:234:GLU:HG3	2.59	0.42
2:D:263:ARG:HD2	2:D:271:VAL:HG23	2.01	0.42
2:H:63:ASP:CB	2:H:78:GLY:HA2	2.49	0.42
1:A:101:MET:HE1	1:A:138:LEU:CD1	2.50	0.42
2:B:163:ASP:OD1	2:B:163:ASP:N	2.52	0.42
1:C:203:ARG:NH1	1:C:212:GLY:O	2.53	0.42
1:E:13:GLY:N	1:E:19:LYS:HD3	2.34	0.42
1:E:237:VAL:HG13	1:E:311:ASP:O	2.20	0.42
2:F:162:LYS:HA	2:F:167:ARG:HG3	2.02	0.42
1:G:340:THR:HG21	2:H:338:PHE:CE2	2.55	0.42
2:B:11:ARG:NH2	2:B:107:GLU:OE1	2.51	0.42
2:H:-1:SER:HB2	2:H:125:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:ASP:HA	2:B:165:PRO:HD3	1.94	0.42
2:B:63:ASP:CB	2:B:78:GLY:HA2	2.50	0.42
2:B:46:VAL:HA	2:B:47:GLY:HA2	1.59	0.41
2:F:236:LEU:HD23	2:F:236:LEU:HA	1.89	0.41
2:B:6:LEU:HB2	2:B:12:ILE:HG22	2.02	0.41
1:C:355:SER:O	1:C:393:VAL:HG22	2.20	0.41
1:E:201:ILE:H	1:E:201:ILE:HD13	1.85	0.41
1:G:203:ARG:H	1:G:203:ARG:HG2	1.52	0.41
1:G:249:VAL:HA	1:G:250:PRO:HD2	1.73	0.41
1:G:408:GLY:HA2	1:G:424:VAL:HG13	2.01	0.41
1:G:93:GLY:O	1:G:131:GLN:HG3	2.20	0.41
1:A:345:PRO:HG3	1:A:412:MET:HE3	2.01	0.41
2:B:37:ARG:HA	2:B:58:LEU:O	2.20	0.41
2:B:39:ARG:HG3	2:B:57:THR:OG1	2.19	0.41
1:E:36:LYS:O	1:E:40:GLU:HG3	2.21	0.41
2:F:263:ARG:NH1	2:F:270:THR:O	2.47	0.41
2:B:268:ARG:O	2:B:268:ARG:HD2	2.20	0.41
2:B:328:ASP:HB3	5:B:438:HOH:O	2.20	0.41
2:F:265:ALA:O	2:F:267:SER:N	2.54	0.41
2:F:73:LYS:HE2	2:F:99:SER:OG	2.20	0.41
1:G:127:SER:O	1:G:133:ARG:HD2	2.20	0.41
1:G:152:ASN:CG	1:G:153:LYS:H	2.23	0.41
2:H:153:GLU:HG3	2:H:154:ASP:N	2.36	0.41
2:H:40:THR:HB	2:H:41:SER:H	1.36	0.41
1:A:203:ARG:HH11	1:A:211:ASN:C	2.23	0.41
1:A:203:ARG:HH21	1:A:203:ARG:HG2	1.86	0.41
1:C:268:MET:HG3	1:C:322:VAL:HG23	2.02	0.41
1:E:216:VAL:HA	1:E:219:LEU:HD12	2.02	0.41
2:F:266:LYS:HD2	2:F:266:LYS:HA	1.87	0.41
2:F:315:VAL:O	2:F:320:GLY:N	2.47	0.41
1:A:236:PRO:HG3	1:A:407:LEU:HD21	2.02	0.41
2:D:141:LEU:HB3	2:D:153:GLU:HB3	2.03	0.41
2:D:128:THR:O	2:D:192:PRO:HD2	2.21	0.41
1:E:9:LEU:HD11	1:E:219:LEU:CD2	2.50	0.41
1:E:401:PHE:CE1	1:E:405:PRO:HB3	2.56	0.41
2:F:62:LEU:HD12	2:F:62:LEU:HA	1.91	0.41
1:G:154:MET:HB2	1:G:192:VAL:O	2.21	0.41
1:G:95:ARG:HH22	1:G:417:ARG:HD3	1.85	0.41
2:H:40:THR:HG21	2:H:94:HIS:NE2	2.36	0.41
1:A:141:THR:HG21	1:A:421:ILE:CG2	2.51	0.41
2:B:222:VAL:HG21	2:B:241:VAL:CG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:ILE:HD12	1:C:135:HIS:HB3	2.03	0.41
1:G:22:LEU:HA	1:G:194:ALA:HB1	2.03	0.41
2:B:75:ARG:HD2	2:B:75:ARG:HH11	1.76	0.41
1:G:138:LEU:HA	1:G:141:THR:HG23	2.03	0.41
2:B:40:THR:HB	2:B:41:SER:H	1.51	0.41
2:B:5:VAL:HG21	2:B:10:ARG:HG2	2.02	0.41
1:E:19:LYS:NZ	3:E:501:GTP:O1B	2.50	0.41
1:A:4:LYS:HA	1:A:5:PRO:HD3	1.78	0.40
2:D:44:VAL:HA	2:D:45:PRO:HD3	1.83	0.40
2:H:294:ASP:OD1	2:H:326:PRO:HA	2.21	0.40
1:A:32:TYR:C	1:A:33:ILE:HD12	2.42	0.40
2:B:259:GLU:OE2	2:B:262:ARG:NH2	2.54	0.40
2:D:7:ASP:CG	2:D:11:ARG:H	2.24	0.40
2:D:245:LEU:HB3	2:D:251:VAL:HG21	2.03	0.40
2:H:226:MET:HE3	2:H:226:MET:HB3	1.98	0.40
2:H:237:ARG:HG3	2:H:254:GLU:HG2	2.02	0.40
2:B:245:LEU:HD12	2:B:245:LEU:HA	1.85	0.40
2:D:317:SER:OG	2:D:318:MET:HG3	2.21	0.40
2:D:61:ARG:O	2:D:78:GLY:HA3	2.21	0.40
1:E:9:LEU:HD11	1:E:219:LEU:HD22	2.03	0.40
1:E:432:VAL:HA	5:E:701:HOH:O	2.22	0.40
1:E:65:GLU:HG2	1:E:70:ILE:O	2.22	0.40
1:A:173:LEU:HA	1:A:173:LEU:HD12	1.95	0.40
2:B:198:GLY:HA2	2:B:224:THR:HG22	2.03	0.40
1:C:156:ALA:HA	1:C:157:PRO:HD3	1.99	0.40
1:C:224:PRO:HA	1:C:225:PRO:HD3	1.89	0.40
1:C:281:MET:HB3	1:C:286:LEU:HD11	2.02	0.40
1:E:32:TYR:OH	1:E:80:GLU:HG2	2.21	0.40
1:E:338:ALA:HB1	1:E:379:PHE:HB2	2.04	0.40
2:F:56:MET:HE2	2:F:89:VAL:HG21	2.04	0.40
1:A:154:MET:CE	1:A:166:TYR:HB2	2.51	0.40
1:A:203:ARG:NH1	1:A:212:GLY:O	2.54	0.40
2:D:187:ALA:HB2	2:D:214:MET:HE1	2.04	0.40
2:D:272:ALA:HA	5:D:572:HOH:O	2.20	0.40
2:F:24:TRP:O	2:F:28:ILE:HG23	2.21	0.40
2:F:322:VAL:O	5:F:530:HOH:O	2.22	0.40
2:F:349:VAL:O	2:F:354:ARG:NH1	2.53	0.40
2:H:292:LEU:HB2	2:H:341:VAL:HG13	2.02	0.40

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	430/447 (96%)	412 (96%)	17 (4%)	1 (0%)	47	58
1	C	429/447 (96%)	407 (95%)	22 (5%)	0	100	100
1	E	429/447 (96%)	410 (96%)	19 (4%)	0	100	100
1	G	430/447 (96%)	406 (94%)	20 (5%)	4 (1%)	17	20
2	B	355/376 (94%)	344 (97%)	8 (2%)	3 (1%)	19	23
2	D	355/376 (94%)	340 (96%)	12 (3%)	3 (1%)	19	23
2	F	353/376 (94%)	331 (94%)	17 (5%)	5 (1%)	11	11
2	H	354/376 (94%)	337 (95%)	14 (4%)	3 (1%)	19	23
All	All	3135/3292 (95%)	2987 (95%)	129 (4%)	19 (1%)	25	31

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	123	GLY
2	F	127	GLY
2	F	266	LYS
1	G	127	SER
2	H	110	LYS
2	H	352	GLU
1	A	337	SER
2	B	158	ARG
2	D	125	ALA
1	G	51	GLU
1	G	350	HIS
2	H	274	THR
2	B	274	THR
2	F	274	THR
2	F	330	PRO
2	D	274	THR
2	F	46	VAL

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Mol	Chain	Res	Type
2	D	45	PRO
1	G	432	VAL

### 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	356/378 (94%)	315 (88%)	41 (12%)	5	6
1	C	361/378 (96%)	319 (88%)	42 (12%)	5	6
1	E	359/378 (95%)	328 (91%)	31 (9%)	10	12
1	G	355/378 (94%)	314 (88%)	41 (12%)	5	6
2	B	284/311 (91%)	238 (84%)	46 (16%)	2	2
2	D	286/311 (92%)	236 (82%)	50 (18%)	2	2
2	F	279/311 (90%)	230 (82%)	49 (18%)	2	1
2	H	280/311 (90%)	231 (82%)	49 (18%)	2	2
All	All	2560/2756 (93%)	2211 (86%)	349 (14%)	3	3

All (349) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LEU
1	A	48	ARG
1	A	58	ILE
1	A	59	LEU
1	A	61	LYS
1	A	66	ARG
1	A	68	ARG
1	A	77	MET
1	A	85	VAL
1	A	95	ARG
1	A	101	MET
1	A	113	LEU
1	A	115	VAL

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Mol	Chain	Res	Type
1	A	137	LEU
1	A	141	THR
1	A	142	MET
1	A	145	GLU
1	A	147	ILE
1	A	149	VAL
1	A	165	ARG
1	A	169	VAL
1	A	173	LEU
1	A	180	LEU
1	A	184	VAL
1	A	187	ILE
1	A	201	ILE
1	A	221	GLN
1	A	233	LEU
1	A	242	SER
1	A	248	THR
1	A	249	VAL
1	A	268	MET
1	A	346	VAL
1	A	349	VAL
1	A	364	LYS
1	A	371	GLN
1	A	373	VAL
1	A	393	VAL
1	A	406	GLN
1	A	432	VAL
1	A	435	LYS
2	B	2	ARG
2	B	5	VAL
2	B	6	LEU
2	B	15	LEU
2	B	21	GLU
2	B	25	LEU
2	B	31	ARG
2	B	38	ILE
2	B	42	ARG
2	B	53	ARG
2	B	55	VAL
2	B	62	LEU
2	B	65	ILE
2	B	74	LEU

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Mol	Chain	Res	Type
2	B	75	ARG
2	B	104	LEU
2	B	106	VAL
2	B	113	SER
2	B	119	ARG
2	B	120	LEU
2	B	128	THR
2	B	131	ILE
2	B	138	GLU
2	B	144	LEU
2	B	181	ARG
2	B	210	VAL
2	B	224	THR
2	B	245	LEU
2	B	248	LEU
2	B	250	ILE
2	B	268	ARG
2	B	274	THR
2	B	283	ARG
2	B	289	THR
2	B	291	LEU
2	B	292	LEU
2	B	293	VAL
2	B	297	LEU
2	B	310	GLU
2	B	314	LEU
2	B	321	ARG
2	B	322	VAL
2	B	328	ASP
2	B	337	SER
2	B	341	VAL
2	B	344	LEU
1	C	4	LYS
1	C	11	VAL
1	C	21	THR
1	C	29	ARG
1	C	30	LEU
1	C	58	ILE
1	C	66	ARG
1	C	68	ARG
1	C	74	LEU
1	C	78	LYS

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Mol	Chain	Res	Type
1	C	95	ARG
1	C	98	VAL
1	C	113	LEU
1	C	131	GLN
1	C	137	LEU
1	C	140	ARG
1	C	141	THR
1	C	142	MET
1	C	147	ILE
1	C	149	VAL
1	C	154	MET
1	C	164	LYS
1	C	165	ARG
1	C	180	LEU
1	C	184	VAL
1	C	190	ILE
1	C	193	SER
1	C	201	ILE
1	C	203	ARG
1	C	221	GLN
1	C	239	ASN
1	C	253	ARG
1	C	265	VAL
1	C	268	MET
1	C	277	ARG
1	C	324	GLU
1	C	340	THR
1	C	346	VAL
1	C	349	VAL
1	C	371	GLN
1	C	373	VAL
1	C	406	GLN
2	D	0	HIS
2	D	10	ARG
2	D	15	LEU
2	D	16	ARG
2	D	21	GLU
2	D	25	LEU
2	D	31	ARG
2	D	38	ILE
2	D	50	ARG
2	D	51	LYS

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Mol	Chain	Res	Type
2	D	55	VAL
2	D	58	LEU
2	D	62	LEU
2	D	65	ILE
2	D	73	LYS
2	D	74	LEU
2	D	81	VAL
2	D	85	ASP
2	D	93	ARG
2	D	99	SER
2	D	104	LEU
2	D	113	SER
2	D	131	ILE
2	D	137	ASP
2	D	159	LEU
2	D	168	GLU
2	D	175	VAL
2	D	191	SER
2	D	204	THR
2	D	210	VAL
2	D	224	THR
2	D	233	ARG
2	D	239	GLU
2	D	240	SER
2	D	245	LEU
2	D	246	ARG
2	D	248	LEU
2	D	266	LYS
2	D	268	ARG
2	D	271	VAL
2	D	274	THR
2	D	289	THR
2	D	291	LEU
2	D	292	LEU
2	D	297	LEU
2	D	304	VAL
2	D	314	LEU
2	D	321	ARG
2	D	341	VAL
2	D	344	LEU
1	E	26	LEU
1	E	27	LEU

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Mol	Chain	Res	Type
1	E	66	ARG
1	E	68	ARG
1	E	78	LYS
1	E	95	ARG
1	E	113	LEU
1	E	127	SER
1	E	137	LEU
1	E	141	THR
1	E	142	MET
1	E	165	ARG
1	E	167	GLU
1	E	183	GLN
1	E	184	VAL
1	E	200	LEU
1	E	201	ILE
1	E	233	LEU
1	E	237	VAL
1	E	239	ASN
1	E	242	SER
1	E	249	VAL
1	E	253	ARG
1	E	260	ARG
1	E	268	MET
1	E	272	VAL
1	E	349	VAL
1	E	364	LYS
1	E	406	GLN
1	E	407	LEU
1	E	415	MET
2	F	3	VAL
2	F	6	LEU
2	F	21	GLU
2	F	25	LEU
2	F	27	ARG
2	F	38	ILE
2	F	55	VAL
2	F	58	LEU
2	F	62	LEU
2	F	65	ILE
2	F	68	GLN
2	F	74	LEU
2	F	81	VAL

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Mol	Chain	Res	Type
2	F	95	SER
2	F	99	SER
2	F	104	LEU
2	F	114	GLU
2	F	117	LEU
2	F	120	LEU
2	F	126	ARG
2	F	128	THR
2	F	131	ILE
2	F	134	VAL
2	F	144	LEU
2	F	153	GLU
2	F	167	ARG
2	F	181	ARG
2	F	204	THR
2	F	210	VAL
2	F	224	THR
2	F	226	MET
2	F	233	ARG
2	F	239	GLU
2	F	245	LEU
2	F	248	LEU
2	F	256	VAL
2	F	264	ILE
2	F	291	LEU
2	F	292	LEU
2	F	294	ASP
2	F	297	LEU
2	F	312	LEU
2	F	314	LEU
2	F	315	VAL
2	F	322	VAL
2	F	328	ASP
2	F	337	SER
2	F	341	VAL
2	F	344	LEU
1	G	9	LEU
1	G	25	HIS
1	G	27	LEU
1	G	34	GLU
1	G	35	GLU
1	G	58	ILE

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Mol	Chain	Res	Type
1	G	59	LEU
1	G	62	MET
1	G	68	ARG
1	G	74	LEU
1	G	77	MET
1	G	95	ARG
1	G	113	LEU
1	G	128	THR
1	G	131	GLN
1	G	137	LEU
1	G	141	THR
1	G	142	MET
1	G	149	VAL
1	G	154	MET
1	G	158	ASP
1	G	160	ASN
1	G	165	ARG
1	G	187	ILE
1	G	201	ILE
1	G	203	ARG
1	G	206	ASN
1	G	235	ILE
1	G	237	VAL
1	G	249	VAL
1	G	253	ARG
1	G	265	VAL
1	G	272	VAL
1	G	300	ARG
1	G	329	ARG
1	G	346	VAL
1	G	361	ILE
1	G	391	LYS
1	G	406	GLN
1	G	412	MET
1	G	415	MET
2	H	2	ARG
2	H	3	VAL
2	H	4	GLU
2	H	10	ARG
2	H	15	LEU
2	H	18	GLU
2	H	25	LEU

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Mol	Chain	Res	Type
2	H	31	ARG
2	H	40	THR
2	H	53	ARG
2	H	65	ILE
2	H	74	LEU
2	H	89	VAL
2	H	104	LEU
2	H	106	VAL
2	H	113	SER
2	H	120	LEU
2	H	131	ILE
2	H	134	VAL
2	H	167	ARG
2	H	168	GLU
2	H	181	ARG
2	H	201	GLN
2	H	204	THR
2	H	222	VAL
2	H	224	THR
2	H	225	SER
2	H	226	MET
2	H	233	ARG
2	H	237	ARG
2	H	238	ARG
2	H	239	GLU
2	H	240	SER
2	H	245	LEU
2	H	248	LEU
2	H	256	VAL
2	H	267	SER
2	H	274	THR
2	H	283	ARG
2	H	289	THR
2	H	291	LEU
2	H	292	LEU
2	H	297	LEU
2	H	302	ASP
2	H	314	LEU
2	H	322	VAL
2	H	337	SER
2	H	341	VAL
2	H	344	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	135	HIS
1	G	107	GLN

### 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 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	GTP	E	501	4	26,34,34	0.91	1 (3%)	33,54,54	1.83	6 (18%)
3	GTP	G	501	4	26,34,34	1.01	1 (3%)	33,54,54	1.75	7 (21%)
3	GTP	A	501	4	26,34,34	0.89	1 (3%)	33,54,54	1.73	6 (18%)
3	GTP	C	501	4	26,34,34	0.98	1 (3%)	33,54,54	1.84	6 (18%)

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	GTP	E	501	4	-	4/18/38/38	0/3/3/3
3	GTP	G	501	4	-	3/18/38/38	0/3/3/3
3	GTP	A	501	4	-	4/18/38/38	0/3/3/3
3	GTP	C	501	4	-	1/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	501	GTP	C6-N1	3.01	1.38	1.33
3	C	501	GTP	C6-N1	2.93	1.38	1.33
3	A	501	GTP	C6-N1	2.71	1.37	1.33
3	E	501	GTP	C6-N1	2.67	1.37	1.33

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	501	GTP	N3-C2-N1	-5.17	120.32	127.22
3	C	501	GTP	N3-C2-N1	-5.15	120.35	127.22
3	E	501	GTP	N3-C2-N1	-4.97	120.59	127.22
3	A	501	GTP	N3-C2-N1	-4.61	121.07	127.22
3	E	501	GTP	PB-O3B-PG	-4.26	118.20	132.83
3	C	501	GTP	C2-N3-C4	3.90	119.81	115.36
3	A	501	GTP	C2-N3-C4	3.77	119.67	115.36
3	G	501	GTP	C2-N3-C4	3.72	119.61	115.36
3	E	501	GTP	C5-C6-N1	-3.60	118.51	123.43
3	C	501	GTP	C5-C6-N1	-3.51	118.62	123.43
3	E	501	GTP	PA-O3A-PB	-3.49	120.84	132.83
3	G	501	GTP	C5-C6-N1	-3.39	118.80	123.43
3	C	501	GTP	PB-O3B-PG	-3.37	121.25	132.83
3	A	501	GTP	PA-O3A-PB	-3.36	121.28	132.83
3	A	501	GTP	C5-C6-N1	-3.35	118.85	123.43
3	E	501	GTP	C2-N3-C4	3.35	119.18	115.36
3	A	501	GTP	PB-O3B-PG	-3.32	121.43	132.83
3	G	501	GTP	PB-O3B-PG	-3.18	121.92	132.83
3	E	501	GTP	C6-N1-C2	3.18	120.98	115.93
3	C	501	GTP	C6-N1-C2	3.02	120.72	115.93
3	G	501	GTP	C6-N1-C2	2.97	120.65	115.93
3	C	501	GTP	PA-O3A-PB	-2.58	123.96	132.83
3	A	501	GTP	C6-N1-C2	2.50	119.90	115.93
3	G	501	GTP	C3'-C2'-C1'	2.36	104.53	100.98
3	G	501	GTP	PA-O3A-PB	-2.22	125.19	132.83

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	501	GTP	C5'-O5'-PA-O1A
3	G	501	GTP	C5'-O5'-PA-O1A
3	A	501	GTP	C5'-O5'-PA-O1A
3	G	501	GTP	C5'-O5'-PA-O3A
3	A	501	GTP	C5'-O5'-PA-O3A
3	G	501	GTP	C5'-O5'-PA-O2A
3	A	501	GTP	O4'-C4'-C5'-O5'
3	A	501	GTP	C3'-C4'-C5'-O5'
3	E	501	GTP	C3'-C4'-C5'-O5'
3	E	501	GTP	O4'-C4'-C5'-O5'
3	C	501	GTP	O4'-C4'-C5'-O5'
3	E	501	GTP	C5'-O5'-PA-O3A

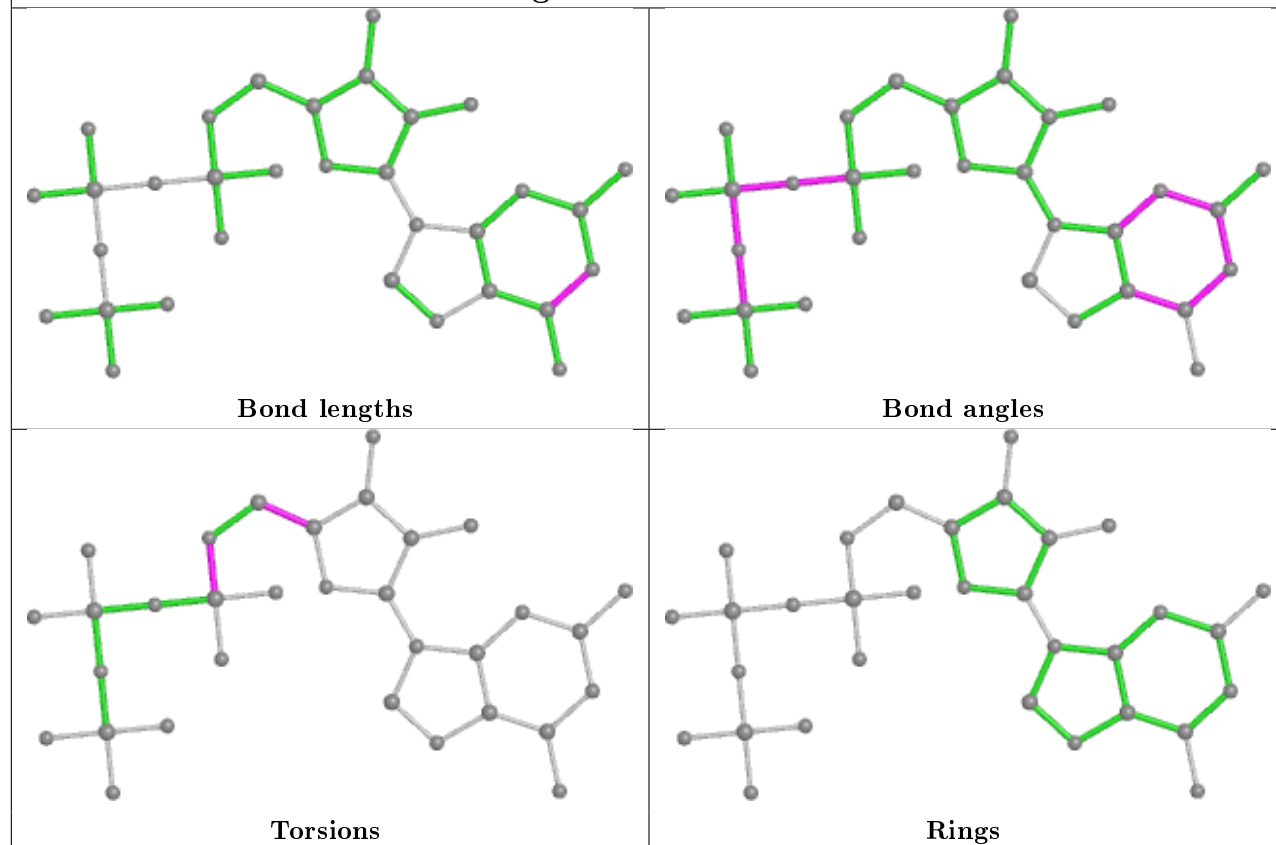
There are no ring outliers.

3 monomers are involved in 10 short contacts:

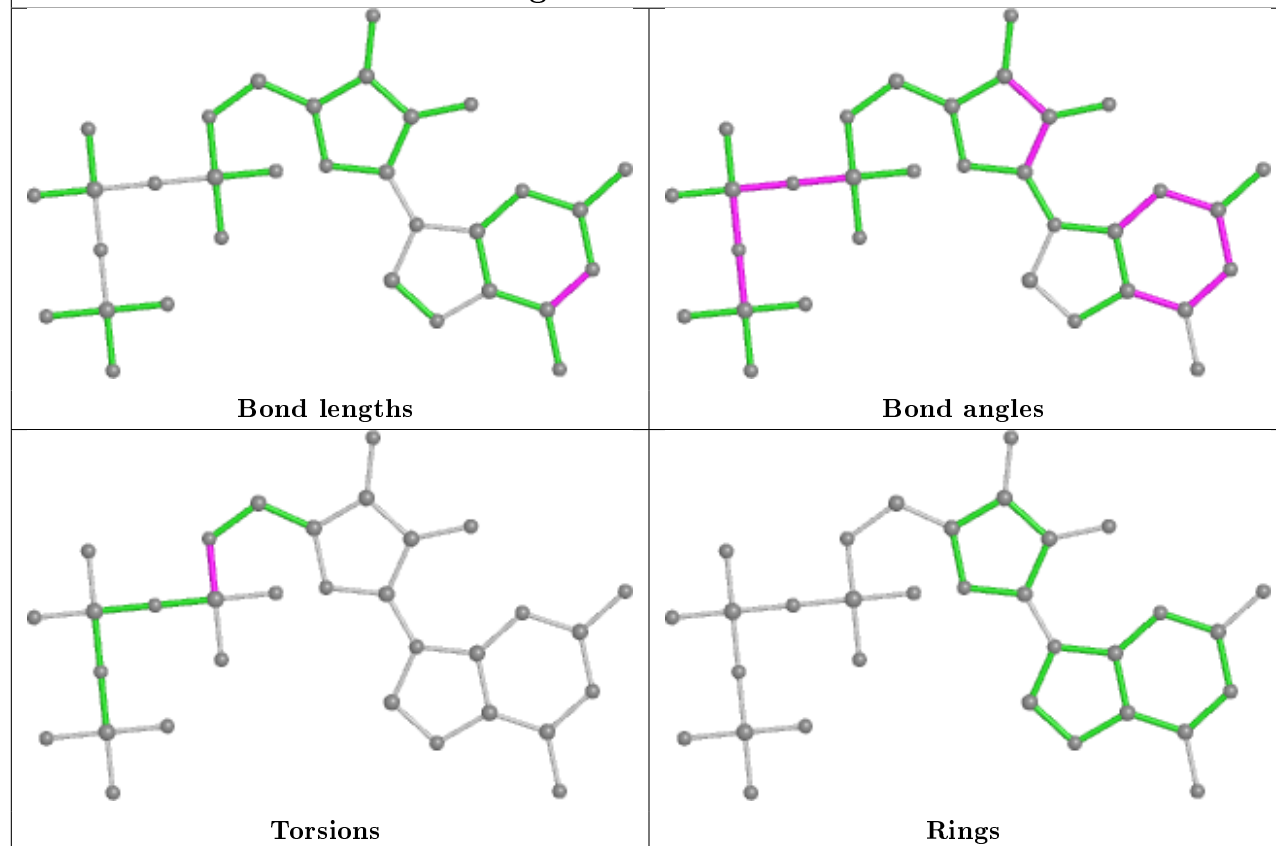
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	501	GTP	1	0
3	G	501	GTP	6	0
3	A	501	GTP	3	0

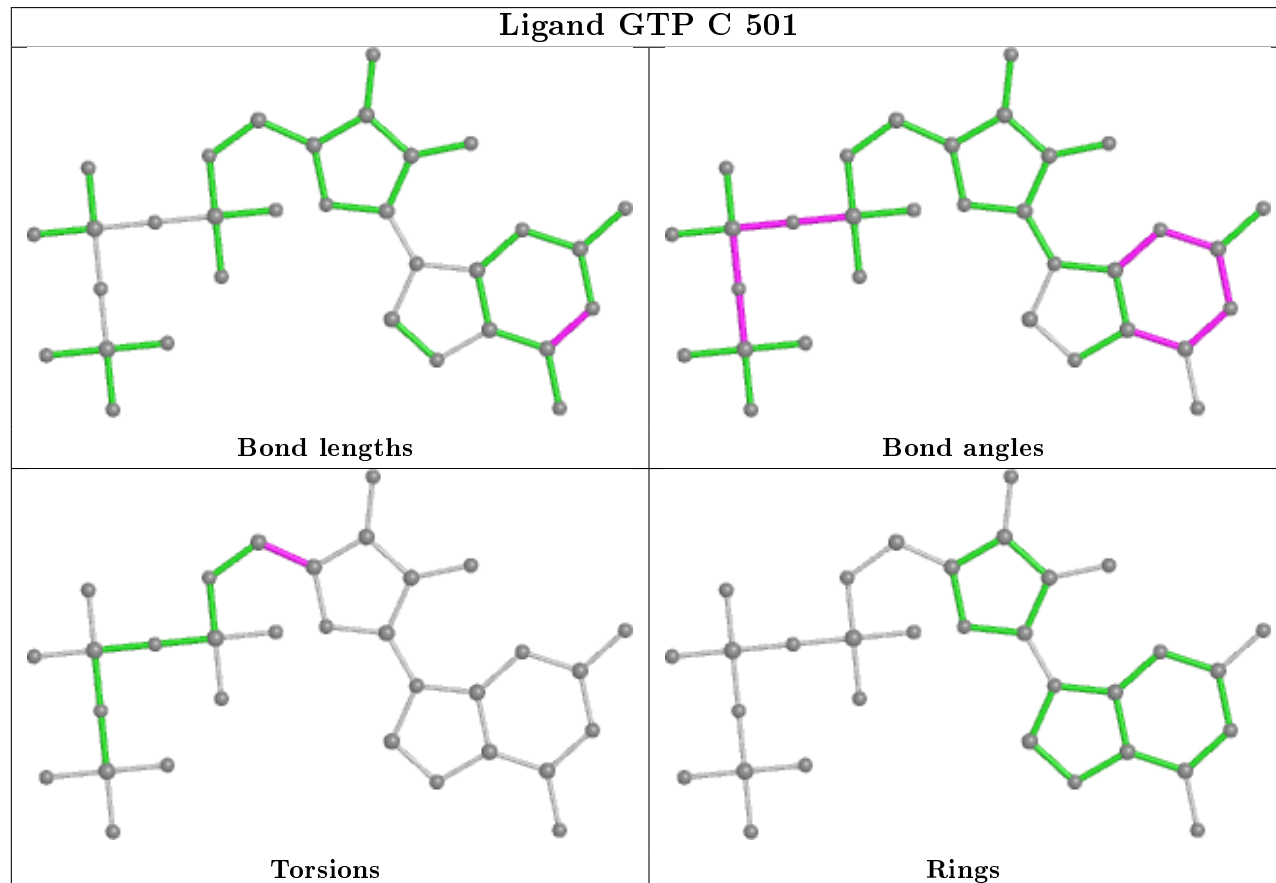
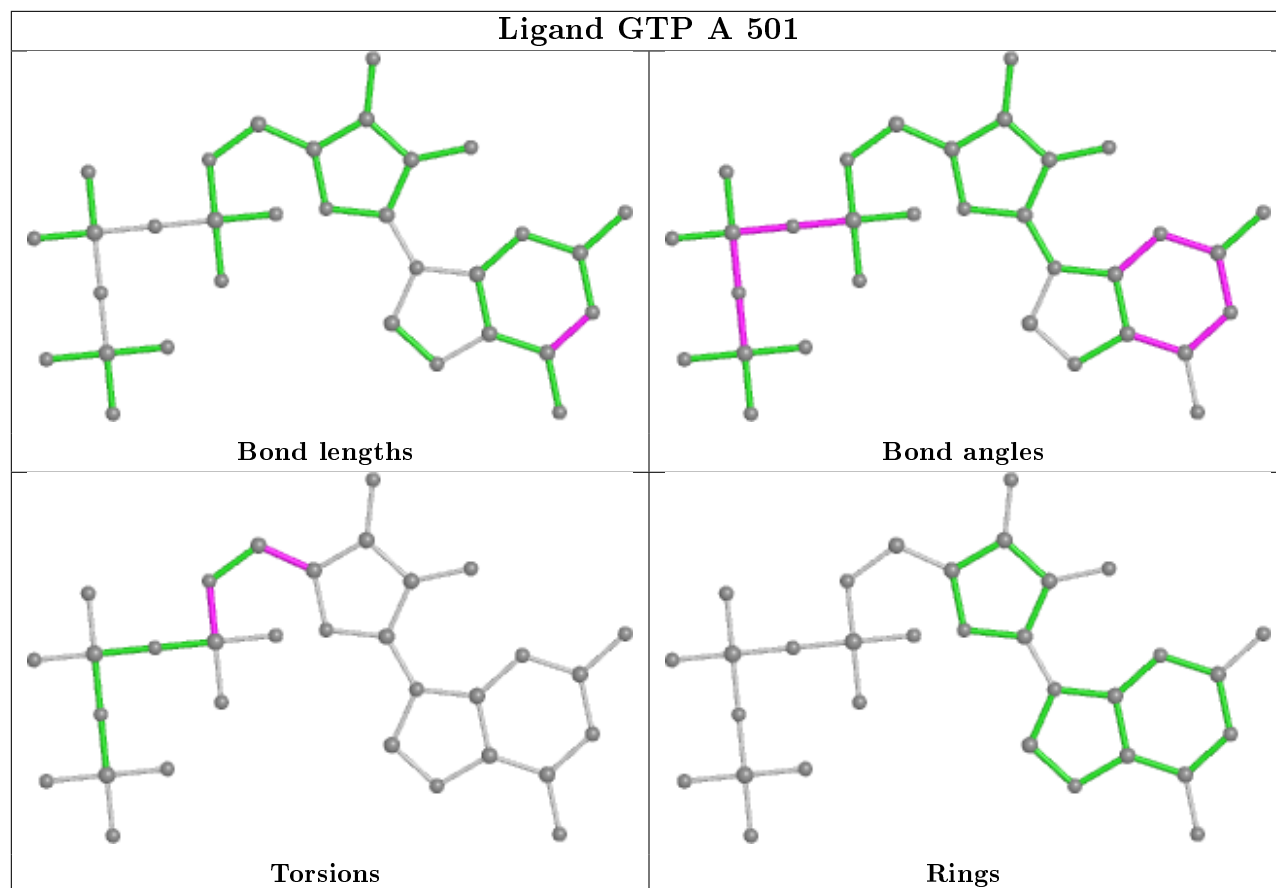
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

## Ligand GTP E 501



## Ligand GTP G 501





## 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	432/447 (96%)	-0.20	6 (1%) 75 80	20, 38, 62, 83	0
1	C	431/447 (96%)	-0.16	6 (1%) 75 80	24, 43, 69, 83	0
1	E	430/447 (96%)	-0.20	7 (1%) 72 77	27, 43, 63, 78	0
1	G	432/447 (96%)	0.11	23 (5%) 26 33	29, 50, 81, 91	0
2	B	357/376 (94%)	-0.36	7 (1%) 65 71	25, 39, 69, 82	0
2	D	357/376 (94%)	-0.38	7 (1%) 65 71	24, 40, 69, 84	0
2	F	355/376 (94%)	-0.38	6 (1%) 70 76	24, 41, 70, 88	0
2	H	356/376 (94%)	-0.27	10 (2%) 53 60	27, 45, 72, 88	0
All	All	3150/3292 (95%)	-0.22	72 (2%) 60 67	20, 43, 71, 91	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	432	VAL	7.3
1	A	432	VAL	4.5
1	A	433	ASP	4.3
2	B	44	VAL	4.1
2	F	46	VAL	4.1
1	G	49	GLY	3.9
1	G	22	LEU	3.5
1	G	368	LYS	3.5
2	H	87	PHE	3.5
1	G	208	PRO	3.5
1	A	435	LYS	3.5
1	G	372	VAL	3.4
1	G	373	VAL	3.4
1	G	205	PRO	3.3
1	C	432	VAL	3.2
1	A	434	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	433	ASP	3.2
2	D	44	VAL	3.1
1	G	11	VAL	3.0
2	H	55	VAL	2.9
1	G	229	VAL	2.9
1	C	205	PRO	2.9
2	B	85	ASP	2.9
2	H	85	ASP	2.9
1	C	229	VAL	2.8
1	E	74	LEU	2.8
1	G	433	ASP	2.8
2	B	355	ARG	2.8
2	H	54	VAL	2.7
2	D	46	VAL	2.6
1	C	22	LEU	2.6
2	H	8	ASN	2.6
2	B	2	ARG	2.6
2	F	158	ARG	2.6
1	E	11	VAL	2.6
2	D	85	ASP	2.6
2	B	46	VAL	2.5
2	D	87	PHE	2.5
2	H	44	VAL	2.5
1	G	114	VAL	2.5
1	G	23	VAL	2.5
2	F	85	ASP	2.5
2	D	54	VAL	2.4
1	E	230	ASP	2.4
1	E	48	ARG	2.4
1	G	226	ALA	2.4
2	F	88	GLY	2.4
1	G	375	GLN	2.4
1	G	103	THR	2.4
1	G	209	TRP	2.3
2	D	-1	SER	2.3
1	E	375	GLN	2.3
2	H	2	ARG	2.3
1	G	371	GLN	2.3
1	G	74	LEU	2.2
1	G	370	GLY	2.2
1	A	22	LEU	2.2
1	G	50	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	351	THR	2.2
1	C	230	ASP	2.2
1	E	368	LYS	2.1
2	D	355	ARG	2.1
2	B	87	PHE	2.1
2	H	84	PRO	2.1
1	A	11	VAL	2.1
1	E	73[A]	ASP	2.1
2	F	54	VAL	2.1
2	B	89	VAL	2.1
2	F	8	ASN	2.1
2	H	46	VAL	2.1
1	G	206	ASN	2.0
2	H	158	ARG	2.0

## 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.

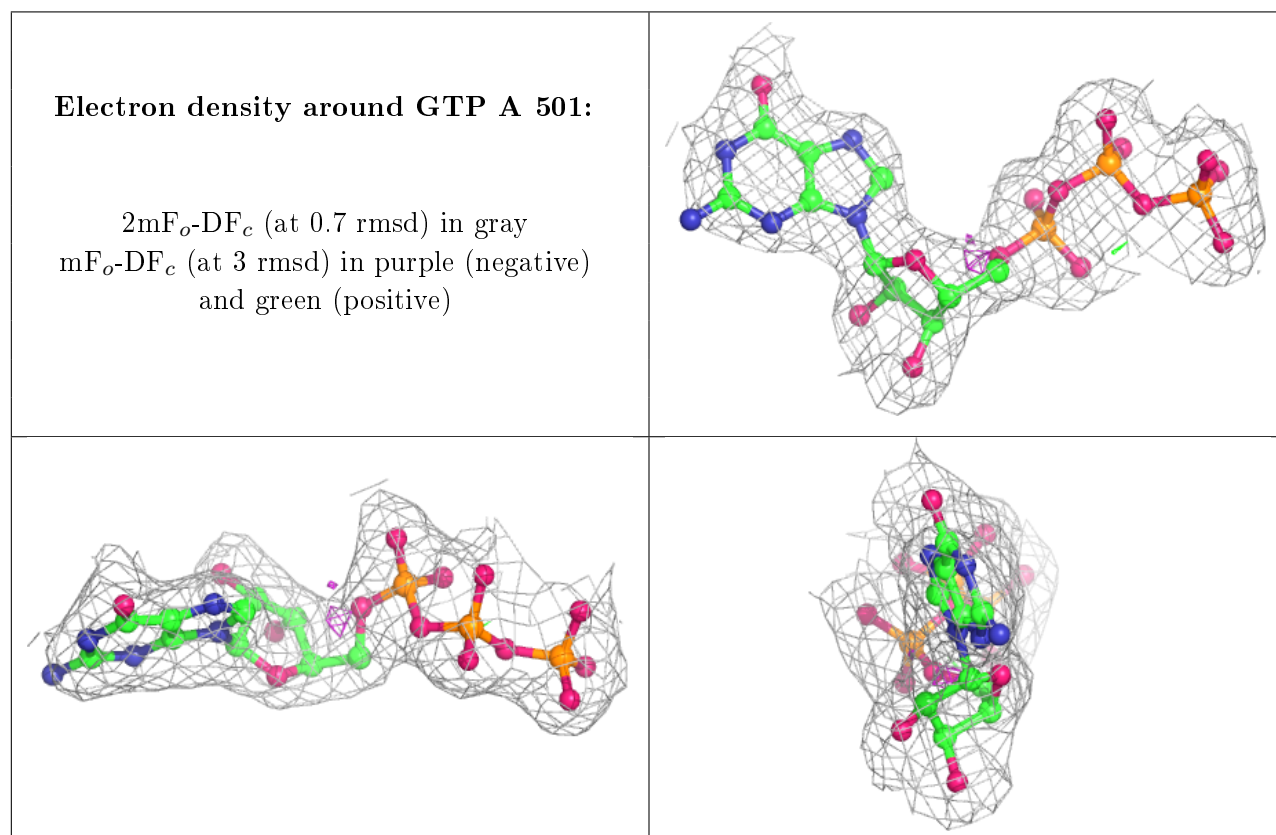
## 6.4 Ligands ⓘ

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. 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	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	MG	G	502	1/1	0.95	0.17	50,50,50,50	0
3	GTP	A	501	32/32	0.97	0.15	26,43,51,61	0
3	GTP	G	501	32/32	0.97	0.15	41,58,66,70	0
3	GTP	C	501	32/32	0.98	0.14	32,46,57,57	0
3	GTP	E	501	32/32	0.98	0.11	31,42,50,51	0
4	MG	A	502	1/1	0.98	0.16	33,33,33,33	0
4	MG	C	502	1/1	0.98	0.19	37,37,37,37	0
4	MG	E	502	1/1	0.99	0.15	38,38,38,38	0

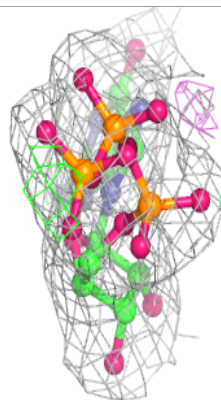
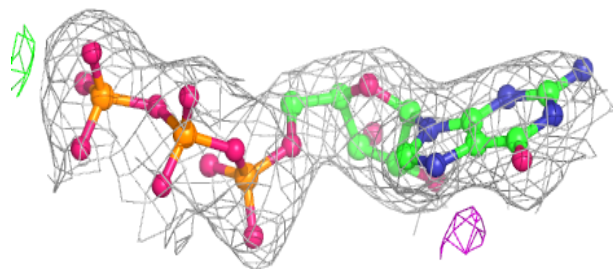
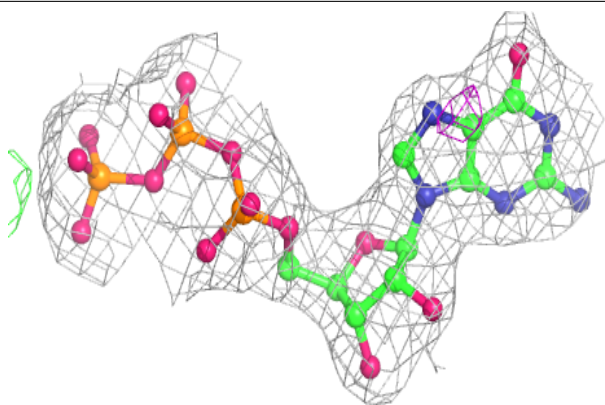


The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

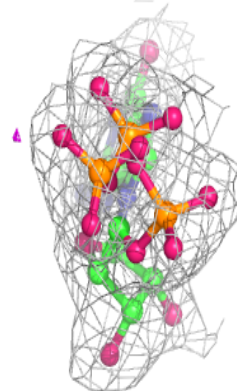
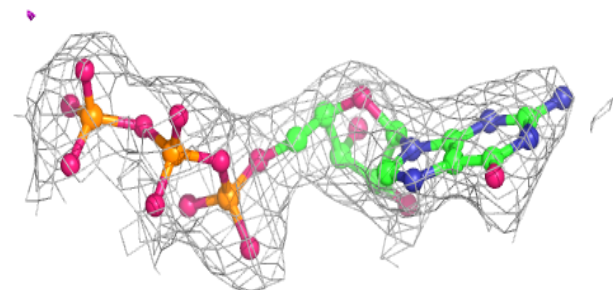
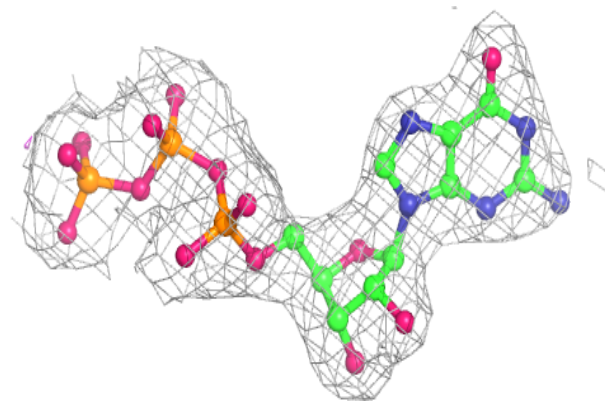


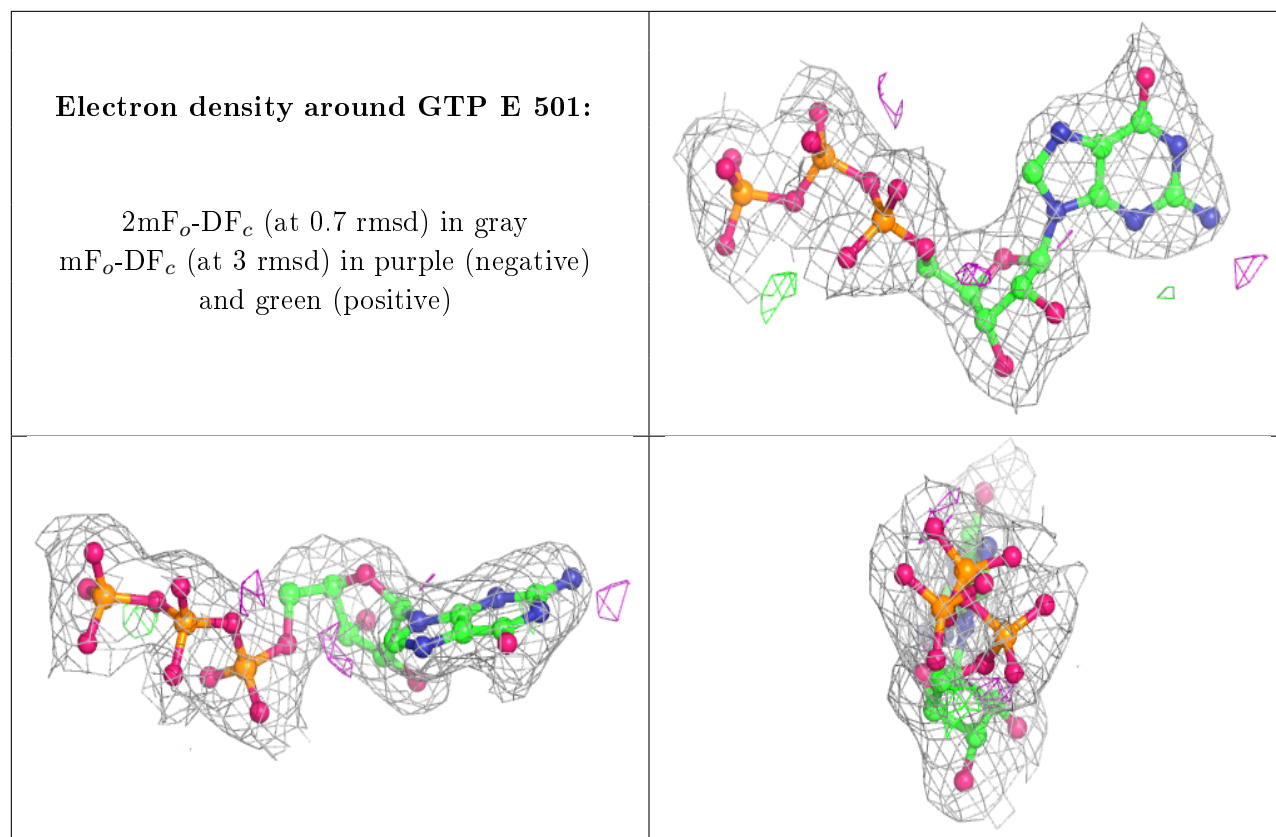
**Electron density around GTP G 501:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around GTP C 501:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.