



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:43 PM GMT

PDB ID : 1UVL  
Title : The structural basis for RNA specificity and Ca<sup>2+</sup> inhibition of an RNA-dependent RNA polymerase phi6p2 with 5nt rna conformation B  
Authors : Salgado, P.S.; Makeyev, E.V.; Butcher, S.; Bamford, D.; Stuart, D.I.; Grimes, J.M.  
Deposited on : 2004-01-21  
Resolution : 2.00 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

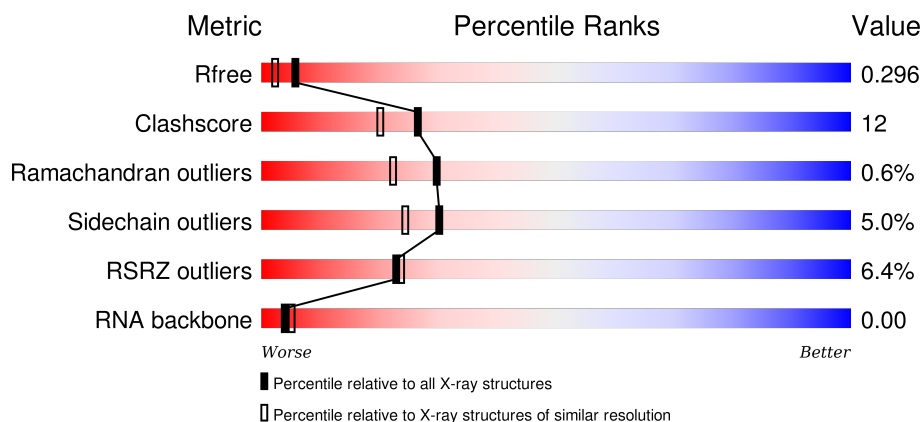
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)
RNA backbone	2183	1002 (2.72-1.30)

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. 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	664	<div> <div>4%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	C	664	<div> <div>4%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	E	664	<div> <div>9%</div> <div>77%</div> <div>21%</div> <div>.</div> </div>
2	B	5	<div> <div>40%</div> <div>40%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	5	<div><div></div><div>60%</div><div>40%</div><div>60%</div></div>
2	F	5	<div><div></div><div>100%</div><div>40%</div><div>60%</div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 16089 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 RNA-DEPENDENT RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	C	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	E	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	456	MET	ILE	CONFLICT	UNP P11124
C	456	MET	ILE	CONFLICT	UNP P11124
E	456	MET	ILE	CONFLICT	UNP P11124

- Molecule 2 is a RNA chain called 5'-R(\*UP\*UP\*UP\*CP\*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	P	0	0	0
			97	45	12	36	4			
2	D	5	Total	C	N	O	P	0	0	0
			97	45	12	36	4			
2	F	5	Total	C	N	O	P	0	0	0
			97	45	12	36	4			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

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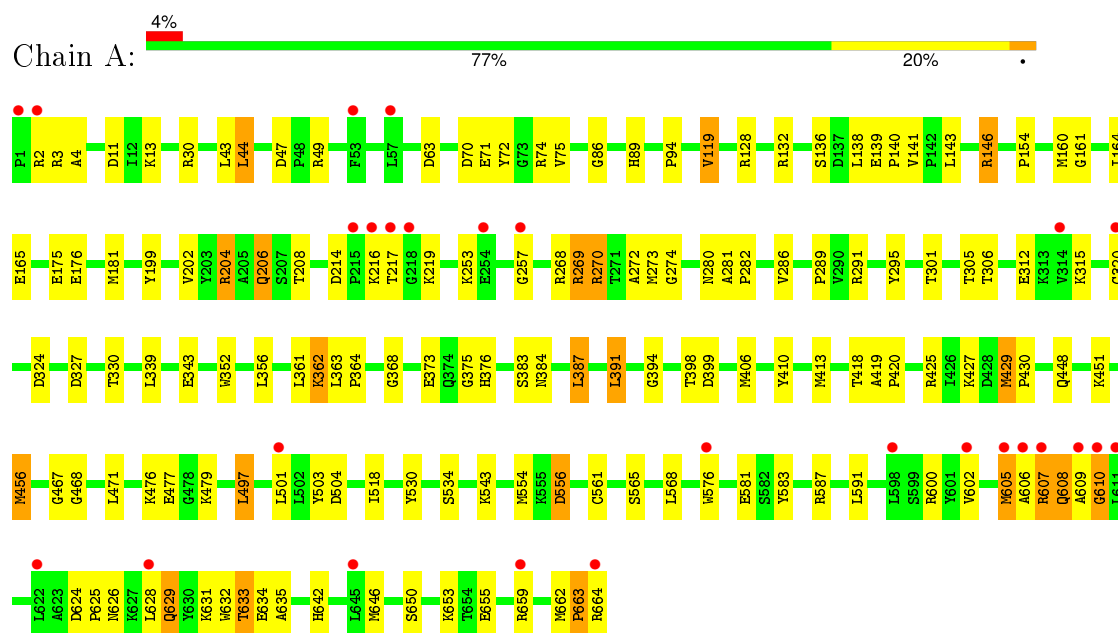
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total	Mn	0	0
			1	1		

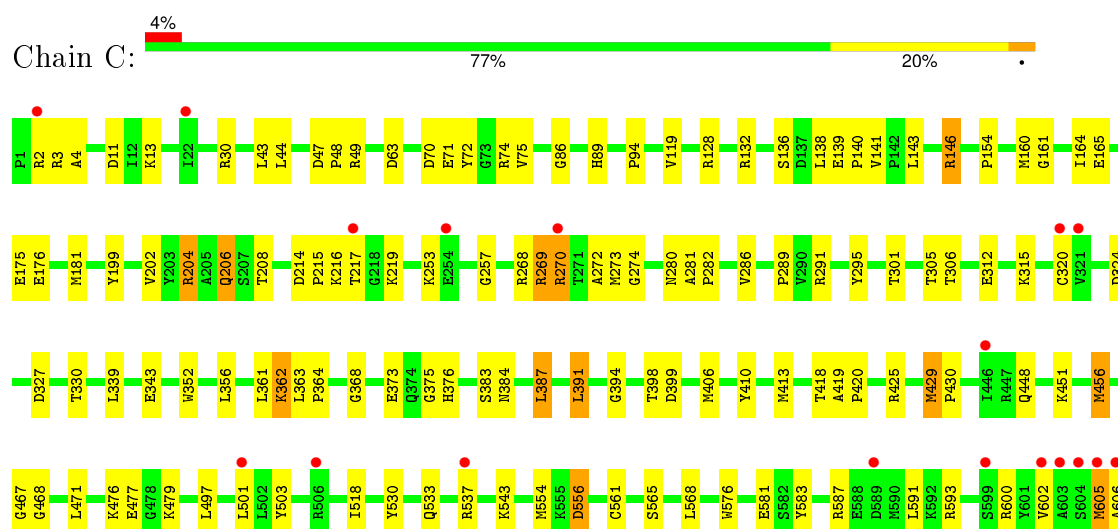
### 3 Residue-property plots [i](#)

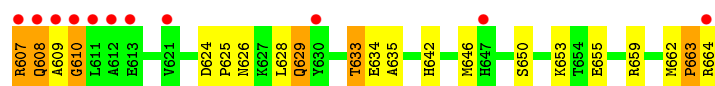
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: RNA-DEPENDENT RNA POLYMERASE

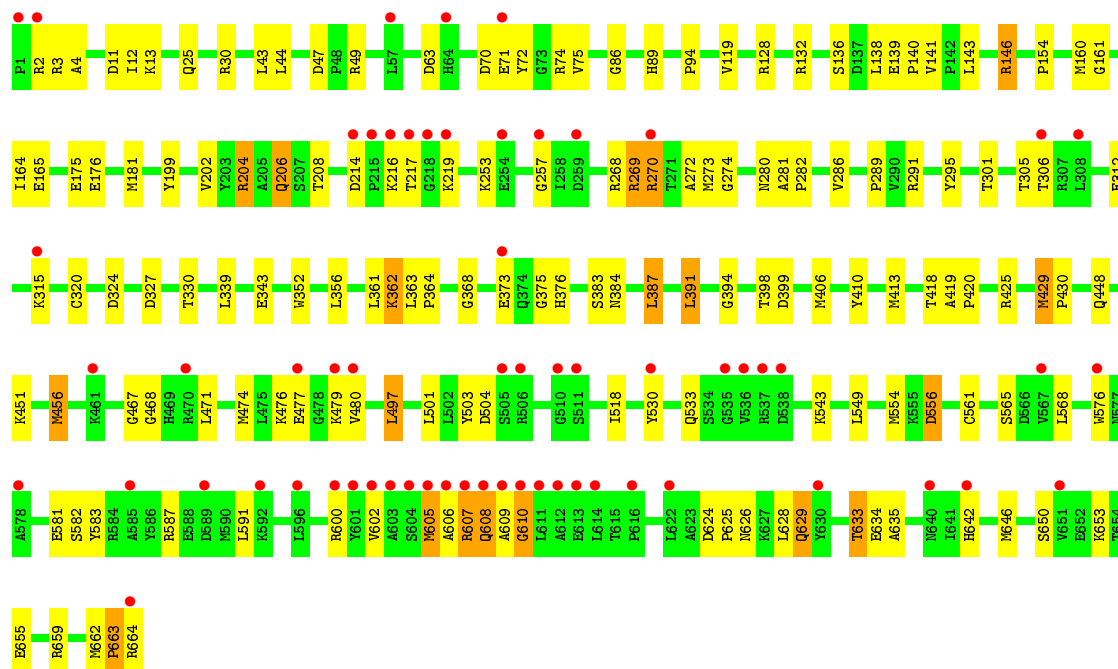
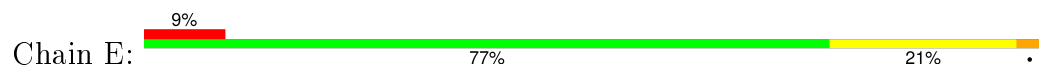


#### • Molecule 1: RNA-DEPENDENT RNA POLYMERASE





● Molecule 1: RNA-DEPENDENT RNA POLYMERASE



● Molecule 2: 5'-R(\*UP\*UP\*UP\*CP\*CP)-3'



● Molecule 2: 5'-R(\*UP\*UP\*UP\*CP\*CP)-3'



● Molecule 2: 5'-R(\*UP\*UP\*UP\*CP\*CP)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.95Å 91.88Å 140.76Å 90.00° 101.56° 90.00°	Depositor
Resolution (Å)	19.82 – 2.00 19.82 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (19.82-2.00) 99.2 (19.82-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 2.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.281 , 0.299 0.277 , 0.296	Depositor DCC
$R_{free}$ test set	8877 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.3	Xtriage
Anisotropy	0.675	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 36.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 176845 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	16089	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.01	2/5396 (0.0%)	1.04	13/7297 (0.2%)
1	C	1.01	2/5396 (0.0%)	1.04	13/7297 (0.2%)
1	E	1.01	2/5396 (0.0%)	1.04	13/7297 (0.2%)
2	B	1.10	0/106	1.63	5/162 (3.1%)
2	D	1.10	0/106	1.63	5/162 (3.1%)
2	F	1.10	0/106	1.63	5/162 (3.1%)
All	All	1.01	6/16506 (0.0%)	1.06	54/22377 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	E	0	1
2	B	1	2
2	D	1	2
2	F	1	2
All	All	3	9

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	581	GLU	CG-CD	6.75	1.62	1.51
1	A	581	GLU	CG-CD	6.71	1.62	1.51
1	E	581	GLU	CG-CD	6.69	1.61	1.51
1	E	176	GLU	CD-OE1	5.30	1.31	1.25
1	A	176	GLU	CD-OE1	5.28	1.31	1.25
1	C	176	GLU	CD-OE1	5.28	1.31	1.25

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	U	N1-C1'-C2'	8.76	125.38	114.00
2	F	4	U	N1-C1'-C2'	8.75	125.38	114.00
2	D	4	U	N1-C1'-C2'	8.73	125.35	114.00
1	C	136	SER	C-N-CA	-8.22	101.14	121.70
1	A	136	SER	C-N-CA	-8.22	101.16	121.70
1	E	136	SER	C-N-CA	-8.21	101.18	121.70
1	A	146	ARG	NE-CZ-NH1	8.03	124.31	120.30
1	E	146	ARG	NE-CZ-NH1	8.02	124.31	120.30
1	C	146	ARG	NE-CZ-NH1	7.97	124.29	120.30
2	D	4	U	O4'-C1'-N1	7.69	114.35	108.20
2	B	4	U	O4'-C1'-N1	7.65	114.32	108.20
2	F	4	U	O4'-C1'-N1	7.59	114.28	108.20
2	F	4	U	C1'-O4'-C4'	-7.54	103.87	109.90
2	B	4	U	C1'-O4'-C4'	-7.52	103.89	109.90
1	A	146	ARG	NE-CZ-NH2	-7.51	116.54	120.30
2	D	4	U	C1'-O4'-C4'	-7.51	103.89	109.90
1	E	146	ARG	NE-CZ-NH2	-7.51	116.55	120.30
1	A	425	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	C	146	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	E	425	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	C	425	ARG	NE-CZ-NH2	-7.33	116.63	120.30
1	A	206	GLN	N-CA-C	-6.68	92.95	111.00
1	E	206	GLN	N-CA-C	-6.68	92.96	111.00
1	C	206	GLN	N-CA-C	-6.67	93.00	111.00
1	C	11	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	A	11	ASP	CB-CG-OD2	-5.96	112.94	118.30
1	E	11	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	C	362	LYS	CD-CE-NZ	-5.84	98.26	111.70
1	A	362	LYS	CD-CE-NZ	-5.84	98.27	111.70
1	E	362	LYS	CD-CE-NZ	-5.84	98.27	111.70
1	E	3	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	3	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	C	3	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	C	204	ARG	NE-CZ-NH2	-5.44	117.58	120.30
2	F	7	C	N1-C1'-C2'	5.41	121.03	114.00
2	D	7	C	N1-C1'-C2'	5.40	121.02	114.00
2	B	7	C	N1-C1'-C2'	5.39	121.01	114.00
1	A	204	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	E	269	ARG	NE-CZ-NH1	-5.37	117.62	120.30
1	C	269	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	A	269	ARG	NE-CZ-NH1	-5.32	117.64	120.30
2	F	4	U	C5'-C4'-C3'	5.32	124.51	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	U	C5'-C4'-C3'	5.31	124.50	116.00
2	D	4	U	C5'-C4'-C3'	5.31	124.49	116.00
1	E	204	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	141	VAL	C-N-CD	5.28	139.49	128.40
1	E	141	VAL	C-N-CD	5.28	139.48	128.40
1	C	141	VAL	C-N-CD	5.28	139.48	128.40
1	A	425	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	E	556	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	C	556	ASP	CB-CG-OD2	-5.17	113.64	118.30
1	C	425	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	556	ASP	CB-CG-OD2	-5.15	113.66	118.30
1	E	425	ARG	NE-CZ-NH1	5.13	122.86	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3	U	C1'
2	D	3	U	C1'
2	F	3	U	C1'

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	199	TYR	Sidechain
2	B	3	U	Sidechain
2	B	4	U	Sidechain
1	C	199	TYR	Sidechain
2	D	3	U	Sidechain
2	D	4	U	Sidechain
1	E	199	TYR	Sidechain
2	F	3	U	Sidechain
2	F	4	U	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5265	0	5165	123	0
1	C	5265	0	5165	122	1
1	E	5265	0	5165	125	1
2	B	97	0	54	21	0
2	D	97	0	54	22	0
2	F	97	0	54	21	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
All	All	16089	0	15657	386	1

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 12.

All (386) 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:554:MET:HE3	1:C:568:LEU:HD11	1.26	1.17
1:A:451:LYS:HE2	2:B:7:C:N4	1.60	1.15
1:E:451:LYS:HE2	2:F:7:C:N4	1.60	1.14
1:C:451:LYS:HE2	2:D:7:C:N4	1.60	1.14
1:A:554:MET:HE3	1:A:568:LEU:HD11	1.25	1.13
1:E:217:THR:HG23	1:E:219:LYS:H	1.06	1.10
1:A:217:THR:HG23	1:A:219:LYS:H	1.06	1.09
1:C:217:THR:HG23	1:C:219:LYS:H	1.06	1.07
1:E:554:MET:HE3	1:E:568:LEU:HD11	1.29	1.05
1:C:214:ASP:HB3	1:C:217:THR:HG22	1.41	1.02
1:C:270:ARG:HG3	1:C:270:ARG:HH11	1.25	1.02
1:A:214:ASP:HB3	1:A:217:THR:HG22	1.41	1.00
1:A:270:ARG:HH11	1:A:270:ARG:HG3	1.25	0.99
1:E:320:CYS:SG	1:E:456:MET:HE3	2.03	0.98
1:E:270:ARG:HH11	1:E:270:ARG:HG3	1.25	0.98
1:E:214:ASP:HB3	1:E:217:THR:HG22	1.41	0.98
1:A:320:CYS:SG	1:A:456:MET:HE3	2.05	0.97
1:C:606:ALA:HB3	1:C:609:ALA:HB2	1.49	0.95
1:E:606:ALA:HB3	1:E:609:ALA:HB2	1.49	0.95
1:C:320:CYS:SG	1:C:456:MET:HE3	2.06	0.94
1:A:606:ALA:HB3	1:A:609:ALA:HB2	1.49	0.93
1:A:427:LYS:HE2	1:E:12:ILE:HG21	1.49	0.91
1:E:295:TYR:HH	2:F:7:C:H5	1.21	0.89
1:E:295:TYR:OH	2:F:7:C:H5	1.57	0.88
1:C:295:TYR:OH	2:D:7:C:H5	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:TYR:OH	2:B:7:C:H5	1.57	0.87
1:E:217:THR:HG23	1:E:219:LYS:N	1.90	0.87
1:A:364:PRO:HA	1:A:387:LEU:HD22	1.57	0.86
1:C:554:MET:CE	1:C:568:LEU:HD11	2.05	0.86
1:C:364:PRO:HA	1:C:387:LEU:HD22	1.57	0.86
1:C:217:THR:HG23	1:C:219:LYS:N	1.90	0.85
1:E:554:MET:CE	1:E:568:LEU:HD11	2.05	0.85
1:A:217:THR:HG23	1:A:219:LYS:N	1.90	0.85
1:A:554:MET:CE	1:A:568:LEU:HD11	2.05	0.85
1:E:364:PRO:HA	1:E:387:LEU:HD22	1.57	0.84
1:A:320:CYS:SG	1:A:456:MET:CE	2.66	0.84
1:C:214:ASP:HB3	1:C:217:THR:CG2	2.09	0.83
1:C:320:CYS:SG	1:C:456:MET:CE	2.66	0.83
1:E:320:CYS:SG	1:E:456:MET:CE	2.66	0.83
1:E:214:ASP:HB3	1:E:217:THR:CG2	2.09	0.83
1:A:214:ASP:HB3	1:A:217:THR:CG2	2.09	0.83
1:E:270:ARG:HG3	1:E:270:ARG:NH1	1.94	0.82
1:E:128:ARG:HB2	1:E:429:MET:HE1	1.65	0.78
1:A:128:ARG:HB2	1:A:429:MET:HE1	1.64	0.78
1:C:451:LYS:CE	2:D:7:C:N4	2.47	0.76
1:E:606:ALA:O	1:E:608:GLN:N	2.17	0.74
1:A:270:ARG:NH1	1:A:270:ARG:HG3	1.94	0.73
1:A:2:ARG:HD2	1:A:2:ARG:O	1.89	0.73
1:E:2:ARG:HD2	1:E:2:ARG:O	1.89	0.72
1:C:606:ALA:O	1:C:608:GLN:N	2.17	0.72
1:A:606:ALA:O	1:A:608:GLN:N	2.17	0.72
1:C:2:ARG:O	1:C:2:ARG:HD2	1.89	0.72
1:C:270:ARG:HG3	1:C:270:ARG:NH1	1.93	0.71
1:A:606:ALA:HB3	1:A:609:ALA:CB	2.20	0.71
1:A:72:TYR:CE1	1:A:476:LYS:HD3	2.26	0.71
1:A:451:LYS:CE	2:B:7:C:N4	2.47	0.71
1:E:202:VAL:HG11	2:F:4:U:H3'	1.72	0.71
1:C:72:TYR:CE1	1:C:476:LYS:HD3	2.26	0.71
1:A:202:VAL:HG11	2:B:4:U:H3'	1.72	0.71
1:A:608:GLN:HE22	1:C:593:ARG:CZ	2.04	0.71
1:C:128:ARG:HB2	1:C:429:MET:HE1	1.72	0.71
1:C:606:ALA:HB3	1:C:609:ALA:CB	2.19	0.71
1:C:202:VAL:HG11	2:D:4:U:H3'	1.72	0.71
1:E:607:ARG:O	1:E:608:GLN:HG3	1.91	0.70
1:E:606:ALA:HB3	1:E:609:ALA:CB	2.20	0.70
2:B:4:U:O2'	2:B:5:U:P	2.49	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:ARG:HB2	1:A:600:ARG:HH11	1.56	0.70
1:E:451:LYS:CE	2:F:7:C:N4	2.47	0.70
2:D:4:U:O2'	2:D:5:U:P	2.49	0.70
2:F:4:U:O2'	2:F:5:U:P	2.49	0.70
1:A:607:ARG:O	1:A:608:GLN:HG3	1.91	0.70
1:E:72:TYR:CE1	1:E:476:LYS:HD3	2.26	0.69
1:E:600:ARG:HB2	1:E:600:ARG:HH11	1.56	0.69
1:A:663:PRO:O	1:A:664:ARG:CZ	2.41	0.69
1:C:607:ARG:O	1:C:608:GLN:HG3	1.91	0.69
1:E:663:PRO:O	1:E:664:ARG:CZ	2.41	0.69
1:C:663:PRO:O	1:C:664:ARG:CZ	2.41	0.68
1:C:600:ARG:HB2	1:C:600:ARG:HH11	1.56	0.68
1:A:128:ARG:CB	1:A:429:MET:HE1	2.23	0.68
1:E:606:ALA:CB	1:E:609:ALA:HB2	2.25	0.66
1:A:534:SER:O	1:C:48:PRO:HG2	1.96	0.66
1:A:650:SER:OG	1:A:653:LYS:HD2	1.96	0.66
1:C:602:VAL:HB	1:C:605:MET:HB2	1.78	0.66
1:A:128:ARG:HB2	1:A:429:MET:CE	2.25	0.66
1:C:650:SER:OG	1:C:653:LYS:HD2	1.96	0.65
1:E:629:GLN:HE22	2:F:7:C:H5'	1.62	0.65
1:C:451:LYS:HE2	2:D:7:C:H41	1.55	0.65
1:C:128:ARG:HB2	1:C:429:MET:CE	2.25	0.65
1:C:629:GLN:HE22	2:D:7:C:H5'	1.62	0.65
1:A:427:LYS:HE2	1:E:12:ILE:CG2	2.26	0.65
1:E:602:VAL:HB	1:E:605:MET:HB2	1.78	0.65
1:A:451:LYS:HE2	2:B:7:C:H41	1.55	0.65
1:E:128:ARG:HB2	1:E:429:MET:CE	2.25	0.65
1:C:202:VAL:HG23	1:C:272:ALA:HB3	1.79	0.65
1:A:202:VAL:HG23	1:A:272:ALA:HB3	1.79	0.65
1:C:74:ARG:HB3	1:C:503:TYR:CD2	2.33	0.64
1:E:650:SER:OG	1:E:653:LYS:HD2	1.96	0.64
1:A:606:ALA:CB	1:A:609:ALA:HB2	2.25	0.64
1:A:74:ARG:HB3	1:A:503:TYR:CD2	2.33	0.64
1:C:606:ALA:CB	1:C:609:ALA:HB2	2.25	0.64
1:E:202:VAL:CG2	1:E:272:ALA:HB3	2.28	0.64
1:C:295:TYR:OH	2:D:7:C:C5	2.36	0.64
1:A:214:ASP:CB	1:A:217:THR:HG22	2.23	0.64
1:A:202:VAL:CG2	1:A:272:ALA:HB3	2.28	0.64
1:E:74:ARG:HB3	1:E:503:TYR:CD2	2.33	0.63
1:A:602:VAL:HB	1:A:605:MET:HB2	1.78	0.63
1:E:128:ARG:CB	1:E:429:MET:HE1	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:GLN:HE22	1:C:593:ARG:NH1	1.97	0.63
1:E:202:VAL:HG23	1:E:272:ALA:HB3	1.79	0.63
1:E:30:ARG:O	1:E:376:HIS:HE1	1.81	0.63
1:A:119:VAL:O	1:E:25:GLN:HG3	1.98	0.63
1:C:202:VAL:CG2	1:C:272:ALA:HB3	2.28	0.63
1:C:70:ASP:OD2	1:C:74:ARG:HD2	1.99	0.63
1:A:629:GLN:HE22	2:B:7:C:H5'	1.62	0.63
1:C:214:ASP:CB	1:C:217:THR:HG22	2.24	0.62
1:C:30:ARG:O	1:C:376:HIS:HE1	1.81	0.62
1:E:70:ASP:OD2	1:E:74:ARG:HD2	1.99	0.62
1:E:419:ALA:N	1:E:420:PRO:HD3	2.14	0.62
1:A:30:ARG:O	1:A:376:HIS:HE1	1.82	0.62
1:A:477:GLU:HG3	1:A:479:LYS:HE3	1.82	0.62
1:C:419:ALA:N	1:C:420:PRO:HD3	2.14	0.62
1:E:451:LYS:HE2	2:F:7:C:H41	1.55	0.62
1:A:70:ASP:OD2	1:A:74:ARG:HD2	1.99	0.62
1:A:312:GLU:HA	1:A:315:LYS:HE2	1.82	0.62
2:F:4:U:HO2'	2:F:5:U:P	2.22	0.61
1:E:312:GLU:HA	1:E:315:LYS:HE2	1.82	0.61
1:A:419:ALA:N	1:A:420:PRO:HD3	2.14	0.61
1:C:312:GLU:HA	1:C:315:LYS:HE2	1.82	0.61
1:E:600:ARG:NH1	1:E:600:ARG:HB2	2.16	0.61
1:E:477:GLU:HG3	1:E:479:LYS:HE3	1.82	0.61
1:C:477:GLU:HG3	1:C:479:LYS:HE3	1.82	0.61
1:E:418:THR:HG22	1:E:467:GLY:C	2.21	0.61
1:C:418:THR:HG22	1:C:467:GLY:C	2.22	0.61
1:A:600:ARG:NH1	1:A:600:ARG:HB2	2.16	0.60
1:C:456:MET:HE1	1:C:501:LEU:HD22	1.84	0.60
1:E:214:ASP:CB	1:E:217:THR:HG22	2.23	0.60
1:E:295:TYR:OH	2:F:7:C:C5	2.36	0.59
1:A:418:THR:HG22	1:A:467:GLY:C	2.21	0.59
1:A:47:ASP:OD1	1:A:49:ARG:HD3	2.02	0.59
1:C:600:ARG:HB2	1:C:600:ARG:NH1	2.16	0.59
1:A:456:MET:HE1	1:A:501:LEU:HD22	1.84	0.59
1:A:554:MET:HE3	1:A:568:LEU:CD1	2.17	0.58
1:E:47:ASP:OD1	1:E:49:ARG:HD3	2.02	0.58
1:C:47:ASP:OD1	1:C:49:ARG:HD3	2.02	0.58
1:C:629:GLN:HE22	2:D:7:C:C5'	2.17	0.58
2:F:3:U:O2'	2:F:4:U:P	2.62	0.58
2:D:4:U:HO2'	2:D:5:U:P	2.26	0.58
2:B:3:U:O2'	2:B:4:U:P	2.62	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:629:GLN:HE22	2:F:7:C:C5'	2.16	0.58
2:D:3:U:O2'	2:D:4:U:P	2.62	0.58
1:E:456:MET:HE1	1:E:501:LEU:HD22	1.84	0.57
2:B:4:U:O2'	2:B:5:U:OP1	2.22	0.57
1:A:629:GLN:HE22	2:B:7:C:C5'	2.17	0.57
1:C:181:MET:SD	1:C:356:LEU:HD23	2.45	0.57
1:A:181:MET:SD	1:A:356:LEU:HD23	2.45	0.57
1:E:181:MET:SD	1:E:356:LEU:HD23	2.45	0.57
1:A:270:ARG:NH1	1:A:270:ARG:CG	2.66	0.57
1:A:606:ALA:C	1:A:608:GLN:H	2.07	0.57
1:C:655:GLU:HG2	1:C:659:ARG:NH1	2.20	0.57
1:C:128:ARG:HB3	1:C:429:MET:HE3	1.85	0.57
1:E:128:ARG:CB	1:E:429:MET:CE	2.83	0.56
1:A:175:GLU:HA	1:A:352:TRP:CE3	2.40	0.56
1:E:391:LEU:HD13	1:E:398:THR:HG23	1.88	0.56
1:A:629:GLN:HG2	2:B:6:C:C4	2.41	0.56
1:A:655:GLU:HG2	1:A:659:ARG:NH1	2.20	0.56
1:E:175:GLU:HA	1:E:352:TRP:CE3	2.40	0.56
1:C:629:GLN:HG2	2:D:6:C:C4	2.41	0.56
1:C:175:GLU:HA	1:C:352:TRP:CE3	2.40	0.56
1:E:161:GLY:O	1:E:165:GLU:HG3	2.06	0.56
1:C:128:ARG:CB	1:C:429:MET:CE	2.83	0.56
1:C:391:LEU:HD13	1:C:398:THR:HG23	1.88	0.56
1:E:655:GLU:HG2	1:E:659:ARG:NH1	2.20	0.56
1:A:391:LEU:HD13	1:A:398:THR:HG23	1.88	0.55
2:F:4:U:O2'	2:F:5:U:OP1	2.22	0.55
1:A:268:ARG:NH1	1:A:270:ARG:HH22	2.05	0.55
1:E:629:GLN:HG2	2:F:6:C:C4	2.41	0.55
1:C:270:ARG:CG	1:C:270:ARG:NH1	2.66	0.55
1:C:161:GLY:O	1:C:165:GLU:HG3	2.06	0.55
1:A:161:GLY:O	1:A:165:GLU:HG3	2.06	0.54
1:C:606:ALA:C	1:C:608:GLN:H	2.07	0.54
1:E:268:ARG:NH1	1:E:270:ARG:HH22	2.04	0.54
1:A:128:ARG:CB	1:A:429:MET:CE	2.83	0.54
1:C:268:ARG:NH1	1:C:270:ARG:HH22	2.04	0.54
1:E:606:ALA:C	1:E:608:GLN:H	2.07	0.53
1:E:391:LEU:HD13	1:E:398:THR:CG2	2.40	0.52
1:C:518:ILE:HB	1:C:561:CYS:SG	2.50	0.52
1:E:518:ILE:HB	1:E:561:CYS:SG	2.50	0.52
1:A:268:ARG:CZ	1:A:270:ARG:NH2	2.73	0.52
1:A:600:ARG:HH11	1:A:600:ARG:CB	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:ARG:HD2	1:C:343:GLU:OE2	2.10	0.52
1:C:391:LEU:HD13	1:C:398:THR:CG2	2.40	0.52
1:C:268:ARG:CZ	1:C:270:ARG:NH2	2.73	0.52
1:A:391:LEU:HD13	1:A:398:THR:CG2	2.40	0.52
1:E:268:ARG:CZ	1:E:270:ARG:NH2	2.73	0.52
1:A:518:ILE:HB	1:A:561:CYS:SG	2.50	0.51
1:A:286:VAL:O	1:A:289:PRO:HD2	2.10	0.51
1:C:286:VAL:O	1:C:289:PRO:HD2	2.10	0.51
1:A:132:ARG:HD2	1:A:343:GLU:OE2	2.10	0.51
1:C:600:ARG:CB	1:C:600:ARG:HH11	2.23	0.51
1:A:13:LYS:NZ	1:A:383:SER:OG	2.44	0.51
1:E:286:VAL:O	1:E:289:PRO:HD2	2.10	0.51
1:C:13:LYS:NZ	1:C:383:SER:OG	2.44	0.51
1:A:274:GLY:HA2	2:B:5:U:O2'	2.11	0.51
1:E:13:LYS:NZ	1:E:383:SER:OG	2.44	0.51
1:A:633:THR:HA	2:B:7:C:H2'	1.93	0.51
1:E:633:THR:HA	2:F:7:C:H2'	1.93	0.51
1:C:633:THR:HA	2:D:7:C:H2'	1.93	0.50
1:E:600:ARG:CB	1:E:600:ARG:HH11	2.23	0.50
1:E:274:GLY:HA2	2:F:5:U:O2'	2.11	0.50
1:E:132:ARG:HD2	1:E:343:GLU:OE2	2.10	0.50
2:B:4:U:O2'	2:B:5:U:O5'	2.29	0.50
2:D:4:U:O2'	2:D:5:U:O5'	2.29	0.50
1:C:274:GLY:HA2	2:D:5:U:O2'	2.11	0.50
1:A:86:GLY:O	1:A:89:HIS:HD2	1.95	0.50
2:F:4:U:O2'	2:F:5:U:O5'	2.29	0.50
1:E:86:GLY:O	1:E:89:HIS:HD2	1.94	0.50
1:A:295:TYR:OH	2:B:7:C:C5	2.36	0.49
1:C:86:GLY:O	1:C:89:HIS:HD2	1.94	0.49
1:C:554:MET:HE3	1:C:568:LEU:CD1	2.18	0.49
1:C:175:GLU:HA	1:C:352:TRP:CD2	2.48	0.49
1:A:138:LEU:HB2	1:A:662:MET:SD	2.53	0.49
1:C:280:ASN:ND2	1:C:394:GLY:O	2.44	0.49
1:E:138:LEU:HB2	1:E:662:MET:SD	2.53	0.49
1:A:175:GLU:HA	1:A:352:TRP:CD2	2.48	0.49
1:E:175:GLU:HA	1:E:352:TRP:CD2	2.48	0.49
1:C:138:LEU:HB2	1:C:662:MET:SD	2.52	0.49
1:E:554:MET:CE	1:E:568:LEU:CD1	2.86	0.49
2:D:4:U:O2'	2:D:5:U:OP1	2.22	0.48
1:E:291:ARG:HD3	2:F:7:C:C6	2.49	0.48
1:A:291:ARG:HD3	2:B:7:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:7:C:O2	2:F:7:C:H3'	2.14	0.48
1:E:281:ALA:HB3	1:E:282:PRO:CD	2.44	0.47
1:C:364:PRO:HA	1:C:387:LEU:CD2	2.38	0.47
1:A:280:ASN:ND2	1:A:394:GLY:O	2.44	0.47
1:C:281:ALA:HB3	1:C:282:PRO:CD	2.44	0.47
1:A:364:PRO:HA	1:A:387:LEU:CD2	2.37	0.47
2:B:7:C:O2	2:B:7:C:H3'	2.14	0.47
1:C:128:ARG:CB	1:C:429:MET:HE3	2.43	0.47
1:C:2:ARG:NH1	1:C:4:ALA:HB2	2.30	0.47
2:D:3:U:O2'	2:D:3:U:C6	2.60	0.47
1:C:554:MET:CE	1:C:568:LEU:CD1	2.86	0.47
1:C:291:ARG:HD3	2:D:7:C:C6	2.49	0.47
1:A:2:ARG:NH1	1:A:4:ALA:HB2	2.30	0.47
1:E:497:LEU:HD12	1:E:497:LEU:HA	1.77	0.47
1:E:305:THR:OG1	1:E:306:THR:N	2.47	0.47
1:E:568:LEU:HA	1:E:568:LEU:HD23	1.63	0.47
1:A:624:ASP:OD1	1:A:626:ASN:HB2	2.15	0.47
1:A:305:THR:OG1	1:A:306:THR:N	2.47	0.47
1:A:281:ALA:HB3	1:A:282:PRO:CD	2.44	0.46
1:E:624:ASP:OD1	1:E:626:ASN:HB2	2.15	0.46
1:E:2:ARG:NH1	1:E:4:ALA:HB2	2.30	0.46
1:A:554:MET:CE	1:A:568:LEU:CD1	2.86	0.46
1:A:608:GLN:NE2	1:C:593:ARG:NH1	2.63	0.46
1:E:281:ALA:N	1:E:282:PRO:HD2	2.31	0.46
1:A:633:THR:HG23	1:A:635:ALA:H	1.81	0.46
2:D:7:C:O2	2:D:7:C:H3'	2.14	0.46
1:C:281:ALA:N	1:C:282:PRO:HD2	2.30	0.46
1:A:361:LEU:C	1:A:362:LYS:HG2	2.36	0.46
1:A:281:ALA:N	1:A:282:PRO:HD2	2.30	0.45
1:E:361:LEU:C	1:E:362:LYS:HG2	2.36	0.45
1:C:583:TYR:CZ	1:C:587:ARG:HD3	2.52	0.45
1:C:139:GLU:HA	1:C:140:PRO:HD3	1.66	0.45
2:F:3:U:O2'	2:F:4:U:O5'	2.34	0.45
2:B:3:U:O2'	2:B:4:U:O5'	2.34	0.45
2:D:3:U:O2'	2:D:4:U:O5'	2.34	0.45
1:A:583:TYR:CZ	1:A:587:ARG:HD3	2.51	0.45
1:C:624:ASP:OD1	1:C:626:ASN:HB2	2.15	0.45
1:E:633:THR:HG23	1:E:635:ALA:H	1.81	0.45
1:E:280:ASN:ND2	1:E:394:GLY:O	2.44	0.45
1:C:633:THR:HG23	1:C:635:ALA:H	1.81	0.45
1:A:568:LEU:HD23	1:A:568:LEU:HA	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:GLY:O	1:A:89:HIS:CD2	2.70	0.45
1:A:406:MET:HB3	1:A:410:TYR:CE2	2.52	0.45
1:C:406:MET:HB3	1:C:410:TYR:CE2	2.52	0.45
1:E:583:TYR:CZ	1:E:587:ARG:HD3	2.51	0.45
1:C:650:SER:OG	1:C:653:LYS:HB2	2.17	0.45
1:E:86:GLY:O	1:E:89:HIS:CD2	2.70	0.45
1:C:305:THR:OG1	1:C:306:THR:N	2.47	0.45
2:B:4:U:HO2'	2:B:5:U:P	2.29	0.45
1:C:86:GLY:O	1:C:89:HIS:CD2	2.70	0.44
1:C:642:HIS:CE1	1:C:646:MET:HG3	2.53	0.44
1:A:650:SER:OG	1:A:653:LYS:HB2	2.17	0.44
1:E:406:MET:HB3	1:E:410:TYR:CE2	2.52	0.44
1:C:607:ARG:O	1:C:608:GLN:CG	2.64	0.44
1:E:655:GLU:HG2	1:E:659:ARG:HH12	1.82	0.44
1:E:650:SER:OG	1:E:653:LYS:HB2	2.17	0.44
1:E:413:MET:HE3	1:E:471:LEU:HD21	1.99	0.44
1:C:204:ARG:HD2	1:C:530:TYR:OH	2.18	0.44
1:E:642:HIS:CE1	1:E:646:MET:HG3	2.52	0.44
1:C:327:ASP:CG	1:C:330:THR:OG1	2.57	0.44
1:E:543:LYS:O	1:E:625:PRO:HD2	2.18	0.43
1:E:474:MET:HE3	1:E:480:VAL:HB	2.00	0.43
1:C:413:MET:HE3	1:C:471:LEU:HD21	1.99	0.43
1:E:663:PRO:O	1:E:664:ARG:NH2	2.51	0.43
1:C:663:PRO:O	1:C:664:ARG:NH2	2.51	0.43
1:C:655:GLU:HG2	1:C:659:ARG:HH12	1.82	0.43
1:A:543:LYS:O	1:A:625:PRO:HD2	2.18	0.43
1:A:663:PRO:O	1:A:664:ARG:NH2	2.51	0.43
1:C:628:LEU:O	2:D:7:C:H3'	2.18	0.43
1:A:655:GLU:HG2	1:A:659:ARG:HH12	1.82	0.43
1:C:543:LYS:O	1:C:625:PRO:HD2	2.18	0.43
1:A:204:ARG:HD2	1:A:530:TYR:OH	2.18	0.43
1:E:327:ASP:CG	1:E:330:THR:OG1	2.57	0.43
1:C:143:LEU:HD23	1:C:143:LEU:C	2.38	0.43
2:B:3:U:O2'	2:B:3:U:C6	2.60	0.43
1:A:642:HIS:CE1	1:A:646:MET:HG3	2.53	0.43
1:C:568:LEU:HA	1:C:568:LEU:HD23	1.63	0.43
1:E:606:ALA:C	1:E:608:GLN:N	2.71	0.43
1:A:327:ASP:CG	1:A:330:THR:OG1	2.57	0.43
1:E:270:ARG:HH11	1:E:270:ARG:CG	2.07	0.43
1:E:364:PRO:HA	1:E:387:LEU:CD2	2.37	0.43
1:C:361:LEU:C	1:C:362:LYS:HG2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:LEU:O	2:B:7:C:H3'	2.18	0.43
1:A:44:LEU:HD11	1:C:257:GLY:HA3	2.00	0.43
1:E:628:LEU:O	2:F:7:C:H3'	2.18	0.42
1:E:363:LEU:HA	1:E:364:PRO:HD3	1.84	0.42
1:E:204:ARG:HD2	1:E:530:TYR:OH	2.18	0.42
1:E:628:LEU:HD12	1:E:628:LEU:HA	1.79	0.42
1:E:609:ALA:O	1:E:610:GLY:O	2.37	0.42
1:A:607:ARG:O	1:A:608:GLN:CG	2.64	0.42
1:A:143:LEU:HD23	1:A:143:LEU:C	2.38	0.42
1:E:143:LEU:HD23	1:E:143:LEU:C	2.38	0.42
1:A:609:ALA:O	1:A:610:GLY:O	2.37	0.42
1:A:399:ASP:N	1:A:399:ASP:OD1	2.53	0.42
1:E:399:ASP:N	1:E:399:ASP:OD1	2.53	0.42
1:C:628:LEU:HD12	1:C:628:LEU:HA	1.79	0.42
1:A:497:LEU:HD12	1:A:497:LEU:HA	1.77	0.42
1:A:413:MET:HE3	1:A:471:LEU:HD21	2.01	0.42
1:C:633:THR:O	1:C:634:GLU:C	2.58	0.42
1:A:160:MET:O	1:A:164:ILE:HG12	2.20	0.42
1:E:533:GLN:OE1	1:E:543:LYS:N	2.42	0.42
1:E:270:ARG:NH1	1:E:270:ARG:CG	2.66	0.42
1:C:664:ARG:NE	1:C:664:ARG:HA	2.35	0.42
1:C:418:THR:HG21	1:C:468:GLY:HA2	2.01	0.42
1:C:609:ALA:O	1:C:610:GLY:O	2.37	0.42
1:E:607:ARG:O	1:E:608:GLN:CG	2.64	0.42
1:E:418:THR:HG21	1:E:468:GLY:HA2	2.01	0.42
1:A:418:THR:HG21	1:A:468:GLY:HA2	2.01	0.42
1:C:160:MET:O	1:C:164:ILE:HG12	2.20	0.42
1:E:139:GLU:HA	1:E:140:PRO:HD3	1.66	0.42
1:C:399:ASP:N	1:C:399:ASP:OD1	2.53	0.42
1:E:664:ARG:HA	1:E:664:ARG:NE	2.35	0.41
1:E:160:MET:O	1:E:164:ILE:HG12	2.20	0.41
1:A:633:THR:O	1:A:634:GLU:C	2.58	0.41
1:A:387:LEU:HA	1:A:387:LEU:HD12	1.87	0.41
1:A:301:THR:HG23	1:A:448:GLN:HG3	2.01	0.41
1:E:301:THR:HG23	1:E:448:GLN:HG3	2.02	0.41
1:C:368:GLY:O	1:C:375:GLY:HA3	2.21	0.41
1:A:363:LEU:HA	1:A:364:PRO:HD3	1.84	0.41
1:E:429:MET:CB	1:E:430:PRO:HD3	2.51	0.41
1:C:175:GLU:HG3	1:C:352:TRP:CD1	2.56	0.41
1:A:456:MET:HB3	1:A:456:MET:HE3	1.91	0.41
1:C:429:MET:CB	1:C:430:PRO:HD3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:LYS:O	1:C:257:GLY:HA2	2.21	0.41
1:C:206:GLN:HG2	1:C:208:THR:O	2.21	0.41
1:A:631:LYS:HE3	1:A:632:TRP:CZ2	2.56	0.41
1:A:175:GLU:HG3	1:A:352:TRP:CD1	2.56	0.41
1:A:368:GLY:O	1:A:375:GLY:HA3	2.21	0.41
1:E:253:LYS:O	1:E:257:GLY:HA2	2.21	0.41
1:A:504:ASP:OD1	1:A:504:ASP:C	2.59	0.41
1:E:549:LEU:HD23	1:E:549:LEU:HA	1.79	0.41
1:E:605:MET:O	1:E:606:ALA:C	2.59	0.41
1:E:72:TYR:CZ	1:E:476:LYS:HD3	2.56	0.41
1:A:664:ARG:HA	1:A:664:ARG:NE	2.35	0.41
1:E:175:GLU:HG3	1:E:352:TRP:CD1	2.56	0.41
1:C:339:LEU:HD23	1:C:339:LEU:C	2.42	0.41
1:E:504:ASP:C	1:E:504:ASP:OD1	2.59	0.41
1:E:206:GLN:HG2	1:E:208:THR:O	2.21	0.41
1:E:339:LEU:C	1:E:339:LEU:HD23	2.42	0.41
1:A:253:LYS:O	1:A:257:GLY:HA2	2.21	0.41
1:E:633:THR:O	1:E:634:GLU:C	2.58	0.40
1:E:387:LEU:HA	1:E:387:LEU:HD12	1.87	0.40
1:A:429:MET:CB	1:A:430:PRO:HD3	2.51	0.40
1:C:281:ALA:HB3	1:C:282:PRO:HD3	2.02	0.40
1:C:533:GLN:OE1	1:C:543:LYS:N	2.42	0.40
1:A:206:GLN:HG2	1:A:208:THR:O	2.21	0.40
1:C:301:THR:HG23	1:C:448:GLN:HG3	2.01	0.40
1:C:214:ASP:HA	1:C:215:PRO:HD3	1.82	0.40
1:A:139:GLU:HA	1:A:140:PRO:HD3	1.66	0.40
1:E:607:ARG:O	1:E:608:GLN:CB	2.70	0.40
2:D:4:U:O4'	2:D:4:U:O2	2.40	0.40
1:A:339:LEU:C	1:A:339:LEU:HD23	2.42	0.40
1:E:368:GLY:O	1:E:375:GLY:HA3	2.21	0.40
1:C:363:LEU:HA	1:C:364:PRO:HD3	1.84	0.40
1:C:602:VAL:CB	1:C:605:MET:HB2	2.51	0.40
1:C:419:ALA:N	1:C:420:PRO:CD	2.82	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:537:ARG:NH2	1:E:582:SER:N[1_655]	2.18	0.02

## 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	662/664 (100%)	638 (96%)	20 (3%)	4 (1%)	30	22
1	C	662/664 (100%)	638 (96%)	20 (3%)	4 (1%)	30	22
1	E	662/664 (100%)	638 (96%)	20 (3%)	4 (1%)	30	22
All	All	1986/1992 (100%)	1914 (96%)	60 (3%)	12 (1%)	30	22

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	607	ARG
1	A	608	GLN
1	A	610	GLY
1	C	607	ARG
1	C	608	GLN
1	C	610	GLY
1	E	607	ARG
1	E	608	GLN
1	E	610	GLY
1	A	663	PRO
1	C	663	PRO
1	E	663	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	557/557 (100%)	529 (95%)	28 (5%)	30	24
1	C	557/557 (100%)	529 (95%)	28 (5%)	30	24
1	E	557/557 (100%)	529 (95%)	28 (5%)	30	24
All	All	1671/1671 (100%)	1587 (95%)	84 (5%)	30	24

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	44	LEU
1	A	63	ASP
1	A	71	GLU
1	A	75	VAL
1	A	94	PRO
1	A	119	VAL
1	A	146	ARG
1	A	154	PRO
1	A	216	LYS
1	A	269	ARG
1	A	270	ARG
1	A	273	MET
1	A	324	ASP
1	A	373	GLU
1	A	384	ASN
1	A	387	LEU
1	A	391	LEU
1	A	429	MET
1	A	456	MET
1	A	497	LEU
1	A	556	ASP
1	A	565	SER
1	A	576	TRP
1	A	591	LEU
1	A	605	MET
1	A	629	GLN
1	A	633	THR
1	C	43	LEU
1	C	44	LEU
1	C	63	ASP

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Mol	Chain	Res	Type
1	C	71	GLU
1	C	75	VAL
1	C	94	PRO
1	C	119	VAL
1	C	146	ARG
1	C	154	PRO
1	C	216	LYS
1	C	269	ARG
1	C	270	ARG
1	C	273	MET
1	C	324	ASP
1	C	373	GLU
1	C	384	ASN
1	C	387	LEU
1	C	391	LEU
1	C	429	MET
1	C	456	MET
1	C	497	LEU
1	C	556	ASP
1	C	565	SER
1	C	576	TRP
1	C	591	LEU
1	C	605	MET
1	C	629	GLN
1	C	633	THR
1	E	43	LEU
1	E	44	LEU
1	E	63	ASP
1	E	71	GLU
1	E	75	VAL
1	E	94	PRO
1	E	119	VAL
1	E	146	ARG
1	E	154	PRO
1	E	216	LYS
1	E	269	ARG
1	E	270	ARG
1	E	273	MET
1	E	324	ASP
1	E	373	GLU
1	E	384	ASN
1	E	387	LEU

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Mol	Chain	Res	Type
1	E	391	LEU
1	E	429	MET
1	E	456	MET
1	E	497	LEU
1	E	556	ASP
1	E	565	SER
1	E	576	TRP
1	E	591	LEU
1	E	605	MET
1	E	629	GLN
1	E	633	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	89	HIS
1	A	191	GLN
1	A	239	GLN
1	A	309	ASN
1	A	376	HIS
1	A	608	GLN
1	A	626	ASN
1	A	629	GLN
1	A	647	HIS
1	C	26	GLN
1	C	89	HIS
1	C	191	GLN
1	C	239	GLN
1	C	309	ASN
1	C	376	HIS
1	C	626	ASN
1	C	629	GLN
1	C	647	HIS
1	E	26	GLN
1	E	89	HIS
1	E	191	GLN
1	E	239	GLN
1	E	309	ASN
1	E	376	HIS
1	E	626	ASN
1	E	629	GLN

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Mol	Chain	Res	Type
1	E	647	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	5/5 (100%)	4 (80%)	2 (40%)
2	D	5/5 (100%)	4 (80%)	2 (40%)
2	F	5/5 (100%)	4 (80%)	2 (40%)
All	All	15/15 (100%)	12 (80%)	6 (40%)

All (12) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	4	U
2	B	5	U
2	B	6	C
2	B	7	C
2	D	4	U
2	D	5	U
2	D	6	C
2	D	7	C
2	F	4	U
2	F	5	U
2	F	6	C
2	F	7	C

All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	3	U
2	B	4	U
2	D	3	U
2	D	4	U
2	F	3	U
2	F	4	U

## 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	664/664 (100%)	0.30	27 (4%)	41 42	25, 39, 64, 124	0
1	C	664/664 (100%)	0.37	29 (4%)	38 39	25, 39, 64, 124	0
1	E	664/664 (100%)	0.56	62 (9%)	11 11	25, 39, 64, 124	0
2	B	5/5 (100%)	2.39	2 (40%)	0 1	85, 93, 137, 151	0
2	D	5/5 (100%)	3.15	3 (60%)	0 1	85, 93, 137, 151	0
2	F	5/5 (100%)	4.02	5 (100%)	0 0	85, 93, 137, 151	0
All	All	2007/2007 (100%)	0.43	128 (6%)	23 24	25, 40, 66, 151	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	607	ARG	11.4
1	C	607	ARG	11.0
1	E	608	GLN	10.9
1	C	608	GLN	10.4
1	E	603	ALA	10.2
1	C	609	ALA	9.4
1	A	606	ALA	8.5
1	E	604	SER	8.1
1	C	603	ALA	8.1
1	E	610	GLY	7.2
1	C	606	ALA	7.1
1	C	604	SER	6.9
1	E	606	ALA	6.9
2	F	7	C	6.8
1	A	664	ARG	6.4
1	E	609	ALA	6.2
2	F	6	C	5.9
1	E	612	ALA	5.9
1	E	535	GLY	5.8

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Mol	Chain	Res	Type	RSRZ
1	E	1	PRO	5.8
1	C	612	ALA	5.6
1	C	537	ARG	5.3
1	E	537	ARG	5.3
2	B	7	C	5.3
1	E	576	TRP	5.3
2	D	7	C	5.3
1	A	607	ARG	5.3
1	E	536	VAL	5.2
1	E	664	ARG	5.2
1	C	664	ARG	5.1
1	A	609	ALA	4.8
1	E	216	LYS	4.7
1	E	215	PRO	4.6
1	A	1	PRO	4.5
1	C	630	TYR	4.5
1	E	308	LEU	4.4
1	E	630	TYR	4.2
2	D	6	C	4.2
1	A	610	GLY	4.1
1	E	605	MET	4.0
1	E	596	LEU	3.9
1	C	2	ARG	3.9
1	E	613	GLU	3.9
1	E	602	VAL	3.7
1	E	600	ARG	3.7
2	D	3	U	3.5
1	E	214	ASP	3.5
1	E	614	LEU	3.5
1	C	610	GLY	3.5
1	E	470	ARG	3.4
1	A	605	MET	3.4
1	E	611	LEU	3.4
1	E	505	SER	3.3
1	A	611	LEU	3.3
1	A	257	GLY	3.3
1	E	257	GLY	3.3
1	C	605	MET	3.2
1	E	592	LYS	3.2
1	A	217	THR	3.2
1	E	601	TYR	3.1
1	E	585	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	E	2	ARG	3.1
1	E	217	THR	3.0
1	E	651	VAL	3.0
1	A	216	LYS	3.0
1	A	2	ARG	3.0
1	C	611	LEU	2.9
2	F	5	U	2.9
1	E	461	LYS	2.9
1	C	22	ILE	2.9
1	E	479	LYS	2.9
1	A	215	PRO	2.9
1	E	254	GLU	2.9
1	E	64	HIS	2.8
1	C	446	ILE	2.8
1	E	218	GLY	2.7
1	A	598	LEU	2.7
2	B	6	C	2.7
1	E	259	ASP	2.6
1	A	254	GLU	2.6
1	A	57	LEU	2.6
1	A	320	CYS	2.6
1	E	219	LYS	2.6
1	C	647	HIS	2.6
1	A	501	LEU	2.5
1	C	254	GLU	2.5
1	E	506	ARG	2.5
1	E	578	ALA	2.4
1	A	645	LEU	2.4
1	E	477	GLU	2.4
1	A	659	ARG	2.4
1	E	567	VAL	2.4
1	E	642	HIS	2.4
1	E	510	GLY	2.3
1	E	315	LYS	2.3
1	A	576	TRP	2.3
2	F	3	U	2.3
1	C	602	VAL	2.2
1	E	480	VAL	2.2
1	E	57	LEU	2.2
1	E	270	ARG	2.2
1	E	640	ASN	2.2
1	A	622	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	506	ARG	2.2
2	F	4	U	2.2
1	C	613	GLU	2.2
1	A	218	GLY	2.2
1	E	616	PRO	2.2
1	E	530	TYR	2.1
1	E	538	ASP	2.1
1	E	589	ASP	2.1
1	C	321	VAL	2.1
1	C	599	SER	2.1
1	A	602	VAL	2.1
1	C	217	THR	2.1
1	C	270	ARG	2.1
1	C	621	VAL	2.1
1	A	628	LEU	2.0
1	C	501	LEU	2.0
1	E	511	SER	2.0
1	A	53	PHE	2.0
1	E	306	THR	2.0
1	C	320	CYS	2.0
1	E	622	LEU	2.0
1	C	589	ASP	2.0
1	E	71	GLU	2.0
1	E	373	GLU	2.0
1	A	314	VAL	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. 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( $\text{\AA}^2$ )	Q<0.9
3	MN	A	1665	1/1	0.98	0.08	-1.55	39,39,39,39	0
3	MN	C	1665	1/1	0.97	0.09	-1.92	39,39,39,39	0
3	MN	E	1665	1/1	0.96	0.05	-4.88	39,39,39,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.