



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:16 am GMT

PDB ID : 4FMB  
Title : VirA-Rab1 complex structure  
Authors : Shao, F.; Zhu, Y.  
Deposited on : 2012-06-16  
Resolution : 3.20 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

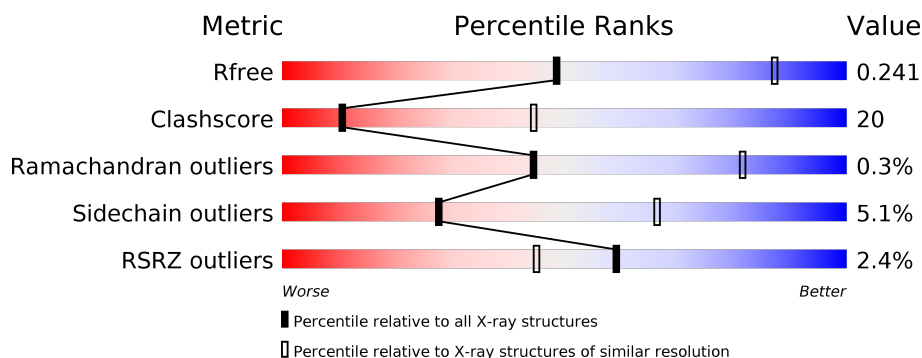
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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. 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	361	<div> <div>16%</div> <div> <div>62%</div> <div>33%</div> <div>• •</div> </div> </div>
1	C	361	<div> <div>63%</div> <div>32%</div> <div>• •</div> </div>
1	E	361	<div> <div>60%</div> <div>36%</div> <div>• •</div> </div>
2	B	171	<div> <div>56%</div> <div>40%</div> <div>•</div> </div>
2	D	171	<div> <div>59%</div> <div>38%</div> <div>•</div> </div>
2	F	171	<div> <div>16%</div> <div>50%</div> <div>47%</div> <div>• •</div> </div>

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
3	AF3	B	201	-	-	-	X
3	AF3	F	201	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12435 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 Cysteine protease-like virA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2750	1741	462	535	12			
1	C	350	Total	C	N	O	S	0	0	0
			2749	1742	461	534	12			
1	E	350	Total	C	N	O	S	0	0	0
			2749	1742	461	534	12			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	GLY	-	EXPRESSION TAG	UNP Q7BU69
A	41	PRO	-	EXPRESSION TAG	UNP Q7BU69
A	42	LEU	-	EXPRESSION TAG	UNP Q7BU69
A	43	GLY	-	EXPRESSION TAG	UNP Q7BU69
A	44	SER	-	EXPRESSION TAG	UNP Q7BU69
C	40	GLY	-	EXPRESSION TAG	UNP Q7BU69
C	41	PRO	-	EXPRESSION TAG	UNP Q7BU69
C	42	LEU	-	EXPRESSION TAG	UNP Q7BU69
C	43	GLY	-	EXPRESSION TAG	UNP Q7BU69
C	44	SER	-	EXPRESSION TAG	UNP Q7BU69
E	40	GLY	-	EXPRESSION TAG	UNP Q7BU69
E	41	PRO	-	EXPRESSION TAG	UNP Q7BU69
E	42	LEU	-	EXPRESSION TAG	UNP Q7BU69
E	43	GLY	-	EXPRESSION TAG	UNP Q7BU69
E	44	SER	-	EXPRESSION TAG	UNP Q7BU69

- Molecule 2 is a protein called Ras-related protein Rab-1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	171	Total	C	N	O	S	0	0	0
			1362	867	223	267	5			

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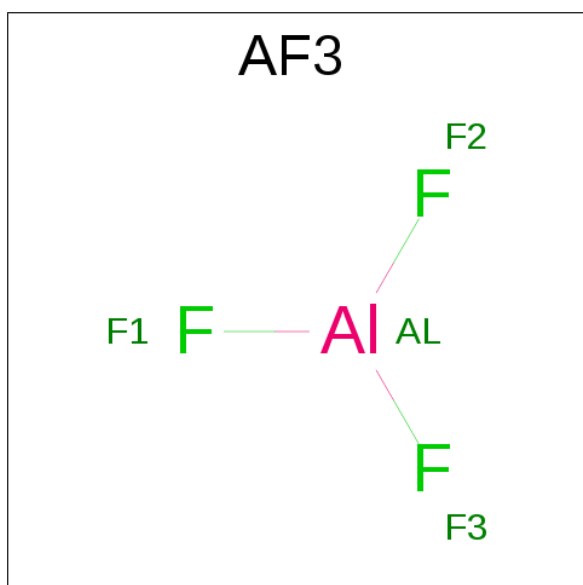
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	171	Total	C	N	O	S	0	0	0
			1362	867	223	267	5			
2	F	170	Total	C	N	O	S	0	0	0
			1355	862	222	266	5			

There are 3 discrepancies between the modelled and reference sequences:

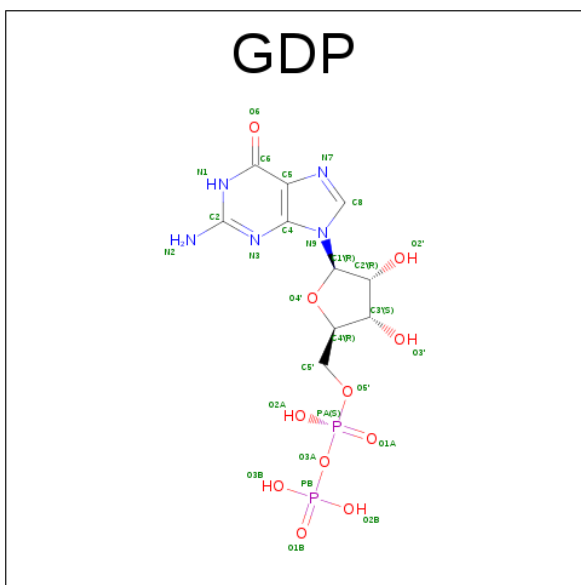
Chain	Residue	Modelled	Actual	Comment	Reference
B	10	ALA	TYR	SEE REMARK 999	UNP P62820
D	10	ALA	TYR	SEE REMARK 999	UNP P62820
F	10	ALA	TYR	SEE REMARK 999	UNP P62820

- Molecule 3 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula:  $\text{AlF}_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	Al	F	0	0
			4	1	3		
3	D	1	Total	Al	F	0	0
			4	1	3		
3	F	1	Total	Al	F	0	0
			4	1	3		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$ ).



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

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

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	3	Total O 3 3	0	0
6	C	1	Total O 1 1	0	0
6	D	2	Total O 2 2	0	0

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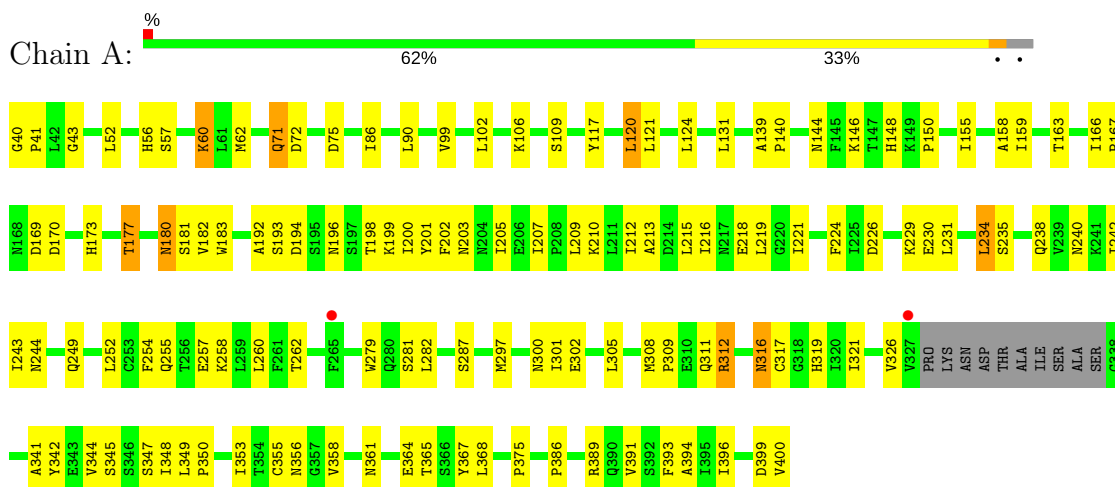
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	O	0	0
			1	1		
6	F	2	Total	O	0	0
			2	2		

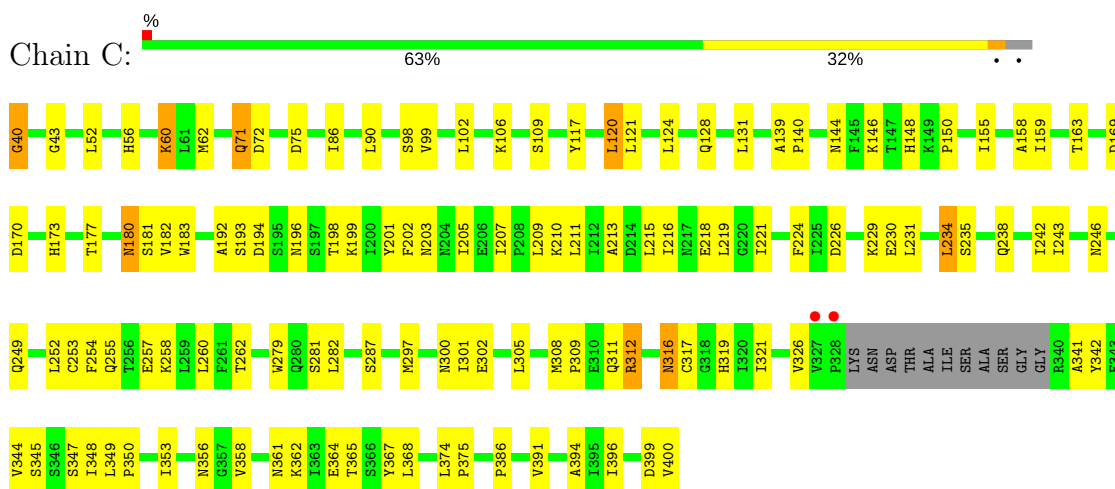
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

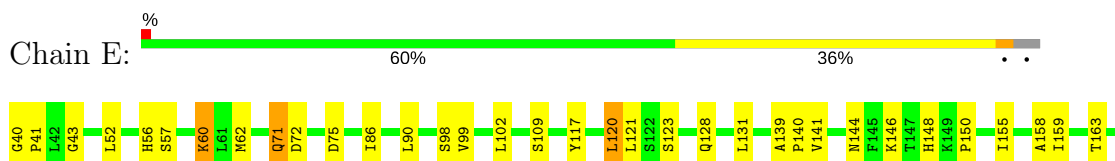
#### • Molecule 1: Cysteine protease-like virA



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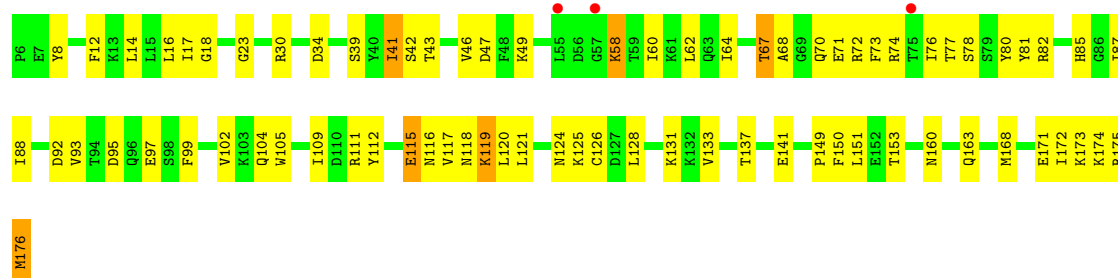
#### • Molecule 1: Cysteine protease-like virA



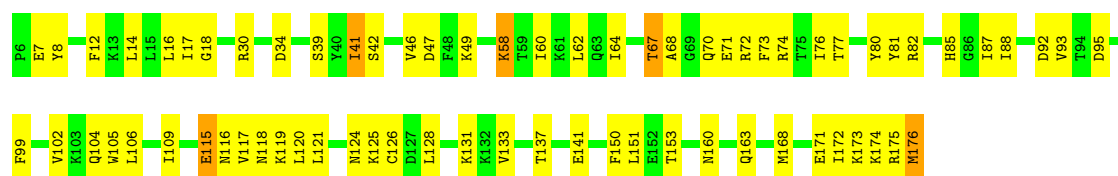




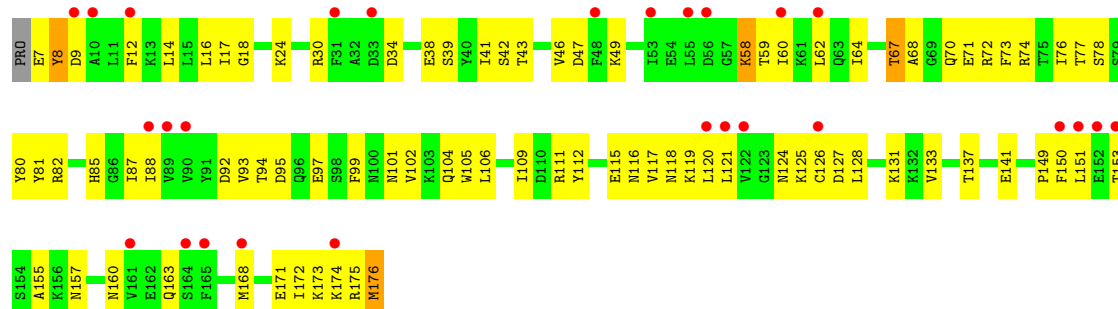
• Molecule 2: Ras-related protein Rab-1A



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• Molecule 2: Ras-related protein Rab-1A



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	186.12Å 127.31Å 107.33Å 90.00° 94.45° 90.00°	Depositor
Resolution (Å)	50.00 – 3.20 48.54 – 3.20	Depositor EDS
% Data completeness (in resolution range)	93.2 (50.00-3.20) 91.7 (48.54-3.20)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 3.19Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.228 , 0.247 0.227 , 0.241	Depositor DCC
$R_{free}$ test set	1886 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	87.0	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 59.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12435	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.44	0/2809	0.68	3/3810 (0.1%)
1	C	0.45	1/2809 (0.0%)	0.67	3/3812 (0.1%)
1	E	0.45	0/2809	0.63	0/3812
2	B	0.39	0/1384	0.70	5/1868 (0.3%)
2	D	0.40	0/1384	0.70	5/1868 (0.3%)
2	F	0.45	0/1376	0.62	2/1857 (0.1%)
All	All	0.44	1/12571 (0.0%)	0.67	18/17027 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	40	GLY	N-CA	5.63	1.54	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	C	312	ARG	NE-CZ-NH1	10.37	125.49	120.30
1	A	312	ARG	NE-CZ-NH2	-10.31	115.14	120.30
1	C	312	ARG	NE-CZ-NH2	-9.87	115.36	120.30
2	B	82	ARG	NE-CZ-NH2	9.63	125.11	120.30
2	D	82	ARG	NE-CZ-NH2	9.21	124.91	120.30
2	B	82	ARG	NE-CZ-NH1	-9.13	115.74	120.30
2	D	82	ARG	NE-CZ-NH1	-8.92	115.84	120.30
2	D	151	LEU	N-CA-CB	-5.77	98.86	110.40
2	B	151	LEU	N-CA-CB	-5.73	98.94	110.40
1	A	312	ARG	CD-NE-CZ	5.60	131.44	123.60
2	B	120	LEU	N-CA-CB	-5.60	99.20	110.40
1	C	312	ARG	CD-NE-CZ	5.57	131.40	123.60
2	D	120	LEU	N-CA-CB	-5.55	99.29	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	151	LEU	N-CA-CB	-5.45	99.50	110.40
2	D	82	ARG	CD-NE-CZ	5.36	131.10	123.60
2	B	82	ARG	CD-NE-CZ	5.19	130.87	123.60
2	F	120	LEU	N-CA-CB	-5.17	100.07	110.40

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	2750	0	2703	106	0
1	C	2749	0	2704	105	0
1	E	2749	0	2704	111	0
2	B	1362	0	1361	68	0
2	D	1362	0	1361	58	0
2	F	1355	0	1353	77	0
3	B	4	0	0	1	0
3	D	4	0	0	0	0
3	F	4	0	0	1	0
4	B	28	0	12	4	0
4	D	28	0	12	1	0
4	F	28	0	12	3	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
6	B	3	0	0	0	0
6	C	1	0	0	0	0
6	D	2	0	0	0	0
6	E	1	0	0	0	0
6	F	2	0	0	0	0
All	All	12435	0	12222	505	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.

All (505) 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:C:40:GLY:HA3	1:C:43:GLY:H	1.18	1.06
2:F:118:ASN:HD22	2:F:171:GLU:HG3	1.29	0.97
2:D:118:ASN:HD22	2:D:171:GLU:HG3	1.33	0.94
2:B:118:ASN:HD22	2:B:171:GLU:HG3	1.31	0.92
2:F:67:THR:HG21	2:F:77:THR:HG23	1.53	0.90
1:C:40:GLY:HA3	1:C:43:GLY:N	1.88	0.88
1:E:326:VAL:HG11	1:E:341:ALA:HB3	1.57	0.87
2:D:67:THR:HG21	2:D:77:THR:HG23	1.55	0.87
2:B:67:THR:HG21	2:B:77:THR:HG23	1.55	0.87
2:F:87:ILE:HD12	2:F:109:ILE:HG23	1.59	0.84
1:C:193:SER:HB2	1:C:209:LEU:HD13	1.61	0.83
1:A:40:GLY:HA3	1:A:43:GLY:H	1.44	0.82
1:E:193:SER:HB2	1:E:209:LEU:HD13	1.60	0.82
1:C:235:SER:H	1:C:238:GLN:NE2	1.79	0.80
1:A:193:SER:HB2	1:A:209:LEU:HD13	1.61	0.80
2:D:87:ILE:HD12	2:D:109:ILE:HG23	1.64	0.80
2:B:87:ILE:HD12	2:B:109:ILE:HG23	1.63	0.80
1:C:281:SER:OG	2:D:70:GLN:HG2	1.81	0.80
1:E:281:SER:OG	2:F:70:GLN:HG2	1.83	0.79
1:E:249:GLN:CD	1:E:249:GLN:H	1.85	0.78
1:A:249:GLN:CD	1:A:249:GLN:H	1.86	0.78
1:A:229:LYS:HG2	1:A:230:GLU:N	2.00	0.77
1:A:235:SER:H	1:A:238:GLN:NE2	1.80	0.77
1:E:229:LYS:HG2	1:E:230:GLU:N	2.01	0.76
1:E:235:SER:H	1:E:238:GLN:NE2	1.83	0.75
2:B:160:ASN:HA	2:B:163:GLN:OE1	1.87	0.75
1:C:249:GLN:CD	1:C:249:GLN:H	1.90	0.75
2:F:117:VAL:HG13	2:F:119:LYS:HE2	1.68	0.75
1:E:219:LEU:HD21	1:E:234:LEU:HD11	1.69	0.74
1:E:327:VAL:HB	1:E:328:PRO:HD2	1.68	0.74
2:D:160:ASN:HA	2:D:163:GLN:OE1	1.88	0.74
2:D:46:VAL:HG12	2:D:47:ASP:N	2.02	0.74
1:C:180:ASN:HD22	1:C:181:SER:H	1.35	0.74
1:A:282:LEU:HD21	1:A:367:TYR:HE2	1.54	0.73
2:B:46:VAL:HG12	2:B:47:ASP:N	2.01	0.73
1:A:281:SER:OG	2:B:70:GLN:HG2	1.87	0.73
1:C:235:SER:H	1:C:238:GLN:HE21	1.36	0.73
1:C:326:VAL:HG11	1:C:341:ALA:HB3	1.71	0.73
1:E:243:ILE:HD11	1:E:262:THR:HA	1.69	0.73
1:A:219:LEU:HD21	1:A:234:LEU:HD11	1.71	0.73
1:E:180:ASN:HD22	1:E:181:SER:H	1.36	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ASN:HD22	1:A:181:SER:H	1.36	0.72
1:C:229:LYS:HG2	1:C:230:GLU:N	2.03	0.72
1:E:40:GLY:HA3	1:E:43:GLY:H	1.55	0.72
1:C:243:ILE:HD11	1:C:262:THR:HA	1.72	0.72
2:F:160:ASN:HA	2:F:163:GLN:OE1	1.89	0.71
1:E:40:GLY:N	1:E:41:PRO:HA	2.04	0.71
1:A:235:SER:H	1:A:238:GLN:HE21	1.38	0.71
1:C:219:LEU:HD21	1:C:234:LEU:HD11	1.73	0.71
2:F:46:VAL:HG12	2:F:47:ASP:N	2.05	0.70
2:B:117:VAL:O	2:B:119:LYS:HE2	1.91	0.69
2:D:117:VAL:HG13	2:D:119:LYS:HE2	1.75	0.69
1:A:243:ILE:HD11	1:A:262:THR:HA	1.75	0.68
1:C:282:LEU:HD21	1:C:367:TYR:HE2	1.59	0.68
2:F:118:ASN:ND2	2:F:171:GLU:HG3	2.07	0.67
1:A:146:LYS:HA	1:A:311:GLN:HE21	1.60	0.67
1:A:305:LEU:O	1:A:309:PRO:HG3	1.95	0.66
1:A:196:ASN:HD21	2:B:41:ILE:HG21	1.60	0.66
1:E:308:MET:HB2	1:E:311:GLN:HB3	1.78	0.65
1:E:146:LYS:HA	1:E:311:GLN:HE21	1.60	0.65
1:A:308:MET:HB2	1:A:311:GLN:HB3	1.79	0.65
1:C:305:LEU:O	1:C:309:PRO:HG3	1.97	0.65
1:E:305:LEU:O	1:E:309:PRO:HG3	1.95	0.65
2:F:70:GLN:HE21	2:F:72:ARG:HG2	1.61	0.65
1:C:146:LYS:HA	1:C:311:GLN:HE21	1.61	0.64
2:B:118:ASN:ND2	2:B:171:GLU:HG3	2.09	0.64
1:A:326:VAL:HG11	1:A:341:ALA:HB3	1.78	0.64
1:E:317:CYS:HB2	1:E:349:LEU:HB2	1.78	0.64
2:F:30:ARG:O	2:F:34:ASP:HA	1.98	0.64
2:F:121:LEU:HD23	2:F:150:PHE:CD1	2.33	0.64
1:E:235:SER:H	1:E:238:GLN:HE21	1.43	0.64
1:E:180:ASN:HD22	1:E:181:SER:N	1.97	0.63
2:F:116:ASN:HD22	2:F:175:ARG:NH2	1.95	0.63
1:C:193:SER:HA	1:C:196:ASN:HB2	1.80	0.63
1:C:279:TRP:CZ2	1:C:281:SER:HB2	2.34	0.63
2:B:128:LEU:HD21	4:B:202:GDP:N2	2.14	0.63
2:D:116:ASN:HD22	2:D:175:ARG:NH2	1.97	0.63
1:A:155:ILE:O	1:A:159:ILE:HG13	1.98	0.63
1:A:317:CYS:HB2	1:A:349:LEU:HB2	1.79	0.62
2:B:128:LEU:HD21	4:B:202:GDP:HN21	1.65	0.62
1:A:180:ASN:HD22	1:A:181:SER:N	1.97	0.62
1:C:308:MET:HB2	1:C:311:GLN:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:LYS:HG2	1:E:230:GLU:H	1.65	0.62
1:A:193:SER:HA	1:A:196:ASN:HB2	1.81	0.62
2:B:121:LEU:HD23	2:B:150:PHE:CD1	2.34	0.62
2:D:70:GLN:HE21	2:D:72:ARG:HG2	1.65	0.62
1:A:229:LYS:HG2	1:A:230:GLU:H	1.62	0.62
1:C:180:ASN:HD22	1:C:181:SER:N	1.97	0.62
1:C:317:CYS:HB2	1:C:349:LEU:HB2	1.81	0.61
1:C:229:LYS:HG2	1:C:230:GLU:H	1.65	0.61
1:A:282:LEU:HD21	1:A:367:TYR:CE2	2.36	0.61
2:D:99:PHE:O	2:D:102:VAL:HG23	2.01	0.61
1:E:300:ASN:ND2	1:E:353:ILE:H	1.98	0.61
1:A:180:ASN:ND2	1:A:181:SER:N	2.49	0.61
1:E:180:ASN:ND2	1:E:181:SER:N	2.49	0.61
1:A:300:ASN:ND2	1:A:353:ILE:H	1.99	0.60
1:C:180:ASN:ND2	1:C:181:SER:H	1.99	0.60
2:D:117:VAL:O	2:D:119:LYS:HE2	2.00	0.60
2:B:70:GLN:HE21	2:B:72:ARG:HG2	1.67	0.60
2:B:116:ASN:HD22	2:B:175:ARG:NH2	1.97	0.60
1:C:155:ILE:O	1:C:159:ILE:HG13	2.01	0.60
1:C:180:ASN:ND2	1:C:181:SER:N	2.49	0.60
1:A:180:ASN:ND2	1:A:181:SER:H	2.00	0.60
2:D:92:ASP:HB3	2:D:95:ASP:HB3	1.85	0.59
1:E:282:LEU:HD21	1:E:367:TYR:HE2	1.65	0.59
2:B:30:ARG:O	2:B:34:ASP:HA	2.02	0.59
1:A:279:TRP:CZ2	1:A:281:SER:HB2	2.37	0.59
1:C:117:TYR:CE2	1:C:121:LEU:HD11	2.38	0.59
2:B:60:ILE:N	2:B:60:ILE:HD12	2.18	0.59
1:C:182:VAL:HG13	1:C:183:TRP:N	2.16	0.59
2:D:121:LEU:HD23	2:D:150:PHE:CD1	2.38	0.59
2:F:58:LYS:HA	2:F:58:LYS:HE3	1.85	0.59
1:E:235:SER:OG	1:E:238:GLN:HG3	2.02	0.59
2:B:92:ASP:HB3	2:B:95:ASP:HB3	1.84	0.58
1:C:196:ASN:HD21	2:D:41:ILE:HG21	1.68	0.58
1:E:193:SER:HA	1:E:196:ASN:HB2	1.85	0.58
1:E:182:VAL:HG13	1:E:183:TRP:N	2.17	0.58
1:E:180:ASN:ND2	1:E:181:SER:H	2.00	0.58
1:E:243:ILE:HD13	1:E:262:THR:OG1	2.03	0.58
1:A:117:TYR:CE2	1:A:121:LEU:HD11	2.38	0.58
2:B:46:VAL:CG1	2:B:47:ASP:N	2.66	0.58
1:C:243:ILE:HD13	1:C:262:THR:OG1	2.04	0.58
2:D:118:ASN:ND2	2:D:171:GLU:HG3	2.11	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:99:PHE:O	2:B:102:VAL:HG23	2.04	0.58
1:E:155:ILE:O	1:E:159:ILE:HG13	2.03	0.58
1:E:301:ILE:HG22	1:E:305:LEU:HD23	1.85	0.58
2:F:92:ASP:HB3	2:F:95:ASP:HB3	1.85	0.58
1:C:300:ASN:ND2	1:C:353:ILE:H	2.01	0.57
1:E:213:ALA:O	1:E:216:ILE:HG22	2.03	0.57
2:D:58:LYS:HE3	2:D:58:LYS:HA	1.86	0.57
2:D:60:ILE:HD12	2:D:60:ILE:N	2.18	0.57
2:B:58:LYS:HE3	2:B:58:LYS:HA	1.86	0.57
2:D:30:ARG:O	2:D:34:ASP:HA	2.05	0.57
1:A:235:SER:OG	1:A:238:GLN:HG3	2.05	0.57
2:D:46:VAL:CG1	2:D:47:ASP:N	2.66	0.57
2:F:60:ILE:HD12	2:F:60:ILE:N	2.20	0.57
1:A:182:VAL:HG13	1:A:183:TRP:N	2.19	0.57
1:A:231:LEU:HB2	1:A:375:PRO:HB2	1.87	0.57
1:A:301:ILE:HG22	1:A:305:LEU:HD23	1.85	0.56
1:C:226:ASP:HB3	1:C:229:LYS:HB2	1.87	0.56
1:C:40:GLY:CA	1:C:43:GLY:H	2.06	0.56
1:E:249:GLN:HA	1:E:258:LYS:NZ	2.20	0.56
1:E:326:VAL:HG12	1:E:341:ALA:O	2.05	0.56
1:E:192:ALA:HB2	2:F:39:SER:HA	1.88	0.56
1:E:350:PRO:HD2	1:E:361:ASN:O	2.05	0.56
2:F:117:VAL:O	2:F:119:LYS:HE2	2.05	0.56
1:A:163:THR:HG22	1:A:394:ALA:CB	2.36	0.56
2:D:46:VAL:HG12	2:D:47:ASP:H	1.70	0.56
1:E:319:HIS:HB3	1:E:321:ILE:HD11	1.88	0.56
2:F:46:VAL:CG1	2:F:47:ASP:N	2.69	0.56
1:C:121:LEU:HD22	1:C:131:LEU:HD13	1.87	0.56
1:A:226:ASP:HB3	1:A:229:LYS:HB2	1.89	0.55
1:C:282:LEU:HD21	1:C:367:TYR:CE2	2.38	0.55
1:C:300:ASN:HD22	1:C:353:ILE:H	1.54	0.55
2:D:14:LEU:N	2:D:14:LEU:HD12	2.21	0.55
1:C:193:SER:CB	1:C:209:LEU:HD13	2.35	0.55
1:C:301:ILE:HG22	1:C:305:LEU:HD23	1.87	0.55
1:A:350:PRO:HD2	1:A:361:ASN:O	2.06	0.55
2:F:46:VAL:HG12	2:F:47:ASP:H	1.71	0.55
2:B:46:VAL:HG12	2:B:47:ASP:H	1.68	0.55
1:E:40:GLY:N	1:E:41:PRO:CA	2.69	0.55
2:B:92:ASP:OD1	2:B:125:LYS:HD2	2.06	0.55
1:C:210:LYS:O	1:C:213:ALA:HB3	2.07	0.55
1:E:249:GLN:CD	1:E:249:GLN:N	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:92:ASP:OD1	2:F:125:LYS:HD2	2.07	0.55
2:F:99:PHE:O	2:F:102:VAL:HG23	2.07	0.55
1:A:243:ILE:HD13	1:A:262:THR:OG1	2.08	0.54
1:C:312:ARG:HG3	2:D:49:LYS:NZ	2.21	0.54
1:E:319:HIS:HB3	1:E:321:ILE:CD1	2.37	0.54
2:F:43:THR:HB	3:F:201:AF3:F2	1.97	0.54
1:E:150:PRO:HG3	1:E:358:VAL:HG12	1.90	0.54
1:E:226:ASP:HB3	1:E:229:LYS:HB2	1.88	0.54
1:E:279:TRP:CZ2	1:E:281:SER:HB2	2.42	0.54
1:C:342:TYR:O	1:C:368:LEU:HD12	2.08	0.54
1:C:235:SER:OG	1:C:238:GLN:HG3	2.07	0.54
1:E:210:LYS:O	1:E:213:ALA:HB3	2.06	0.54
1:A:121:LEU:HD22	1:A:131:LEU:HD13	1.88	0.54
1:C:319:HIS:HB3	1:C:321:ILE:HD11	1.88	0.54
2:F:8:TYR:C	2:F:8:TYR:CD2	2.81	0.54
2:F:9:ASP:OD2	2:F:59:THR:N	2.40	0.54
1:C:319:HIS:HB3	1:C:321:ILE:CD1	2.37	0.54
2:F:14:LEU:HD12	2:F:14:LEU:N	2.23	0.54
1:C:213:ALA:O	1:C:216:ILE:HG22	2.08	0.54
1:A:210:LYS:O	1:A:213:ALA:HB3	2.08	0.53
1:C:90:LEU:HD22	1:C:120:LEU:HD11	1.90	0.53
1:A:249:GLN:HA	1:A:258:LYS:NZ	2.24	0.53
1:C:249:GLN:HA	1:C:258:LYS:NZ	2.23	0.53
2:B:14:LEU:HD12	2:B:14:LEU:N	2.22	0.53
2:F:105:TRP:O	2:F:109:ILE:HG13	2.07	0.53
1:C:180:ASN:HD22	1:C:180:ASN:N	2.06	0.53
1:A:213:ALA:O	1:A:216:ILE:HG22	2.09	0.53
1:A:249:GLN:CD	1:A:249:GLN:N	2.60	0.53
1:E:121:LEU:HD22	1:E:131:LEU:HD13	1.91	0.53
1:E:56:HIS:HB3	1:E:60:LYS:HE2	1.90	0.53
1:A:300:ASN:HD22	1:A:353:ILE:H	1.56	0.52
2:B:46:VAL:CG1	2:B:47:ASP:H	2.22	0.52
1:A:193:SER:CB	1:A:209:LEU:HD13	2.35	0.52
1:A:180:ASN:HD22	1:A:180:ASN:N	2.06	0.52
1:E:117:TYR:CE2	1:E:121:LEU:HD11	2.43	0.52
2:B:43:THR:HB	3:B:201:AF3:F2	1.99	0.52
2:F:67:THR:HG21	2:F:77:THR:CG2	2.34	0.52
1:E:300:ASN:HD22	1:E:353:ILE:H	1.57	0.52
2:F:88:ILE:HG12	2:F:168:MET:HE2	1.92	0.52
1:A:312:ARG:HG3	2:B:49:LYS:NZ	2.24	0.52
1:E:163:THR:HG22	1:E:394:ALA:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:105:TRP:O	2:D:109:ILE:HG13	2.10	0.51
1:E:180:ASN:HD22	1:E:180:ASN:N	2.08	0.51
2:D:88:ILE:HG12	2:D:168:MET:HE2	1.92	0.51
2:D:46:VAL:CG1	2:D:47:ASP:H	2.22	0.51
2:B:105:TRP:O	2:B:109:ILE:HG13	2.09	0.51
1:E:216:ILE:HG12	1:E:221:ILE:HB	1.91	0.51
2:F:121:LEU:HD23	2:F:150:PHE:HD1	1.75	0.51
2:D:128:LEU:HD21	4:D:202:GDP:N2	2.26	0.51
1:E:202:PHE:CD2	1:E:260:LEU:HD21	2.46	0.51
1:C:144:ASN:ND2	1:C:146:LYS:H	2.08	0.51
2:F:77:THR:HG22	2:F:81:TYR:HE1	1.75	0.51
2:F:70:GLN:HG3	2:F:72:ARG:H	1.76	0.51
1:C:297:MET:O	1:C:301:ILE:HG12	2.11	0.51
1:A:342:TYR:O	1:A:368:LEU:HD12	2.10	0.51
1:C:234:LEU:HD12	1:C:234:LEU:N	2.26	0.51
1:A:192:ALA:HB2	2:B:39:SER:HA	1.93	0.50
1:A:202:PHE:CD2	1:A:260:LEU:HD21	2.46	0.50
2:B:131:LYS:O	2:B:133:VAL:HG13	2.12	0.50
1:E:148:HIS:HA	1:E:312:ARG:O	2.11	0.50
2:F:85:HIS:HB3	2:F:172:ILE:HD13	1.93	0.50
2:F:14:LEU:HD11	2:F:62:LEU:HD22	1.93	0.50
1:C:231:LEU:HB2	1:C:375:PRO:HB2	1.92	0.50
1:E:243:ILE:CD1	1:E:262:THR:HA	2.39	0.50
2:F:99:PHE:HA	2:F:102:VAL:HG23	1.93	0.50
2:F:71:GLU:O	2:F:74:ARG:HG3	2.12	0.50
1:A:163:THR:HG22	1:A:394:ALA:HB2	1.93	0.50
2:F:46:VAL:CG1	2:F:47:ASP:H	2.24	0.50
1:A:71:GLN:H	1:A:71:GLN:CD	2.15	0.50
2:F:131:LYS:O	2:F:133:VAL:HG13	2.11	0.50
2:F:73:PHE:HD1	2:F:76:ILE:HD11	1.77	0.50
2:B:77:THR:HG22	2:B:81:TYR:HE1	1.77	0.50
2:D:67:THR:HG21	2:D:77:THR:CG2	2.36	0.50
1:E:347:SER:OG	1:E:364:GLU:HG3	2.12	0.50
1:E:90:LEU:HD22	1:E:120:LEU:HD11	1.93	0.50
1:C:202:PHE:CD2	1:C:260:LEU:HD21	2.46	0.50
1:A:216:ILE:HG12	1:A:221:ILE:HB	1.94	0.49
1:C:198:THR:HA	1:C:319:HIS:O	2.12	0.49
1:E:193:SER:CB	1:E:209:LEU:HD13	2.36	0.49
2:D:92:ASP:OD1	2:D:125:LYS:HD2	2.12	0.49
1:A:144:ASN:ND2	1:A:146:LYS:H	2.10	0.49
2:D:77:THR:HG22	2:D:81:TYR:HE1	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:24:LYS:HB2	4:F:202:GDP:O3B	2.12	0.49
2:B:73:PHE:HD1	2:B:76:ILE:HD11	1.77	0.49
1:C:71:GLN:H	1:C:71:GLN:CD	2.16	0.49
1:E:234:LEU:HD12	1:E:234:LEU:N	2.27	0.49
1:A:234:LEU:HD12	1:A:234:LEU:N	2.27	0.49
1:C:216:ILE:HG12	1:C:221:ILE:HB	1.93	0.49
2:D:99:PHE:HA	2:D:102:VAL:HG23	1.95	0.49
1:E:282:LEU:HD21	1:E:367:TYR:CE2	2.46	0.49
2:B:85:HIS:HB3	2:B:172:ILE:HD13	1.94	0.49
1:C:56:HIS:HB3	1:C:60:LYS:HE2	1.95	0.49
2:D:85:HIS:HB3	2:D:172:ILE:HD13	1.95	0.49
1:E:71:GLN:CD	1:E:71:GLN:H	2.16	0.49
1:C:144:ASN:ND2	1:C:146:LYS:HB2	2.28	0.49
2:F:64:ILE:N	2:F:64:ILE:HD12	2.27	0.49
2:F:93:VAL:HG21	2:F:126:CYS:HA	1.94	0.49
1:A:148:HIS:HA	1:A:312:ARG:O	2.13	0.49
1:A:170:ASP:OD2	1:A:287:SER:HB2	2.13	0.49
2:F:125:LYS:HE2	4:F:202:GDP:N9	2.28	0.49
2:B:23:GLY:HA2	4:B:202:GDP:O1A	2.13	0.49
1:A:177:THR:HG21	2:B:71:GLU:HG2	1.95	0.49
1:E:326:VAL:CG1	1:E:341:ALA:HB3	2.37	0.49
2:F:116:ASN:HD22	2:F:175:ARG:HH22	1.59	0.49
1:A:198:THR:HA	1:A:319:HIS:O	2.13	0.48
1:E:231:LEU:HB2	1:E:375:PRO:HB2	1.95	0.48
1:C:350:PRO:HD2	1:C:361:ASN:O	2.13	0.48
2:B:70:GLN:HG3	2:B:72:ARG:H	1.79	0.48
1:C:163:THR:HG22	1:C:394:ALA:CB	2.43	0.48
2:D:73:PHE:HD1	2:D:76:ILE:HD11	1.79	0.48
1:C:148:HIS:HA	1:C:312:ARG:O	2.13	0.48
2:D:116:ASN:HD22	2:D:175:ARG:HH22	1.60	0.48
1:E:199:LYS:HD3	1:E:201:TYR:OH	2.14	0.48
1:A:199:LYS:HD3	1:A:201:TYR:OH	2.13	0.48
1:A:40:GLY:N	1:A:41:PRO:HA	2.29	0.48
2:B:88:ILE:HG12	2:B:168:MET:HE2	1.96	0.48
1:E:144:ASN:ND2	1:E:146:LYS:H	2.11	0.48
1:E:297:MET:O	1:E:301:ILE:HG12	2.13	0.48
2:D:70:GLN:HG3	2:D:72:ARG:H	1.79	0.48
1:E:191:ARG:HD3	2:F:38:GLU:O	2.14	0.48
1:E:396:ILE:N	1:E:396:ILE:HD12	2.28	0.48
2:F:124:ASN:HA	2:F:153:THR:O	2.14	0.48
1:E:312:ARG:HG3	2:F:49:LYS:NZ	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:ILE:N	1:A:396:ILE:HD12	2.29	0.48
2:B:14:LEU:HD11	2:B:62:LEU:HD22	1.94	0.48
2:B:71:GLU:O	2:B:74:ARG:HG3	2.14	0.48
2:D:7:GLU:OE1	2:D:8:TYR:HD2	1.97	0.48
1:E:198:THR:HA	1:E:319:HIS:O	2.12	0.48
1:C:316:ASN:HD22	1:C:317:CYS:H	1.60	0.48
1:E:342:TYR:O	1:E:368:LEU:HD12	2.13	0.48
2:D:14:LEU:HD11	2:D:62:LEU:HD22	1.96	0.48
2:F:64:ILE:HD12	2:F:64:ILE:H	1.79	0.48
1:A:399:ASP:OD1	1:A:400:VAL:N	2.42	0.48
1:C:326:VAL:HG12	1:C:341:ALA:O	2.13	0.48
1:C:203:ASN:O	1:C:205:ILE:HG13	2.14	0.47
1:C:365:THR:HG23	1:C:391:VAL:HG22	1.96	0.47
2:F:174:LYS:HG2	2:F:174:LYS:O	2.14	0.47
2:B:124:ASN:HA	2:B:153:THR:O	2.14	0.47
1:A:326:VAL:HG12	1:A:341:ALA:O	2.14	0.47
2:D:131:LYS:O	2:D:133:VAL:HG13	2.14	0.47
2:D:174:LYS:HG2	2:D:174:LYS:O	2.15	0.47
1:A:312:ARG:HG3	2:B:49:LYS:HZ3	1.80	0.47
1:C:199:LYS:HD3	1:C:201:TYR:OH	2.14	0.47
2:F:117:VAL:O	2:F:119:LYS:CE	2.63	0.47
1:C:102:LEU:HD12	1:C:102:LEU:N	2.30	0.47
1:C:234:LEU:HB3	1:C:238:GLN:HB2	1.96	0.47
1:C:312:ARG:HG3	2:D:49:LYS:HZ1	1.80	0.47
2:B:121:LEU:HD23	2:B:150:PHE:HD1	1.76	0.47
1:C:106:LYS:HB3	1:C:106:LYS:NZ	2.30	0.47
2:B:124:ASN:O	2:B:125:LYS:HB2	2.15	0.47
2:D:64:ILE:HD12	2:D:64:ILE:N	2.30	0.47
1:C:252:LEU:HD13	1:C:252:LEU:O	2.15	0.46
1:E:218:GLU:HB2	1:E:242:ILE:HD11	1.97	0.46
1:A:150:PRO:HG3	1:A:358:VAL:HG12	1.97	0.46
1:A:319:HIS:HB3	1:A:321:ILE:CD1	2.44	0.46
2:B:64:ILE:HD12	2:B:64:ILE:N	2.31	0.46
1:C:243:ILE:CD1	1:C:262:THR:HA	2.42	0.46
2:D:124:ASN:HA	2:D:153:THR:O	2.15	0.46
2:B:176:MET:HG2	2:B:176:MET:H	1.43	0.46
1:E:163:THR:HG22	1:E:394:ALA:HB2	1.97	0.46
1:E:234:LEU:HB3	1:E:238:GLN:HB2	1.97	0.46
1:A:297:MET:O	1:A:301:ILE:HG12	2.15	0.46
2:B:17:ILE:HG22	2:B:18:GLY:N	2.31	0.46
2:F:176:MET:H	2:F:176:MET:HG2	1.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ASN:ND2	1:A:146:LYS:HB2	2.31	0.46
2:B:174:LYS:O	2:B:174:LYS:HG2	2.15	0.46
1:A:102:LEU:N	1:A:102:LEU:HD12	2.31	0.46
1:A:158:ALA:HA	1:A:396:ILE:HG12	1.97	0.46
1:A:218:GLU:HB2	1:A:242:ILE:HD11	1.98	0.46
2:F:8:TYR:C	2:F:8:TYR:HD2	2.18	0.46
1:A:347:SER:OG	1:A:364:GLU:HG3	2.16	0.46
2:B:12:PHE:HA	2:B:85:HIS:ND1	2.31	0.46
1:C:202:PHE:HB2	1:C:207:ILE:HD11	1.97	0.46
1:C:344:VAL:HG12	1:C:345:SER:N	2.31	0.46
2:D:117:VAL:O	2:D:119:LYS:CE	2.64	0.46
1:A:252:LEU:HD22	1:A:255:GLN:NE2	2.31	0.46
1:A:56:HIS:HB3	1:A:60:LYS:HE2	1.98	0.46
1:E:272:SER:HB3	1:E:380:LEU:HD21	1.97	0.46
2:F:124:ASN:O	2:F:125:LYS:HB2	2.16	0.46
1:A:234:LEU:HB3	1:A:238:GLN:HB2	1.97	0.45
1:A:57:SER:OG	1:A:60:LYS:HB2	2.17	0.45
1:A:202:PHE:HB2	1:A:207:ILE:HD11	1.97	0.45
1:C:170:ASP:OD2	1:C:287:SER:HB2	2.15	0.45
2:F:74:ARG:HH12	2:F:104:GLN:HB3	1.80	0.45
2:D:121:LEU:HD23	2:D:150:PHE:HD1	1.80	0.45
2:F:155:ALA:N	4:F:202:GDP:O6	2.49	0.45
1:A:319:HIS:HB3	1:A:321:ILE:HD11	1.97	0.45
1:E:170:ASP:OD2	1:E:287:SER:HB2	2.17	0.45
2:B:99:PHE:HA	2:B:102:VAL:HG23	1.99	0.45
1:A:192:ALA:CB	2:B:39:SER:HA	2.47	0.45
2:D:12:PHE:HA	2:D:85:HIS:ND1	2.31	0.45
1:E:144:ASN:ND2	1:E:146:LYS:HB2	2.31	0.45
1:E:252:LEU:HD22	1:E:255:GLN:NE2	2.31	0.45
1:A:365:THR:HG23	1:A:391:VAL:HG22	1.99	0.45
2:D:74:ARG:HH12	2:D:104:GLN:HB3	1.82	0.45
1:E:141:VAL:O	1:E:399:ASP:N	2.49	0.45
1:E:128:GLN:NE2	1:E:392:SER:OG	2.42	0.45
1:A:203:ASN:O	1:A:205:ILE:HG13	2.17	0.45
2:B:116:ASN:HD22	2:B:175:ARG:HH22	1.61	0.45
1:C:396:ILE:HD12	1:C:396:ILE:N	2.32	0.45
2:D:71:GLU:O	2:D:74:ARG:HG3	2.16	0.45
1:E:158:ALA:HA	1:E:396:ILE:HG12	1.97	0.45
2:B:67:THR:HG21	2:B:77:THR:CG2	2.37	0.45
2:B:173:LYS:C	2:B:175:ARG:H	2.20	0.44
1:A:344:VAL:HG12	1:A:345:SER:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:102:LEU:HD12	1:E:102:LEU:N	2.32	0.44
1:C:399:ASP:OD1	1:C:400:VAL:N	2.44	0.44
2:D:137:THR:O	2:D:141:GLU:HB2	2.17	0.44
1:E:139:ALA:HA	1:E:140:PRO:HD3	1.75	0.44
1:E:202:PHE:HB2	1:E:207:ILE:HD11	2.00	0.44
1:A:106:LYS:HB3	1:A:106:LYS:NZ	2.32	0.44
2:B:93:VAL:HG21	2:B:126:CYS:HA	1.99	0.44
1:E:192:ALA:O	1:E:196:ASN:HB2	2.17	0.44
1:E:365:THR:HG23	1:E:391:VAL:HG22	1.99	0.44
1:C:252:LEU:HD22	1:C:255:GLN:NE2	2.32	0.44
2:F:137:THR:O	2:F:141:GLU:HB2	2.18	0.44
2:F:46:VAL:HG21	2:F:80:TYR:CE2	2.53	0.44
1:C:192:ALA:O	1:C:196:ASN:HB2	2.18	0.44
2:F:16:LEU:HD13	2:F:64:ILE:CG2	2.48	0.44
1:A:243:ILE:CD1	1:A:262:THR:HA	2.44	0.44
1:A:90:LEU:HD22	1:A:120:LEU:HD11	2.00	0.44
1:C:102:LEU:N	1:C:102:LEU:CD1	2.80	0.44
1:C:52:LEU:HD21	1:C:86:ILE:HD12	2.00	0.44
2:B:16:LEU:HD13	2:B:64:ILE:CG2	2.49	0.43
1:E:344:VAL:HG12	1:E:345:SER:N	2.32	0.43
1:A:254:PHE:HA	1:A:257:GLU:OE1	2.17	0.43
2:B:115:GLU:N	2:B:115:GLU:OE1	2.52	0.43
1:C:218:GLU:HB2	1:C:242:ILE:HD11	1.99	0.43
2:D:16:LEU:HD13	2:D:64:ILE:CG2	2.49	0.43
1:E:52:LEU:HD21	1:E:86:ILE:HD12	2.00	0.43
2:F:12:PHE:HA	2:F:85:HIS:ND1	2.33	0.43
2:F:68:ALA:HB3	2:F:73:PHE:CG	2.53	0.43
1:A:99:VAL:O	1:A:109:SER:HA	2.18	0.43
2:B:92:ASP:CG	2:B:125:LYS:HD2	2.38	0.43
1:E:202:PHE:HD2	1:E:260:LEU:HD21	1.84	0.43
1:E:219:LEU:CD2	1:E:234:LEU:HD11	2.44	0.43
1:E:399:ASP:OD1	1:E:400:VAL:N	2.40	0.43
2:F:95:ASP:OD1	2:F:97:GLU:HB3	2.19	0.43
2:B:74:ARG:HH12	2:B:104:GLN:HB3	1.83	0.43
2:F:111:ARG:O	2:F:111:ARG:HG2	2.19	0.43
1:C:192:ALA:HB2	2:D:39:SER:HA	2.00	0.43
1:A:355:CYS:O	1:C:254:PHE:HZ	2.02	0.43
2:B:64:ILE:HD12	2:B:64:ILE:H	1.83	0.43
1:A:254:PHE:HZ	1:E:355:CYS:O	2.01	0.43
2:B:87:ILE:CD1	2:B:109:ILE:HG23	2.42	0.43
1:A:279:TRP:HZ2	2:B:70:GLN:NE2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:182:VAL:CG1	1:C:183:TRP:N	2.82	0.43
1:E:203:ASN:O	1:E:205:ILE:HG13	2.19	0.43
1:E:374:LEU:HA	1:E:375:PRO:HD3	1.77	0.43
1:C:144:ASN:HD22	1:C:146:LYS:HB2	1.83	0.43
1:A:102:LEU:N	1:A:102:LEU:CD1	2.82	0.43
2:B:46:VAL:HG21	2:B:80:TYR:CE2	2.53	0.43
1:C:150:PRO:HG3	1:C:358:VAL:HG12	2.01	0.43
1:E:356:ASN:HD22	1:E:399:ASP:HA	1.84	0.43
2:F:17:ILE:CG2	2:F:105:TRP:CE3	3.02	0.43
1:A:163:THR:HG22	1:A:394:ALA:HB3	2.01	0.42
1:C:121:LEU:HD22	1:C:131:LEU:CD1	2.49	0.42
1:A:202:PHE:HD2	1:A:260:LEU:HD21	1.84	0.42
1:C:139:ALA:HA	1:C:140:PRO:HD3	1.74	0.42
1:C:356:ASN:HD22	1:C:399:ASP:HA	1.83	0.42
1:E:99:VAL:O	1:E:109:SER:HA	2.19	0.42
2:B:111:ARG:HG2	2:B:111:ARG:O	2.19	0.42
1:C:211:LEU:CD1	1:C:246:ASN:HD22	2.32	0.42
1:E:166:ILE:HG13	1:E:393:PHE:CE1	2.55	0.42
1:A:166:ILE:HG13	1:A:393:PHE:CD1	2.54	0.42
2:B:137:THR:O	2:B:141:GLU:HB2	2.20	0.42
1:E:215:LEU:HA	1:E:242:ILE:HD13	2.01	0.42
1:E:254:PHE:HA	1:E:257:GLU:OE1	2.19	0.42
2:F:173:LYS:C	2:F:175:ARG:H	2.23	0.42
2:D:173:LYS:C	2:D:175:ARG:H	2.23	0.42
1:A:240:ASN:O	1:A:244:ASN:HB2	2.20	0.42
2:D:115:GLU:N	2:D:115:GLU:OE1	2.53	0.42
1:E:211:LEU:CD1	1:E:246:ASN:HD22	2.32	0.42
1:C:99:VAL:O	1:C:109:SER:HA	2.18	0.42
1:C:347:SER:OG	1:C:364:GLU:HG3	2.20	0.42
2:F:94:THR:HG21	2:F:128:LEU:HD12	2.02	0.42
1:A:139:ALA:HA	1:A:140:PRO:HD3	1.75	0.42
2:D:124:ASN:O	2:D:125:LYS:HB2	2.19	0.42
2:D:46:VAL:HG21	2:D:80:TYR:CE2	2.55	0.42
1:A:316:ASN:HD22	1:A:317:CYS:H	1.67	0.42
1:C:202:PHE:HD2	1:C:260:LEU:HD21	1.84	0.42
1:E:146:LYS:CA	1:E:311:GLN:HE21	2.31	0.42
2:F:17:ILE:HG22	2:F:18:GLY:N	2.34	0.42
1:A:356:ASN:HD22	1:A:399:ASP:HA	1.84	0.41
1:C:62:MET:HE3	1:C:124:LEU:HA	2.02	0.41
1:C:254:PHE:HA	1:C:257:GLU:OE1	2.20	0.41
1:E:102:LEU:N	1:E:102:LEU:CD1	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:78:SER:HB2	2:F:112:TYR:CD2	2.55	0.41
1:A:52:LEU:HD21	1:A:86:ILE:HD12	2.01	0.41
1:C:128:GLN:HG3	1:C:364:GLU:OE2	2.20	0.41
1:C:183:TRP:HA	1:C:183:TRP:HE3	1.85	0.41
1:C:158:ALA:O	1:C:362:LYS:HD2	2.19	0.41
1:A:192:ALA:O	1:A:196:ASN:HB2	2.20	0.41
1:C:221:ILE:HD11	1:C:231:LEU:HD11	2.02	0.41
1:E:202:PHE:CE2	1:E:203:ASN:ND2	2.88	0.41
1:A:219:LEU:HD23	1:A:219:LEU:HA	1.89	0.41
1:C:163:THR:HG22	1:C:394:ALA:HB2	2.02	0.41
2:F:127:ASP:HB2	2:F:157:ASN:HD21	1.85	0.41
1:E:121:LEU:HD22	1:E:131:LEU:CD1	2.50	0.41
1:E:191:ARG:NH1	2:F:38:GLU:HB3	2.36	0.41
2:D:93:VAL:HG21	2:D:126:CYS:HA	2.02	0.41
1:E:182:VAL:CG1	1:E:183:TRP:N	2.82	0.41
1:C:374:LEU:HA	1:C:375:PRO:HD3	1.78	0.41
2:F:106:LEU:HD23	2:F:109:ILE:HD12	2.02	0.41
1:C:249:GLN:CD	1:C:249:GLN:N	2.63	0.41
1:E:183:TRP:CZ2	1:E:231:LEU:HG	2.56	0.41
1:E:57:SER:OG	1:E:60:LYS:HB2	2.21	0.41
1:A:146:LYS:CA	1:A:311:GLN:HE21	2.32	0.41
1:E:128:GLN:HG3	1:E:364:GLU:OE2	2.21	0.41
1:E:62:MET:HG3	1:E:123:SER:O	2.21	0.41
2:F:101:ASN:OD1	2:F:104:GLN:NE2	2.54	0.41
1:A:121:LEU:HD22	1:A:131:LEU:CD1	2.50	0.41
2:B:125:LYS:HE2	4:B:202:GDP:N9	2.36	0.41
2:D:68:ALA:HB3	2:D:73:PHE:CG	2.56	0.41
1:A:200:ILE:HD12	1:A:212:ILE:HG13	2.03	0.41
1:A:215:LEU:HA	1:A:242:ILE:HD13	2.03	0.41
1:C:215:LEU:HA	1:C:242:ILE:HD13	2.03	0.41
1:C:219:LEU:HD23	1:C:219:LEU:HA	1.91	0.41
1:E:240:ASN:O	1:E:244:ASN:HB2	2.21	0.41
2:B:78:SER:HB2	2:B:112:TYR:CD2	2.55	0.40
2:B:119:LYS:O	2:B:149:PRO:HD2	2.21	0.40
2:B:95:ASP:OD1	2:B:97:GLU:HB3	2.22	0.40
1:C:316:ASN:ND2	1:C:317:CYS:H	2.18	0.40
2:D:17:ILE:HG22	2:D:18:GLY:N	2.35	0.40
1:E:327:VAL:HB	1:E:328:PRO:CD	2.45	0.40
2:F:119:LYS:O	2:F:149:PRO:HD2	2.22	0.40
2:F:93:VAL:HG22	2:F:124:ASN:O	2.21	0.40
2:F:87:ILE:HD12	2:F:109:ILE:CG2	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:LEU:O	1:A:252:LEU:HD13	2.21	0.40
1:A:282:LEU:CD1	1:A:389:ARG:HD3	2.52	0.40
2:D:176:MET:HG2	2:D:176:MET:H	1.41	0.40
1:E:301:ILE:O	1:E:305:LEU:HD23	2.20	0.40
1:E:163:THR:HG22	1:E:394:ALA:HB3	2.03	0.40
1:A:62:MET:HE3	1:A:124:LEU:HA	2.04	0.40
2:F:92:ASP:CG	2:F:125:LYS:HD2	2.42	0.40
2:F:12:PHE:HB2	2:F:62:LEU:HD23	2.02	0.40
2:B:68:ALA:HB3	2:B:73:PHE:CG	2.57	0.40
1:C:183:TRP:HA	1:C:183:TRP:CE3	2.56	0.40
2:D:106:LEU:HD23	2:D:109:ILE:HD12	2.03	0.40
2:F:87:ILE:CD1	2:F:109:ILE:HG23	2.39	0.40
2:F:118:ASN:HB3	2:F:171:GLU:HG2	2.04	0.40

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	347/361 (96%)	306 (88%)	41 (12%)	0	100	100
1	C	346/361 (96%)	308 (89%)	37 (11%)	1 (0%)	44	81
1	E	346/361 (96%)	305 (88%)	40 (12%)	1 (0%)	44	81
2	B	169/171 (99%)	156 (92%)	12 (7%)	1 (1%)	28	72
2	D	169/171 (99%)	156 (92%)	12 (7%)	1 (1%)	28	72
2	F	168/171 (98%)	154 (92%)	13 (8%)	1 (1%)	28	72
All	All	1545/1596 (97%)	1385 (90%)	155 (10%)	5 (0%)	44	81

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	253	CYS
1	E	280	GLN
2	B	41	ILE
2	D	41	ILE
2	F	41	ILE

### 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	317/326 (97%)	300 (95%)	17 (5%)	26	65
1	C	318/326 (98%)	301 (95%)	17 (5%)	26	65
1	E	318/326 (98%)	300 (94%)	18 (6%)	24	63
2	B	150/150 (100%)	143 (95%)	7 (5%)	30	69
2	D	150/150 (100%)	145 (97%)	5 (3%)	43	78
2	F	149/150 (99%)	141 (95%)	8 (5%)	26	65
All	All	1402/1428 (98%)	1330 (95%)	72 (5%)	28	66

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LYS
1	A	71	GLN
1	A	72	ASP
1	A	75	ASP
1	A	120	LEU
1	A	167	PRO
1	A	169	ASP
1	A	173	HIS
1	A	177	THR
1	A	180	ASN
1	A	194	ASP
1	A	224	PHE
1	A	234	LEU
1	A	302	GLU

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Mol	Chain	Res	Type
1	A	316	ASN
1	A	348	ILE
1	A	386	PRO
2	B	8	TYR
2	B	42	SER
2	B	58	LYS
2	B	67	THR
2	B	115	GLU
2	B	119	LYS
2	B	176	MET
1	C	60	LYS
1	C	71	GLN
1	C	72	ASP
1	C	75	ASP
1	C	98	SER
1	C	120	LEU
1	C	169	ASP
1	C	173	HIS
1	C	177	THR
1	C	180	ASN
1	C	194	ASP
1	C	224	PHE
1	C	234	LEU
1	C	302	GLU
1	C	316	ASN
1	C	348	ILE
1	C	386	PRO
2	D	42	SER
2	D	58	LYS
2	D	67	THR
2	D	115	GLU
2	D	176	MET
1	E	60	LYS
1	E	71	GLN
1	E	72	ASP
1	E	75	ASP
1	E	98	SER
1	E	120	LEU
1	E	169	ASP
1	E	173	HIS
1	E	177	THR
1	E	180	ASN

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Mol	Chain	Res	Type
1	E	194	ASP
1	E	224	PHE
1	E	234	LEU
1	E	302	GLU
1	E	316	ASN
1	E	328	PRO
1	E	348	ILE
1	E	386	PRO
2	F	7	GLU
2	F	8	TYR
2	F	42	SER
2	F	58	LYS
2	F	67	THR
2	F	82	ARG
2	F	115	GLU
2	F	176	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	HIS
1	A	71	GLN
1	A	128	GLN
1	A	144	ASN
1	A	168	ASN
1	A	180	ASN
1	A	184	HIS
1	A	196	ASN
1	A	238	GLN
1	A	240	ASN
1	A	250	GLN
1	A	255	GLN
1	A	300	ASN
1	A	316	ASN
1	A	319	HIS
1	A	356	ASN
2	B	70	GLN
2	B	101	ASN
2	B	104	GLN
2	B	157	ASN
1	C	49	HIS
1	C	71	GLN

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Mol	Chain	Res	Type
1	C	144	ASN
1	C	168	ASN
1	C	180	ASN
1	C	196	ASN
1	C	238	GLN
1	C	240	ASN
1	C	250	GLN
1	C	255	GLN
1	C	300	ASN
1	C	316	ASN
1	C	319	HIS
1	C	356	ASN
1	C	390	GLN
2	D	70	GLN
2	D	101	ASN
2	D	104	GLN
2	D	157	ASN
1	E	49	HIS
1	E	71	GLN
1	E	128	GLN
1	E	144	ASN
1	E	168	ASN
1	E	180	ASN
1	E	238	GLN
1	E	240	ASN
1	E	250	GLN
1	E	255	GLN
1	E	300	ASN
1	E	316	ASN
1	E	319	HIS
1	E	356	ASN
1	E	390	GLN
2	F	70	GLN
2	F	101	ASN
2	F	104	GLN
2	F	116	ASN
2	F	157	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	AF3	B	201	4,6	0,3,3	0.00	-	0,3,3	0.00	-
4	GDP	B	202	3,5	25,30,30	1.78	5 (20%)	26,47,47	2.65	9 (34%)
3	AF3	D	201	4,6	0,3,3	0.00	-	0,3,3	0.00	-
4	GDP	D	202	3,5	25,30,30	1.64	4 (16%)	26,47,47	1.88	6 (23%)
3	AF3	F	201	4,6	0,3,3	0.00	-	0,3,3	0.00	-
4	GDP	F	202	3,5	25,30,30	1.96	4 (16%)	26,47,47	2.14	7 (26%)

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	AF3	B	201	4,6	-	0/0/0/0	0/0/0/0
4	GDP	B	202	3,5	-	0/12/32/32	0/3/3/3
3	AF3	D	201	4,6	-	0/0/0/0	0/0/0/0
4	GDP	D	202	3,5	-	0/12/32/32	0/3/3/3
3	AF3	F	201	4,6	-	0/0/0/0	0/0/0/0
4	GDP	F	202	3,5	-	0/12/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	202	GDP	O4'-C4'	-2.17	1.40	1.45
4	B	202	GDP	C2-N2	2.07	1.38	1.34
4	B	202	GDP	PB-O1B	2.72	1.60	1.50
4	D	202	GDP	C6-C5	2.82	1.46	1.41
4	D	202	GDP	PB-O3A	3.03	1.65	1.60
4	F	202	GDP	PB-O1B	3.03	1.61	1.50
4	F	202	GDP	O4'-C1'	3.31	1.45	1.41
4	D	202	GDP	PB-O1B	3.60	1.63	1.50
4	B	202	GDP	C6-C5	4.13	1.49	1.41
4	D	202	GDP	O6-C6	4.77	1.36	1.24
4	B	202	GDP	O6-C6	4.93	1.36	1.24
4	F	202	GDP	O6-C6	5.09	1.37	1.24
4	F	202	GDP	C6-C5	5.51	1.51	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	202	GDP	N3-C2-N1	-5.15	119.93	127.46
4	B	202	GDP	O4'-C4'-C3'	-4.98	95.27	105.17
4	D	202	GDP	C5-C6-N1	-4.83	116.60	123.48
4	B	202	GDP	C5-C6-N1	-4.39	117.23	123.48
4	F	202	GDP	C5-C6-N1	-4.24	117.45	123.48
4	F	202	GDP	C4-C5-N7	-4.05	105.50	109.41
4	B	202	GDP	C4-C5-N7	-3.42	106.10	109.41
4	D	202	GDP	N3-C2-N1	-3.06	122.98	127.46
4	F	202	GDP	N3-C2-N1	-2.35	124.03	127.46
4	B	202	GDP	N2-C2-N1	2.11	120.62	117.24
4	F	202	GDP	C6-N1-C2	2.15	119.15	116.06
4	D	202	GDP	N2-C2-N1	2.89	121.87	117.24
4	B	202	GDP	O3B-PB-O2B	3.02	119.80	107.61
4	F	202	GDP	O3B-PB-O2B	3.05	119.90	107.61
4	D	202	GDP	C6-N1-C2	3.20	120.66	116.06
4	D	202	GDP	C2-N3-C4	3.44	119.18	115.16
4	D	202	GDP	O3B-PB-O2B	3.45	121.53	107.61
4	B	202	GDP	O3'-C3'-C4'	3.60	121.60	111.09
4	B	202	GDP	C6-N1-C2	3.82	121.55	116.06
4	F	202	GDP	O3'-C3'-C4'	4.01	122.79	111.09
4	F	202	GDP	C2-N3-C4	5.56	121.65	115.16
4	B	202	GDP	C2-N3-C4	6.24	122.45	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	AF3	1	0
4	B	202	GDP	4	0
4	D	202	GDP	1	0
3	F	201	AF3	1	0
4	F	202	GDP	3	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

### 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	351/361 (97%)	0.03	2 (0%) 89 83	71, 94, 122, 143	0
1	C	350/361 (96%)	-0.07	2 (0%) 89 83	73, 95, 123, 143	0
1	E	350/361 (96%)	0.01	3 (0%) 84 75	71, 95, 123, 144	0
2	B	171/171 (100%)	0.32	3 (1%) 69 55	90, 116, 139, 148	0
2	D	171/171 (100%)	0.19	0 100 100	91, 116, 139, 146	0
2	F	170/171 (99%)	0.85	27 (15%) 2 1	94, 119, 140, 148	0
All	All	1563/1596 (97%)	0.14	37 (2%) 59 45	71, 104, 136, 148	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	VAL	5.5
2	F	164	SER	4.1
1	E	328	PRO	3.9
1	C	328	PRO	3.9
2	F	55	LEU	3.8
2	F	12	PHE	3.6
2	F	165	PHE	3.5
2	F	152	GLU	3.4
2	F	150	PHE	3.4
2	F	121	LEU	3.3
2	F	126	CYS	3.2
2	F	53	ILE	3.2
2	F	161	VAL	3.1
2	F	120	LEU	3.0
2	B	55	LEU	3.0
2	F	89	VAL	2.8
2	F	88	ILE	2.8
2	F	174	LYS	2.7
1	E	223	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
2	F	60	ILE	2.7
2	F	90	VAL	2.5
2	F	62	LEU	2.4
1	E	327	VAL	2.4
2	F	151	LEU	2.3
2	B	57	GLY	2.3
1	C	327	VAL	2.3
2	F	31	PHE	2.3
2	F	33	ASP	2.3
2	F	56	ASP	2.3
2	F	122	VAL	2.3
1	A	265	PHE	2.2
2	F	48	PHE	2.2
2	F	153	THR	2.1
2	F	9	ASP	2.1
2	F	10	ALA	2.0
2	B	75	THR	2.0
2	F	168	MET	2.0

## 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	AF3	F	201	4/4	0.99	0.33	2.95	116,116,116,116	0
3	AF3	B	201	4/4	0.99	0.34	2.00	72,72,72,72	0
5	MG	B	203	1/1	0.77	0.29	0.78	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	AF3	D	201	4/4	0.98	0.23	0.68	89,89,89,89	0
5	MG	F	203	1/1	0.65	0.22	0.03	102,102,102,102	0
4	GDP	F	202	28/28	0.81	0.26	-0.25	116,116,116,116	0
4	GDP	B	202	28/28	0.97	0.23	-0.38	72,72,72,72	0
5	MG	D	203	1/1	0.82	0.18	-0.87	102,102,102,102	0
4	GDP	D	202	28/28	0.96	0.17	-0.93	89,89,89,89	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.