



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:50 PM GMT

PDB ID : 3V6D
Title : Crystal structure of HIV-1 reverse transcriptase (RT) cross-linked with AZT-terminated DNA
Authors : Das, K.; Martinez, S.E.; Arnold, E.
Deposited on : 2011-12-19
Resolution : 2.70 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

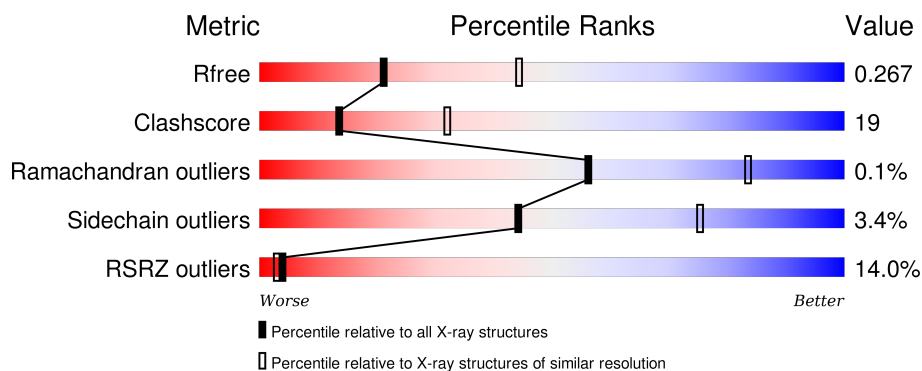
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	556	<div> <div>18%</div> <div>62%</div> <div>35%</div> <div>.</div> </div>
1	C	556	<div> <div>17%</div> <div>58%</div> <div>40%</div> <div>.</div> </div>
2	B	428	<div> <div>7%</div> <div>65%</div> <div>30%</div> <div>.</div> </div>
2	D	428	<div> <div>11%</div> <div>60%</div> <div>36%</div> <div>.</div> </div>
3	E	27	<div> <div>19%</div> <div>30%</div> <div>37%</div> <div>22%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
3	T	27	
4	F	21	
4	P	21	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17627 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 HIV-1 REVERSE TRANSCRIPTASE P66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4511	2920	751	832	8			
1	C	554	Total	C	N	O	S	0	0	0
			4506	2917	750	831	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP P03366
A	0	VAL	-	EXPRESSION TAG	UNP P03366
A	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
A	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
A	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366
C	-1	MET	-	EXPRESSION TAG	UNP P03366
C	0	VAL	-	EXPRESSION TAG	UNP P03366
C	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
C	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
C	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366

- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE P51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			
2	D	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
D	280	SER	CYS	ENGINEERED MUTATION	UNP P03366

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*TP*GP*GP*AP*AP*GP*GP*CP*GP*CP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			
3	E	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			

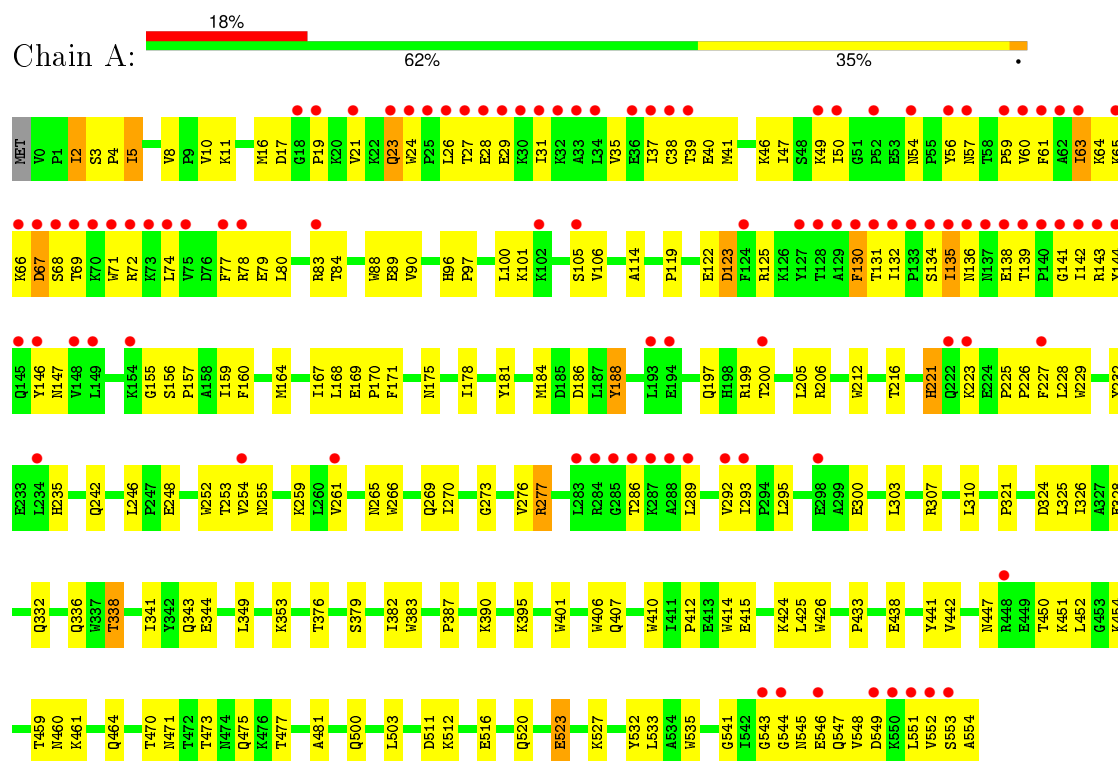
- Molecule 4 is a DNA chain called DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(ATM))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	P	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			
4	F	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			

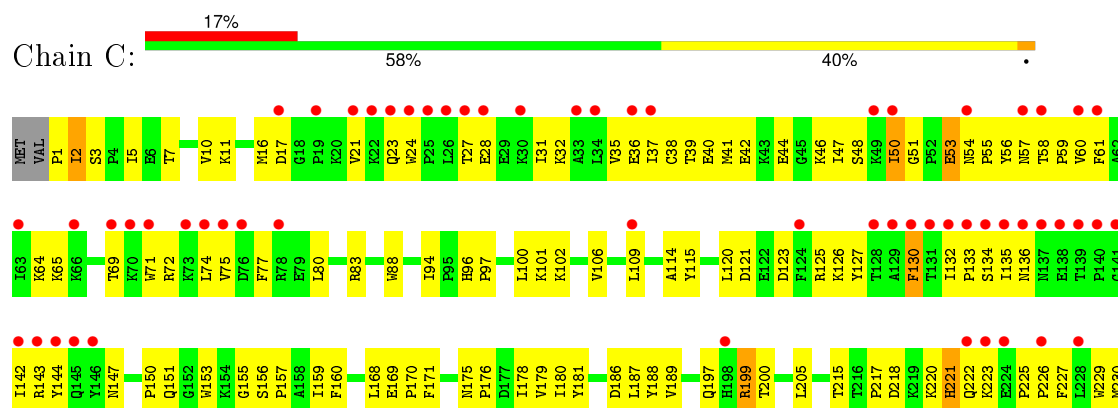
3 Residue-property plots

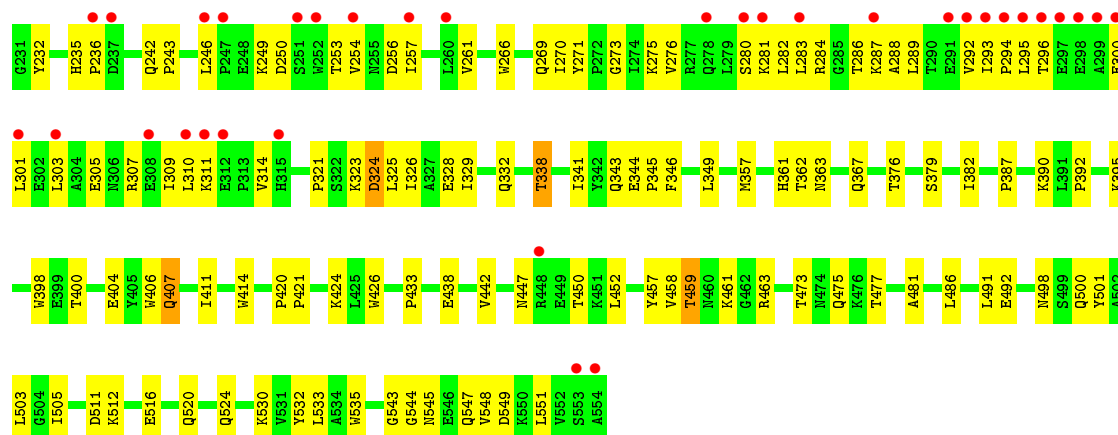
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 subunit

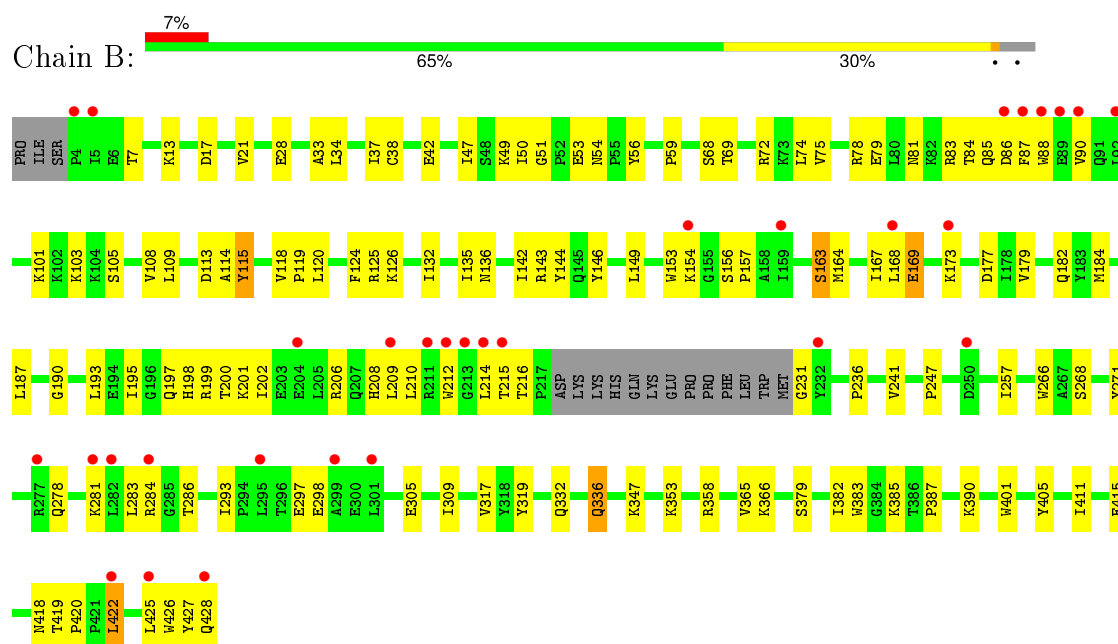


- Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 subunit

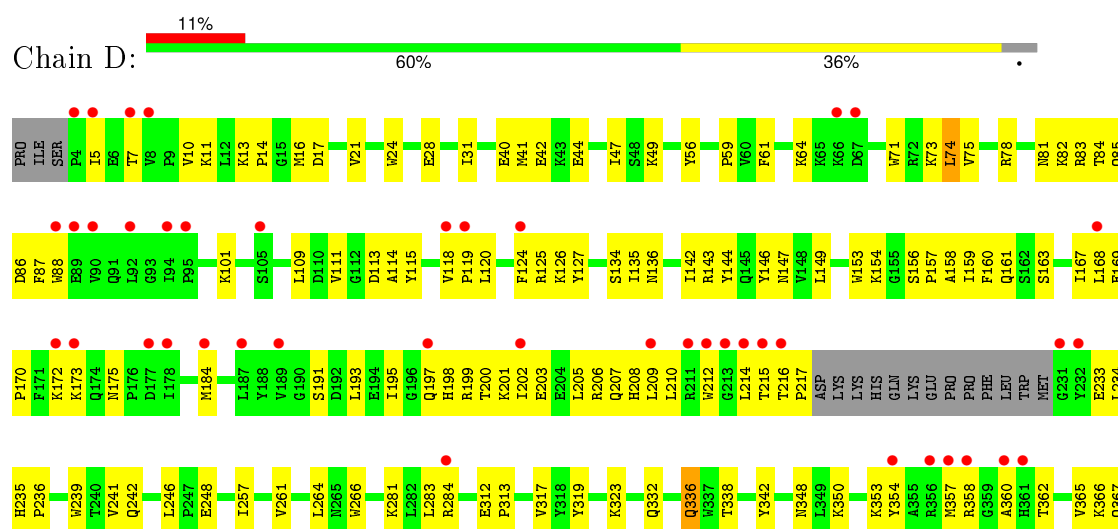


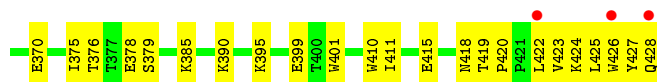


• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 subunit



• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 subunit

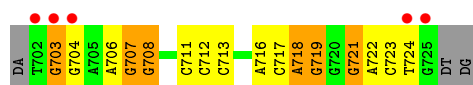




- Molecule 3: DNA (5'-D(*AP*TP*GP*GP*AP*AP*GP*GP*CP*GP*CP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')



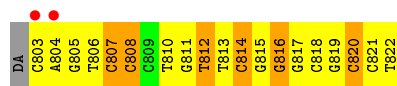
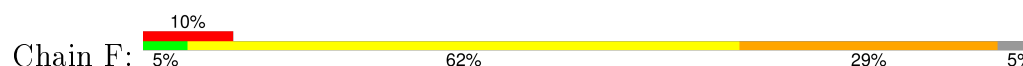
- Molecule 3: DNA (5'-D(*AP*TP*GP*GP*AP*AP*GP*GP*CP*GP*CP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*GP*TP*G)-3')



- Molecule 4: DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(M RG)P*CP*GP*CP*CP*(ATM))-3')



- Molecule 4: DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(M RG)P*CP*GP*CP*CP*(ATM))-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.48 Å 133.17 Å 139.90 Å 90.00° 98.67° 90.00°	Depositor
Resolution (Å)	44.30 – 2.70 48.21 – 2.71	Depositor EDS
% Data completeness (in resolution range)	97.1 (44.30-2.70) 97.8 (48.21-2.71)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.73 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.233 , 0.268 0.234 , 0.267	Depositor DCC
R_{free} test set	2606 reflections (3.12%)	DCC
Wilson B-factor (Å ²)	67.4	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 86162 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17627	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0/4629	0.61	1/6290 (0.0%)
1	C	0.45	0/4624	0.58	0/6282
2	B	0.48	0/3497	0.60	0/4751
2	D	0.46	0/3497	0.61	0/4751
3	E	0.79	0/560	1.44	10/864 (1.2%)
3	T	0.80	0/560	1.48	11/864 (1.3%)
4	F	0.82	0/400	1.58	9/612 (1.5%)
4	P	0.78	0/400	1.52	6/612 (1.0%)
All	All	0.51	0/18167	0.76	37/25026 (0.1%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	810	DT	O4'-C1'-N1	9.89	114.92	108.00
4	F	807	DC	O4'-C1'-N1	8.96	114.27	108.00
4	P	816	DG	O4'-C1'-N9	8.78	114.14	108.00
3	E	721	DG	O4'-C1'-N9	-8.59	101.99	108.00
3	T	703	DG	O4'-C4'-C3'	-7.75	101.35	106.00
3	T	719	DG	C1'-O4'-C4'	-7.44	102.66	110.10
3	T	703	DG	O4'-C1'-N9	7.26	113.08	108.00
4	F	811	DG	O4'-C1'-N9	7.20	113.04	108.00
3	T	708	DG	O4'-C1'-N9	7.18	113.03	108.00
4	F	810	DT	N3-C4-O4	6.99	124.10	119.90
3	E	707	DG	O4'-C4'-C3'	-6.80	101.78	104.50
3	E	718	DA	O4'-C1'-N9	6.60	112.62	108.00
3	E	719	DG	C1'-O4'-C4'	-6.50	103.60	110.10
4	F	810	DT	C5-C4-O4	-6.46	120.38	124.90
3	T	708	DG	N9-C4-C5	6.41	107.96	105.40
4	F	812	DT	O4'-C1'-N1	-5.93	103.85	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	820	DC	O4'-C1'-N1	5.86	112.10	108.00
3	E	708	DG	N9-C4-C5	5.78	107.71	105.40
4	F	808	DC	C5'-C4'-C3'	-5.71	103.82	114.10
4	F	816	DG	O4'-C1'-N9	5.64	111.94	108.00
3	E	708	DG	C8-N9-C4	-5.62	104.15	106.40
4	P	807	DC	O4'-C1'-N1	5.55	111.89	108.00
3	E	703	DG	O4'-C1'-N9	5.55	111.88	108.00
3	E	711	DC	O4'-C1'-N1	5.49	111.84	108.00
3	T	708	DG	C8-N9-C4	-5.39	104.24	106.40
3	T	703	DG	C4'-C3'-C2'	-5.39	98.25	103.10
4	P	810	DT	C5-C4-O4	-5.33	121.17	124.90
4	F	820	DC	O4'-C1'-N1	5.23	111.66	108.00
3	E	707	DG	O4'-C1'-N9	5.18	111.63	108.00
3	T	718	DA	C3'-C2'-C1'	-5.18	96.28	102.50
4	F	814	DC	O4'-C1'-C2'	-5.18	101.76	105.90
1	A	4	PRO	N-CA-C	5.17	125.55	112.10
3	T	709	DC	C4'-C3'-C2'	-5.14	98.47	103.10
4	P	808	DC	C5'-C4'-C3'	-5.12	104.89	114.10
3	T	708	DG	C4'-C3'-C2'	-5.09	98.52	103.10
3	E	708	DG	N3-C2-N2	-5.06	116.36	119.90
3	T	720	DG	O4'-C1'-N9	-5.03	104.48	108.00

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	4511	0	4570	174	0
1	C	4506	0	4568	182	0
2	B	3400	0	3433	117	0
2	D	3400	0	3433	135	0
3	E	497	0	268	14	0
3	T	497	0	268	15	0
4	F	408	0	231	27	0
4	P	408	0	231	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	17627	0	17002	643	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 19.

All (643) 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:223:LYS:O	1:C:225:PRO:HD3	1.53	1.09
1:A:541:GLY:HA2	1:A:546:GLU:HB2	1.41	1.01
1:C:500:GLN:HG2	2:D:422:LEU:HD22	1.44	1.00
1:A:459:THR:HG22	1:A:461:LYS:H	1.23	0.99
1:A:2:ILE:HD12	1:A:2:ILE:H	1.26	0.99
1:A:223:LYS:O	1:A:225:PRO:HD3	1.64	0.98
2:B:266:TRP:CD1	2:B:425:LEU:HD22	2.01	0.96
2:D:170:PRO:HB2	2:D:208:HIS:HE1	1.31	0.94
1:A:37:ILE:HD12	1:A:40:GLU:HG3	1.52	0.91
1:A:65:LYS:HB3	1:A:68:SER:HB2	1.52	0.91
1:A:5:ILE:HG22	1:A:212:TRP:HD1	1.37	0.90
2:B:47:ILE:HD12	2:B:144:TYR:CD1	2.08	0.89
1:A:199:ARG:NH2	1:A:223:LYS:HB3	1.89	0.88
1:C:175:ASN:HB3	1:C:178:ILE:HD13	1.55	0.87
1:C:125:ARG:HD3	1:C:147:ASN:HA	1.56	0.87
2:D:115:TYR:HD2	2:D:156:SER:HB3	1.40	0.86
4:P:807:DC:H2''	4:P:808:DC:H5''	1.56	0.85
2:B:109:LEU:HD22	2:B:216:THR:HG21	1.59	0.84
1:C:450:THR:HG21	1:C:452:LEU:HD12	1.60	0.84
1:C:23:GLN:HE22	1:C:60:VAL:HG12	1.43	0.84
1:C:253:THR:HG22	1:C:292:VAL:HG12	1.60	0.83
1:C:199:ARG:NH2	1:C:223:LYS:HB2	1.93	0.83
4:F:817:MRG:N3	4:F:817:MRG:H222	1.94	0.81
2:B:13:LYS:HD2	2:B:85:GLN:HB3	1.63	0.80
1:C:303:LEU:O	1:C:307:ARG:HG3	1.81	0.79
2:B:266:TRP:NE1	2:B:425:LEU:HD22	1.98	0.79
1:A:303:LEU:O	1:A:307:ARG:HG3	1.83	0.79
2:D:87:PHE:HZ	2:D:159:ILE:HG13	1.48	0.79
1:A:199:ARG:HH21	1:A:223:LYS:HB3	1.47	0.78
1:C:438:GLU:OE2	1:C:459:THR:HG21	1.83	0.78
4:F:807:DC:H2''	4:F:808:DC:C5'	2.12	0.78
1:A:459:THR:CG2	1:A:461:LYS:H	1.97	0.78
4:P:807:DC:H2''	4:P:808:DC:C5'	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:266:TRP:CD1	2:D:425:LEU:HD22	2.18	0.78
4:F:807:DC:H2''	4:F:808:DC:H5''	1.65	0.77
1:A:459:THR:HG22	1:A:461:LYS:N	1.97	0.77
1:C:254:VAL:HG21	1:C:286:THR:HG21	1.65	0.77
1:C:459:THR:HG22	1:C:461:LYS:H	1.49	0.77
1:A:438:GLU:OE2	1:A:459:THR:HG21	1.84	0.77
1:A:5:ILE:HG22	1:A:212:TRP:CD1	2.20	0.76
2:D:319:TYR:OH	2:D:385:LYS:HD2	1.84	0.76
2:D:266:TRP:NE1	2:D:425:LEU:HD22	2.00	0.76
1:C:323:LYS:HE2	1:C:344:GLU:OE2	1.85	0.76
1:C:459:THR:CG2	1:C:461:LYS:H	1.98	0.76
2:B:281:LYS:HE3	2:B:284:ARG:NH2	2.01	0.76
1:C:273:GLY:HA2	1:C:338:THR:HG21	1.69	0.75
1:A:541:GLY:CA	1:A:546:GLU:HB2	2.16	0.75
2:B:182:GLN:HG3	2:B:187:LEU:HD12	1.68	0.75
1:A:78:ARG:HH21	3:T:705:DA:H5''	1.52	0.74
1:C:21:VAL:HG23	1:C:59:PRO:HD3	1.67	0.74
1:A:543:GLY:HA2	2:B:283:LEU:O	1.87	0.74
1:C:21:VAL:CG2	1:C:59:PRO:HD3	2.17	0.74
1:C:544:GLY:HA2	1:C:547:GLN:HE21	1.51	0.74
1:A:31:ILE:O	1:A:35:VAL:HG23	1.88	0.74
1:A:503:LEU:HD12	1:A:533:LEU:HD13	1.70	0.73
2:B:114:ALA:H	2:B:214:LEU:HD13	1.53	0.73
2:D:170:PRO:HB2	2:D:208:HIS:CE1	2.20	0.73
1:C:51:GLY:N	1:C:53:GLU:OE2	2.21	0.73
4:F:804:DA:H2'	4:F:805:DG:C8	2.24	0.73
2:D:209:LEU:HD22	2:D:214:LEU:HD23	1.70	0.73
3:E:721:DG:H2''	3:E:722:DA:OP2	1.87	0.72
1:A:21:VAL:HG23	1:A:59:PRO:HD3	1.71	0.72
1:A:511:ASP:OD2	1:A:512:LYS:NZ	2.21	0.72
2:B:33:ALA:O	2:B:37:ILE:HG12	1.89	0.72
2:B:278:GLN:HE21	2:B:298:GLU:HB2	1.52	0.72
1:A:252:TRP:O	1:A:292:VAL:HG23	1.90	0.72
2:D:358:ARG:HB2	2:D:370:GLU:OE2	1.90	0.72
1:A:66:LYS:NZ	1:A:67:ASP:OD2	2.24	0.71
1:A:543:GLY:N	2:B:283:LEU:O	2.23	0.71
1:C:543:GLY:HA2	2:D:283:LEU:O	1.89	0.71
1:A:125:ARG:HG2	1:A:146:TYR:O	1.91	0.71
2:B:68:SER:O	2:B:69:THR:HB	1.90	0.71
1:C:101:LYS:HE2	1:C:321:PRO:HG3	1.72	0.71
2:B:7:THR:HG22	2:B:119:PRO:HB2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:293:ILE:HG13	1:C:294:PRO:HD2	1.72	0.71
2:B:198:HIS:NE2	2:B:202:ILE:HD11	2.06	0.70
2:D:312:GLU:HB3	2:D:313:PRO:HD2	1.74	0.70
2:D:354:TYR:HE2	2:D:375:ILE:HG13	1.57	0.70
1:C:367:GLN:HE22	1:C:512:LYS:HD2	1.57	0.69
2:D:169:GLU:O	2:D:173:LYS:HG2	1.92	0.69
1:C:261:VAL:HG13	1:C:276:VAL:HG11	1.73	0.69
3:E:723:DC:OP1	3:E:723:DC:H4'	1.91	0.69
3:E:723:DC:H5''	3:E:723:DC:H6	1.58	0.69
1:C:77:PHE:CD1	1:C:80:LEU:HD23	2.28	0.69
3:E:716:DA:H2''	3:E:717:DC:OP2	1.91	0.69
1:C:215:THR:HG22	1:C:217:PRO:HD3	1.74	0.68
2:D:342:TYR:HB3	2:D:348:ASN:HD22	1.57	0.68
1:A:544:GLY:O	1:A:548:VAL:HG23	1.94	0.68
2:B:154:LYS:HG2	2:B:184:MET:SD	2.34	0.68
1:A:253:THR:HA	1:A:292:VAL:HA	1.76	0.68
2:D:64:LYS:HE3	2:D:71:TRP:CE2	2.29	0.68
3:T:724:DT:H3	4:P:804:DA:H61	1.42	0.68
2:D:47:ILE:HD12	2:D:144:TYR:CD1	2.28	0.68
1:C:459:THR:HG22	1:C:461:LYS:N	2.08	0.68
4:F:805:DG:H2''	4:F:806:DT:O5'	1.93	0.68
2:D:266:TRP:HD1	2:D:425:LEU:HD13	1.59	0.68
2:D:360:ALA:HA	2:D:367:GLN:NE2	2.08	0.68
2:D:157:PRO:HG3	2:D:184:MET:HA	1.75	0.68
1:C:2:ILE:HD12	1:C:2:ILE:N	2.09	0.68
4:F:804:DA:H2''	4:F:805:DG:O5'	1.94	0.68
1:C:287:LYS:HG3	1:C:288:ALA:H	1.58	0.68
1:A:135:ILE:HG12	1:A:136:ASN:H	1.58	0.67
2:B:336:GLN:HG2	2:B:353:LYS:HD2	1.77	0.67
2:D:115:TYR:CD2	2:D:156:SER:HB3	2.26	0.67
1:A:266:TRP:O	1:A:269:GLN:HG2	1.95	0.67
2:D:163:SER:O	2:D:167:ILE:HG13	1.94	0.67
1:C:246:LEU:HD11	1:C:310:LEU:HD22	1.76	0.67
1:A:41:MET:HB3	1:A:46:LYS:HB2	1.77	0.67
1:A:543:GLY:CA	2:B:283:LEU:O	2.43	0.66
2:B:332:GLN:HB2	2:B:336:GLN:HB3	1.76	0.66
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.76	0.66
2:D:86:ASP:OD1	2:D:87:PHE:N	2.29	0.66
2:D:214:LEU:HD12	2:D:215:THR:H	1.60	0.66
1:C:109:LEU:HD23	1:C:220:LYS:HD2	1.77	0.66
2:D:246:LEU:HD11	2:D:264:LEU:HD21	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:16:MET:HG3	2:D:83:ARG:HG2	1.76	0.66
1:C:100:LEU:HD11	1:C:229:TRP:CZ3	2.31	0.66
2:D:198:HIS:CD2	2:D:202:ILE:HD11	2.31	0.66
1:C:407:GLN:HE22	2:D:418:ASN:HA	1.60	0.66
1:A:500:GLN:HG2	2:B:422:LEU:CD1	2.26	0.66
1:C:32:LYS:O	1:C:36:GLU:HG3	1.97	0.65
4:F:803:DC:H2'	4:F:804:DA:C8	2.32	0.65
2:D:114:ALA:H	2:D:214:LEU:HD13	1.61	0.65
1:A:23:GLN:HG2	1:A:59:PRO:HA	1.79	0.65
1:A:328:GLU:HG3	1:A:390:LYS:HB2	1.79	0.65
2:B:115:TYR:O	2:B:149:LEU:HB2	1.95	0.65
1:A:332:GLN:OE1	1:A:338:THR:HG23	1.96	0.65
4:P:817:MRG:H222	4:P:817:MRG:N3	2.12	0.65
1:C:289:LEU:HD21	4:F:817:MRG:H4'	1.77	0.64
4:F:806:DT:H2'	4:F:807:DC:C6	2.32	0.64
1:C:543:GLY:O	1:C:547:GLN:NE2	2.30	0.64
2:B:114:ALA:N	2:B:214:LEU:HD13	2.12	0.64
2:D:338:THR:HG22	2:D:353:LYS:HG3	1.80	0.64
2:B:81:ASN:ND2	2:B:154:LYS:HG3	2.13	0.64
1:A:253:THR:HG22	1:A:292:VAL:HB	1.79	0.64
1:C:21:VAL:HG22	1:C:57:ASN:O	1.98	0.64
1:C:500:GLN:HG2	2:D:422:LEU:CD2	2.23	0.64
4:F:807:DC:C2'	4:F:808:DC:H5''	2.28	0.63
1:C:503:LEU:CD1	1:C:533:LEU:HG	2.29	0.63
1:C:31:ILE:O	1:C:35:VAL:HG23	1.98	0.63
1:A:276:VAL:O	1:A:276:VAL:HG12	1.96	0.63
1:C:275:LYS:HE2	1:C:332:GLN:NE2	2.13	0.63
1:C:186:ASP:HB2	4:F:822:ATM:N5'	2.13	0.63
2:D:115:TYR:O	2:D:149:LEU:HB2	1.99	0.63
4:P:807:DC:H2'	4:P:808:DC:C6	2.33	0.63
1:A:167:ILE:O	1:A:170:PRO:HD2	1.99	0.63
2:B:56:TYR:HE2	2:B:126:LYS:HE2	1.62	0.63
1:A:78:ARG:NH2	3:T:705:DA:H5''	2.14	0.62
1:A:125:ARG:HE	1:A:147:ASN:HA	1.61	0.62
1:A:60:VAL:HG11	1:A:130:PHE:HD1	1.64	0.62
2:B:193:LEU:HB3	2:B:197:GLN:HB2	1.81	0.62
2:D:78:ARG:O	2:D:82:LYS:HG3	1.99	0.62
3:T:716:DA:H2''	3:T:717:DC:OP2	2.00	0.62
1:A:545:ASN:O	1:A:549:ASP:HB2	2.00	0.62
1:C:226:PRO:HB3	1:C:235:HIS:CE1	2.35	0.62
2:B:195:ILE:HG22	2:B:199:ARG:HE	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:266:TRP:CD1	2:D:425:LEU:HD13	2.34	0.62
2:D:167:ILE:O	2:D:208:HIS:NE2	2.33	0.61
2:D:7:THR:HG22	2:D:119:PRO:HB2	1.82	0.61
1:A:265:ASN:OD1	1:A:353:LYS:NZ	2.24	0.61
1:C:395:LYS:NZ	1:C:414:TRP:O	2.34	0.61
1:A:61:PHE:CE1	3:T:704:DG:C8	2.89	0.61
2:B:169:GLU:O	2:B:173:LYS:HG2	2.00	0.60
1:A:500:GLN:HG2	2:B:422:LEU:HD11	1.84	0.60
3:T:718:DA:H2'	3:T:718:DA:OP2	2.02	0.60
1:C:307:ARG:O	1:C:311:LYS:HG3	2.00	0.60
2:D:13:LYS:HB2	2:D:16:MET:HE3	1.82	0.60
1:A:254:VAL:HG21	1:A:286:THR:HG21	1.82	0.60
1:A:135:ILE:CG2	1:A:138:GLU:HB2	2.31	0.60
2:B:124:PHE:CE2	2:B:153:TRP:CZ2	2.90	0.60
4:F:807:DC:H2''	4:F:808:DC:O5'	2.01	0.60
1:C:61:PHE:HE1	1:C:74:LEU:HD12	1.67	0.59
1:A:175:ASN:HB3	1:A:178:ILE:HG12	1.84	0.59
1:C:109:LEU:CD2	1:C:220:LYS:HD2	2.32	0.59
2:D:40:GLU:HG2	2:D:44:GLU:OE1	2.02	0.59
1:C:37:ILE:O	1:C:40:GLU:HB2	2.02	0.59
2:B:86:ASP:OD1	2:B:87:PHE:N	2.35	0.59
3:T:725:DG:N2	4:P:803:DC:N3	2.39	0.59
2:D:13:LYS:HE3	2:D:16:MET:HE3	1.84	0.59
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.37	0.59
1:C:276:VAL:HG12	1:C:276:VAL:O	2.03	0.59
2:D:109:LEU:HD22	2:D:216:THR:HG21	1.85	0.59
4:F:814:DC:H2''	4:F:815:DG:C8	2.38	0.59
1:C:516:GLU:O	1:C:520:GLN:HG3	2.03	0.59
1:A:5:ILE:CG2	1:A:212:TRP:HD1	2.10	0.58
2:B:167:ILE:HG23	2:B:212:TRP:CG	2.37	0.58
2:B:317:VAL:HG12	2:B:347:LYS:CD	2.32	0.58
1:A:452:LEU:HD23	1:A:470:THR:HA	1.84	0.58
1:C:457:TYR:HE1	1:C:463:ARG:HG2	1.68	0.58
2:B:197:GLN:O	2:B:201:LYS:HG2	2.03	0.58
1:A:24:TRP:CD1	1:A:61:PHE:HE2	2.21	0.58
3:T:717:DC:H2''	3:T:718:DA:OP2	2.02	0.58
1:C:31:ILE:HG23	1:C:133:PRO:O	2.04	0.58
1:C:114:ALA:HB1	1:C:160:PHE:CZ	2.39	0.58
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.84	0.58
2:D:191:SER:OG	2:D:198:HIS:ND1	2.27	0.58
2:B:115:TYR:CD2	2:B:115:TYR:N	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:115:TYR:CD1	2:B:156:SER:HB3	2.39	0.57
2:B:108:VAL:O	2:B:231:GLY:HA3	2.03	0.57
2:D:209:LEU:HD22	2:D:214:LEU:CD2	2.34	0.57
2:B:317:VAL:HG12	2:B:347:LYS:HD3	1.86	0.57
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.86	0.57
1:C:367:GLN:NE2	1:C:512:LYS:HD2	2.18	0.57
2:B:163:SER:O	2:B:167:ILE:HG13	2.04	0.57
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.85	0.57
1:A:406:TRP:CZ2	2:B:420:PRO:HG3	2.39	0.57
2:B:206:ARG:HH21	2:B:210:LEU:HD11	1.68	0.57
2:B:209:LEU:HD22	2:B:214:LEU:HD23	1.85	0.57
2:D:13:LYS:HE3	2:D:16:MET:CE	2.34	0.57
1:C:343:GLN:HG3	1:C:349:LEU:HD11	1.87	0.57
2:B:336:GLN:HG2	2:B:427:TYR:CE1	2.40	0.57
1:C:305:GLU:O	1:C:309:ILE:HG13	2.05	0.57
2:B:266:TRP:CD1	2:B:425:LEU:CD2	2.81	0.56
3:T:713:DC:H2''	3:T:714:DG:H5'	1.88	0.56
2:D:233:GLU:O	2:D:234:LEU:HD23	2.05	0.56
1:A:5:ILE:HD11	1:A:119:PRO:HD2	1.87	0.56
2:D:114:ALA:N	2:D:214:LEU:HD13	2.20	0.56
2:B:278:GLN:NE2	2:B:298:GLU:HB2	2.19	0.56
1:A:464:GLN:NE2	1:A:551:LEU:HD11	2.20	0.56
2:B:88:TRP:CZ2	2:B:154:LYS:HD2	2.40	0.56
2:D:118:VAL:HG12	2:D:119:PRO:O	2.05	0.56
3:E:704:DG:H5''	3:E:704:DG:N3	2.20	0.56
1:C:23:GLN:NE2	1:C:60:VAL:HG12	2.18	0.56
1:C:407:GLN:NE2	2:D:418:ASN:HA	2.20	0.56
2:D:266:TRP:HE1	2:D:425:LEU:HD22	1.70	0.56
1:A:139:THR:HG22	1:A:141:GLY:H	1.71	0.56
1:C:328:GLU:HG3	1:C:390:LYS:HB2	1.88	0.56
1:A:441:TYR:O	1:A:548:VAL:HG21	2.06	0.55
1:C:155:GLY:O	1:C:159:ILE:HG13	2.07	0.55
4:P:807:DC:C2'	4:P:808:DC:H5''	2.31	0.55
2:D:336:GLN:HG2	2:D:427:TYR:CE1	2.42	0.55
1:C:75:VAL:HB	1:C:77:PHE:CE2	2.42	0.55
1:A:186:ASP:HB2	4:P:822:ATM:N5'	2.20	0.55
2:B:358:ARG:HG3	2:B:366:LYS:HD3	1.88	0.55
1:C:473:THR:O	1:C:477:THR:HG23	2.06	0.55
2:D:160:PHE:CD2	2:D:160:PHE:O	2.60	0.55
2:B:115:TYR:HD2	2:B:115:TYR:N	2.05	0.55
4:F:815:DG:H2'	4:F:815:DG:OP2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:GLU:O	1:A:527:LYS:HG3	2.06	0.55
2:D:168:LEU:HB3	2:D:172:LYS:HE3	1.88	0.55
1:A:37:ILE:HA	1:A:40:GLU:CG	2.37	0.54
4:P:815:DG:H2''	4:P:816:DG:O5'	2.05	0.54
1:C:77:PHE:O	1:C:80:LEU:N	2.40	0.54
2:D:195:ILE:O	2:D:199:ARG:HG3	2.07	0.54
1:C:197:GLN:O	1:C:200:THR:HB	2.07	0.54
1:A:206:ARG:NH2	1:A:216:THR:O	2.40	0.54
1:C:295:LEU:HD22	1:C:300:GLU:OE1	2.07	0.54
2:B:85:GLN:HA	2:B:88:TRP:CE2	2.43	0.54
1:C:301:LEU:O	1:C:305:GLU:HG2	2.08	0.54
1:C:97:PRO:HD3	1:C:232:TYR:CE2	2.43	0.54
2:B:195:ILE:HG21	2:B:199:ARG:HH21	1.73	0.54
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.89	0.54
1:A:49:LYS:HE3	1:A:142:ILE:HG23	1.89	0.54
2:D:425:LEU:HD23	2:D:426:TRP:CE2	2.42	0.54
1:C:180:ILE:HA	1:C:188:TYR:O	2.07	0.54
1:A:132:ILE:HB	1:A:142:ILE:O	2.07	0.54
1:A:516:GLU:O	1:A:520:GLN:HG3	2.08	0.54
1:C:130:PHE:CE2	1:C:144:TYR:HB2	2.43	0.53
1:C:287:LYS:HG3	1:C:288:ALA:N	2.23	0.53
1:C:442:VAL:HB	1:C:481:ALA:HB1	1.89	0.53
4:F:817:MRG:H2'	4:F:818:DC:C6	2.43	0.53
2:D:175:ASN:OD1	2:D:201:LYS:NZ	2.34	0.53
2:D:56:TYR:HE2	2:D:126:LYS:HE2	1.73	0.53
1:C:406:TRP:CD1	1:C:407:GLN:HG2	2.44	0.53
1:C:503:LEU:HD11	1:C:533:LEU:HG	1.89	0.53
1:C:363:ASN:HA	1:C:511:ASP:OD1	2.07	0.53
2:D:332:GLN:HB2	2:D:336:GLN:HB3	1.90	0.53
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.91	0.53
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.90	0.53
2:D:64:LYS:HE3	2:D:71:TRP:CZ2	2.44	0.53
1:C:41:MET:HB3	1:C:46:LYS:HB2	1.90	0.53
2:D:87:PHE:CZ	2:D:159:ILE:HG13	2.37	0.53
2:B:281:LYS:HE3	2:B:284:ARG:HH21	1.74	0.53
3:T:713:DC:H2'	3:T:714:DG:C8	2.44	0.53
2:D:210:LEU:HA	2:D:214:LEU:O	2.09	0.53
2:D:395:LYS:HE2	2:D:399:GLU:OE2	2.08	0.53
1:A:123:ASP:N	1:A:123:ASP:OD2	2.42	0.52
1:A:135:ILE:HG23	1:A:138:GLU:HB2	1.90	0.52
1:A:50:ILE:HD12	1:A:54:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:SER:O	2:B:190:GLY:HA2	2.09	0.52
1:A:101:LYS:HE2	1:A:321:PRO:HG3	1.91	0.52
1:A:246:LEU:HD11	1:A:310:LEU:HD22	1.89	0.52
1:A:155:GLY:O	1:A:159:ILE:HG13	2.08	0.52
1:C:199:ARG:HE	1:C:222:GLN:HG2	1.72	0.52
1:C:41:MET:HA	1:C:44:GLU:OE1	2.10	0.52
2:D:111:VAL:HG23	2:D:115:TYR:HE1	1.74	0.52
2:D:16:MET:CG	2:D:83:ARG:HG2	2.39	0.52
1:A:31:ILE:HG21	1:A:135:ILE:HA	1.90	0.52
1:A:390:LYS:HE2	1:A:415:GLU:OE2	2.08	0.52
1:A:464:GLN:NE2	1:A:551:LEU:HD21	2.24	0.52
1:C:24:TRP:CZ3	3:E:703:DG:N2	2.76	0.52
1:C:257:ILE:HG21	1:C:283:LEU:HD21	1.90	0.52
1:C:398:TRP:CZ2	1:C:411:ILE:HG13	2.44	0.52
1:A:255:ASN:HB2	1:A:289:LEU:HG	1.91	0.52
1:A:21:VAL:CG2	1:A:59:PRO:HD3	2.39	0.52
2:B:366:LYS:HG3	2:B:405:TYR:CD1	2.44	0.52
1:C:178:ILE:HD12	1:C:178:ILE:N	2.25	0.51
1:C:249:LYS:HG2	1:C:256:ASP:OD2	2.10	0.51
1:C:21:VAL:HG21	1:C:59:PRO:HD3	1.92	0.51
2:D:419:THR:HG22	2:D:419:THR:O	2.09	0.51
1:A:379:SER:CB	1:A:387:PRO:HD3	2.40	0.51
2:B:79:GLU:HG3	2:B:83:ARG:HE	1.75	0.51
2:D:214:LEU:HD12	2:D:215:THR:N	2.25	0.51
2:B:278:GLN:NE2	2:B:298:GLU:CB	2.74	0.51
1:A:450:THR:HB	1:A:452:LEU:HD12	1.92	0.51
1:C:362:THR:HG21	1:C:367:GLN:HE21	1.75	0.51
1:C:253:THR:CG2	1:C:292:VAL:HG12	2.36	0.51
2:D:198:HIS:O	2:D:202:ILE:HG13	2.10	0.51
1:C:31:ILE:HD12	1:C:133:PRO:HB2	1.93	0.51
1:C:10:VAL:O	1:C:11:LYS:HG3	2.11	0.51
4:F:806:DT:H2''	4:F:807:DC:OP1	2.09	0.51
4:F:804:DA:C2'	4:F:805:DG:C8	2.94	0.51
4:F:807:DC:H2'	4:F:808:DC:C6	2.46	0.51
1:C:186:ASP:CB	4:F:822:ATM:N5'	2.74	0.51
1:A:169:GLU:N	1:A:170:PRO:HD2	2.25	0.51
1:C:126:LYS:HG3	1:C:127:TYR:CD2	2.46	0.51
4:F:817:MRG:N3	4:F:817:MRG:C22	2.72	0.50
2:D:210:LEU:HD12	2:D:214:LEU:O	2.11	0.50
2:D:73:LYS:CE	2:D:146:TYR:OH	2.60	0.50
2:D:109:LEU:HD22	2:D:216:THR:CG2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:365:VAL:HG11	2:D:401:TRP:HB2	1.93	0.50
2:B:317:VAL:O	2:B:317:VAL:HG23	2.11	0.50
2:D:31:ILE:HD12	2:D:135:ILE:HG12	1.92	0.50
1:A:295:LEU:HB2	1:A:300:GLU:OE2	2.11	0.50
2:D:42:GLU:OE2	2:D:49:LYS:HG3	2.11	0.50
2:D:167:ILE:HG23	2:D:212:TRP:CG	2.46	0.50
4:P:806:DT:H2'	4:P:807:DC:C6	2.47	0.50
2:D:354:TYR:CE2	2:D:375:ILE:HG13	2.43	0.50
1:A:473:THR:O	1:A:477:THR:HG23	2.12	0.50
2:D:241:VAL:HG12	2:D:242:GLN:H	1.75	0.50
4:P:803:DC:H2'	4:P:804:DA:C8	2.46	0.50
2:B:101:LYS:O	2:B:236:PRO:HB2	2.12	0.50
1:A:171:PHE:CD2	1:A:205:LEU:HD13	2.46	0.50
1:C:179:VAL:O	1:C:189:VAL:HA	2.12	0.50
1:C:94:ILE:HD11	3:E:708:DG:N2	2.26	0.50
1:A:64:LYS:HE3	1:A:69:THR:O	2.11	0.50
2:B:278:GLN:HG3	2:B:298:GLU:HB3	1.94	0.49
1:A:407:GLN:HE22	2:B:418:ASN:HA	1.76	0.49
2:B:305:GLU:O	2:B:309:ILE:HG13	2.11	0.49
1:A:184:MET:HG2	4:P:822:ATM:H1'	1.94	0.49
2:D:28:GLU:HA	2:D:135:ILE:HD11	1.93	0.49
1:C:329:ILE:O	1:C:392:PRO:HD3	2.12	0.49
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.94	0.49
1:A:63:ILE:O	1:A:72:ARG:HB3	2.12	0.49
1:A:37:ILE:HA	1:A:40:GLU:HG3	1.93	0.49
1:C:38:CYS:HB3	1:C:144:TYR:CE2	2.47	0.49
3:E:722:DA:H2''	3:E:723:DC:H5''	1.94	0.49
2:B:390:LYS:HE2	2:B:415:GLU:OE2	2.12	0.49
1:C:503:LEU:HD22	1:C:535:TRP:HB2	1.93	0.49
1:C:28:GLU:HB2	1:C:135:ILE:HG21	1.95	0.49
1:C:115:TYR:CD2	1:C:151:GLN:HG2	2.47	0.49
3:E:718:DA:H4'	3:E:719:DG:OP1	2.12	0.49
1:A:500:GLN:CD	2:B:422:LEU:HD11	2.32	0.49
1:A:328:GLU:HG3	1:A:390:LYS:CB	2.41	0.49
1:C:296:THR:O	1:C:300:GLU:HB2	2.12	0.49
4:F:819:DG:H2'	4:F:820:DC:C6	2.48	0.49
2:B:69:THR:O	2:B:69:THR:HG22	2.12	0.49
2:B:118:VAL:HG12	2:B:119:PRO:O	2.12	0.49
1:A:130:PHE:H	1:A:130:PHE:HD2	1.59	0.49
1:A:97:PRO:HD3	1:A:232:TYR:CE2	2.47	0.49
2:B:142:ILE:HG22	2:B:144:TYR:CE2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282:LEU:HB3	1:C:293:ILE:HD13	1.95	0.49
1:A:410:TRP:CH2	1:A:412:PRO:HA	2.48	0.49
2:D:199:ARG:HA	2:D:202:ILE:HD12	1.94	0.49
1:A:433:PRO:HD3	1:A:532:TYR:CZ	2.48	0.49
1:A:17:ASP:OD2	1:A:56:TYR:HE1	1.96	0.49
2:B:336:GLN:CG	2:B:353:LYS:HD2	2.43	0.49
1:A:10:VAL:HG12	1:A:11:LYS:H	1.78	0.49
1:C:281:LYS:HG3	1:C:284:ARG:CZ	2.43	0.48
2:D:390:LYS:HE2	2:D:415:GLU:OE2	2.13	0.48
1:C:376:THR:HG21	2:D:401:TRP:CH2	2.48	0.48
1:C:361:HIS:CD2	1:C:505:ILE:HG12	2.48	0.48
1:C:223:LYS:O	1:C:223:LYS:HG2	2.13	0.48
1:A:2:ILE:CD1	1:A:2:ILE:N	2.73	0.48
1:C:276:VAL:HG12	1:C:280:SER:OG	2.12	0.48
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.96	0.48
2:B:281:LYS:O	2:B:284:ARG:HG3	2.14	0.48
2:D:360:ALA:C	2:D:362:THR:H	2.17	0.48
1:A:2:ILE:CD1	1:A:2:ILE:H	1.99	0.48
1:C:37:ILE:HD13	1:C:40:GLU:HG3	1.96	0.48
1:C:50:ILE:HG12	1:C:54:ASN:HD22	1.79	0.48
2:B:109:LEU:HD22	2:B:216:THR:CG2	2.37	0.48
1:A:135:ILE:HG22	1:A:138:GLU:HB2	1.95	0.48
1:A:24:TRP:O	1:A:26:LEU:HG	2.14	0.48
1:C:324:ASP:O	1:C:343:GLN:HG2	2.13	0.48
1:A:10:VAL:HG12	1:A:11:LYS:N	2.29	0.48
2:D:21:VAL:HB	2:D:59:PRO:HD3	1.96	0.48
1:C:130:PHE:HD2	1:C:130:PHE:H	1.60	0.48
4:F:803:DC:H2'	4:F:804:DA:N7	2.28	0.48
2:B:206:ARG:NH2	2:B:210:LEU:HD11	2.29	0.48
2:D:85:GLN:HA	2:D:88:TRP:CE2	2.49	0.48
1:C:171:PHE:CZ	1:C:205:LEU:HB2	2.49	0.48
2:B:56:TYR:HE2	2:B:126:LYS:CE	2.26	0.48
2:B:124:PHE:HE2	2:B:153:TRP:CZ2	2.32	0.47
1:A:376:THR:HG21	2:B:401:TRP:CH2	2.49	0.47
4:P:811:DG:H2''	4:P:812:DT:O5'	2.14	0.47
4:P:807:DC:H4'	4:P:808:DC:OP1	2.15	0.47
1:C:37:ILE:HA	1:C:40:GLU:HG3	1.95	0.47
1:C:115:TYR:HD2	1:C:151:GLN:HG2	1.79	0.47
1:C:545:ASN:O	1:C:549:ASP:HB2	2.14	0.47
1:A:276:VAL:CG1	1:A:276:VAL:O	2.62	0.47
1:C:64:LYS:NZ	1:C:69:THR:HA	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:120:LEU:HD23	2:D:125:ARG:HG2	1.95	0.47
1:C:221:HIS:ND1	1:C:221:HIS:N	2.63	0.47
2:D:84:THR:O	2:D:84:THR:HG22	2.14	0.47
1:A:122:GLU:OE2	1:A:125:ARG:NH1	2.48	0.47
2:D:419:THR:O	2:D:420:PRO:C	2.50	0.47
2:D:203:GLU:O	2:D:207:GLN:HG2	2.14	0.47
1:A:79:GLU:OE1	1:A:83:ARG:NH2	2.48	0.47
1:C:125:ARG:HH11	1:C:147:ASN:HB3	1.79	0.47
1:A:261:VAL:HG22	1:A:276:VAL:HG13	1.97	0.47
1:A:500:GLN:CG	2:B:422:LEU:HD11	2.44	0.47
2:B:164:MET:HE2	2:B:168:LEU:HD11	1.95	0.47
1:A:226:PRO:HB3	1:A:235:HIS:CD2	2.50	0.47
1:C:447:ASN:HB3	1:C:450:THR:HB	1.96	0.47
2:B:214:LEU:HD12	2:B:215:THR:H	1.80	0.47
2:D:17:ASP:O	2:D:83:ARG:HD3	2.15	0.47
1:C:406:TRP:CZ2	2:D:420:PRO:HG3	2.49	0.47
1:A:344:GLU:OE1	1:A:344:GLU:HA	2.15	0.47
1:C:102:LYS:HE2	1:C:236:PRO:O	2.14	0.47
2:B:28:GLU:CB	2:B:135:ILE:HD11	2.45	0.47
1:C:106:VAL:O	1:C:227:PHE:CZ	2.68	0.47
2:D:358:ARG:HB3	2:D:366:LYS:HE2	1.96	0.47
1:A:16:MET:HE2	1:A:83:ARG:HG2	1.97	0.47
1:A:35:VAL:HA	1:A:38:CYS:HB2	1.97	0.46
1:A:114:ALA:HB1	1:A:160:PHE:CE2	2.50	0.46
1:A:8:VAL:O	1:A:10:VAL:HG23	2.16	0.46
1:A:135:ILE:HG12	1:A:136:ASN:N	2.27	0.46
1:C:398:TRP:CH2	1:C:411:ILE:HG13	2.50	0.46
1:C:242:GLN:HB3	1:C:243:PRO:HD2	1.96	0.46
1:A:106:VAL:O	1:A:227:PHE:CZ	2.68	0.46
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.97	0.46
1:A:228:LEU:HD22	1:A:242:GLN:NE2	2.31	0.46
1:C:65:LYS:HE2	1:C:72:ARG:HD3	1.98	0.46
1:C:64:LYS:HD3	1:C:71:TRP:CE2	2.50	0.46
1:A:226:PRO:HB3	1:A:235:HIS:NE2	2.30	0.46
1:C:120:LEU:HG	1:C:121:ASP:N	2.30	0.46
1:A:88:TRP:CD1	2:B:143:ARG:NH1	2.84	0.46
1:A:164:MET:HE2	1:A:168:LEU:HD11	1.96	0.46
2:D:235:HIS:N	2:D:236:PRO:HD3	2.30	0.46
2:B:182:GLN:HG3	2:B:187:LEU:CD1	2.41	0.46
1:C:53:GLU:H	1:C:53:GLU:HG3	1.37	0.46
1:C:548:VAL:HA	1:C:551:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:13:LYS:HB3	2:D:14:PRO:HD2	1.98	0.46
4:F:815:DG:OP2	4:F:815:DG:H8	1.99	0.46
1:A:325:LEU:HD11	1:A:383:TRP:CE3	2.51	0.46
1:C:254:VAL:CG2	1:C:286:THR:HG21	2.42	0.46
2:D:41:MET:HB3	2:D:47:ILE:HG12	1.98	0.46
1:A:186:ASP:CB	4:P:822:ATM:N5'	2.78	0.46
1:C:88:TRP:CD1	2:D:143:ARG:NH1	2.83	0.46
1:C:345:PRO:O	1:C:346:PHE:HB2	2.15	0.46
1:C:169:GLU:N	1:C:170:PRO:HD2	2.31	0.46
3:E:723:DC:H2''	3:E:724:DT:C6	2.51	0.46
2:B:87:PHE:CD2	2:B:87:PHE:C	2.88	0.46
2:B:17:ASP:O	2:B:83:ARG:HD3	2.15	0.46
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.15	0.46
1:A:100:LEU:HD11	1:A:229:TRP:CZ3	2.51	0.46
3:E:723:DC:H5''	3:E:723:DC:C6	2.46	0.45
2:B:197:GLN:O	2:B:200:THR:HB	2.16	0.45
2:B:379:SER:HB3	2:B:385:LYS:O	2.15	0.45
2:D:205:LEU:O	2:D:205:LEU:HD12	2.16	0.45
2:D:191:SER:HB2	2:D:193:LEU:HG	1.99	0.45
1:C:168:LEU:HD11	1:C:187:LEU:HD21	1.99	0.45
2:D:284:ARG:HG2	2:D:284:ARG:HH11	1.81	0.45
1:A:424:LYS:HE3	1:A:426:TRP:CZ3	2.51	0.45
1:A:60:VAL:HG11	1:A:130:PHE:CD1	2.47	0.45
1:A:221:HIS:ND1	1:A:221:HIS:N	2.63	0.45
1:A:8:VAL:HG12	1:A:8:VAL:O	2.16	0.45
1:A:131:THR:HA	1:A:143:ARG:HG2	1.98	0.45
1:C:130:PHE:CD2	1:C:130:PHE:N	2.85	0.45
3:T:725:DG:N2	4:P:803:DC:C2	2.84	0.45
1:A:547:GLN:O	1:A:551:LEU:HB2	2.17	0.45
2:B:103:LYS:HE2	2:B:179:VAL:HG23	1.99	0.45
1:A:64:LYS:HD3	1:A:71:TRP:NE1	2.31	0.45
1:A:80:LEU:O	1:A:84:THR:OG1	2.29	0.45
2:D:114:ALA:HB2	2:D:214:LEU:HD13	1.98	0.45
3:E:721:DG:C2'	3:E:722:DA:OP2	2.61	0.45
1:A:46:LYS:O	1:A:47:ILE:HG23	2.17	0.45
1:A:503:LEU:CD1	1:A:533:LEU:HD13	2.43	0.45
1:C:17:ASP:O	1:C:83:ARG:HD3	2.17	0.45
1:C:362:THR:CG2	1:C:367:GLN:HE21	2.29	0.45
2:B:268:SER:HA	2:B:271:TYR:O	2.16	0.45
3:E:706:DA:H2'	3:E:707:DG:C8	2.52	0.45
2:D:13:LYS:HD3	2:D:85:GLN:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:VAL:CG1	1:A:130:PHE:HD1	2.27	0.44
2:D:101:LYS:O	2:D:236:PRO:HB2	2.17	0.44
2:B:247:PRO:CA	2:B:428:GLN:HE22	2.30	0.44
1:A:27:THR:OG1	1:A:29:GLU:HB3	2.17	0.44
2:D:124:PHE:CE2	2:D:153:TRP:CZ2	3.05	0.44
2:D:323:LYS:O	2:D:385:LYS:NZ	2.50	0.44
2:D:78:ARG:HD3	2:D:411:ILE:O	2.17	0.44
1:C:120:LEU:HG	1:C:121:ASP:H	1.82	0.44
2:D:109:LEU:HA	2:D:109:LEU:HD23	1.87	0.44
1:A:77:PHE:O	1:A:80:LEU:N	2.49	0.44
1:C:47:ILE:HG12	1:C:144:TYR:HB3	2.00	0.44
1:C:21:VAL:CG2	1:C:58:THR:HA	2.48	0.44
4:P:818:DC:H2'	4:P:819:DG:H8	1.83	0.44
2:D:81:ASN:HB3	2:D:154:LYS:HD2	2.00	0.44
2:D:317:VAL:HG23	2:D:317:VAL:O	2.17	0.44
3:E:712:DC:H2''	3:E:713:DC:O5'	2.18	0.44
2:D:239:TRP:CH2	2:D:378:GLU:HA	2.53	0.44
2:B:69:THR:CG2	2:B:69:THR:O	2.65	0.44
1:A:273:GLY:HA2	1:A:338:THR:HG21	1.98	0.44
1:C:253:THR:HG22	1:C:292:VAL:CG1	2.39	0.44
1:C:96:HIS:CG	1:C:97:PRO:HD2	2.53	0.44
1:C:16:MET:CE	1:C:83:ARG:HG2	2.48	0.44
3:T:710:DG:H2'	3:T:711:DC:C6	2.53	0.44
3:T:711:DC:H2''	3:T:712:DC:O5'	2.18	0.44
1:A:181:TYR:HB2	1:A:188:TYR:HB3	1.99	0.44
2:B:42:GLU:OE2	2:B:49:LYS:HG3	2.18	0.44
1:A:37:ILE:HA	1:A:40:GLU:HG2	1.98	0.44
1:C:424:LYS:HE2	1:C:426:TRP:CZ3	2.53	0.44
4:F:819:DG:H2'	4:F:820:DC:H6	1.83	0.44
1:C:433:PRO:HD3	1:C:532:TYR:CZ	2.52	0.44
2:B:195:ILE:O	2:B:199:ARG:HG3	2.18	0.44
1:A:197:GLN:O	1:A:200:THR:HB	2.18	0.44
2:D:281:LYS:O	2:D:284:ARG:HG3	2.18	0.43
1:C:175:ASN:N	1:C:176:PRO:HD3	2.33	0.43
1:A:122:GLU:HB3	1:A:123:ASP:OD2	2.18	0.43
1:C:50:ILE:HD13	1:C:143:ARG:NH1	2.33	0.43
2:D:74:LEU:HD12	2:D:75:VAL:N	2.33	0.43
1:A:500:GLN:HG2	2:B:422:LEU:HD13	1.99	0.43
1:A:382:ILE:O	2:B:136:ASN:HB2	2.19	0.43
1:C:254:VAL:HG21	1:C:286:THR:CG2	2.44	0.43
1:A:259:LYS:HG3	4:P:819:DG:OP1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:428:GLN:HA	2:D:428:GLN:OE1	2.18	0.43
1:A:130:PHE:N	1:A:130:PHE:CD2	2.87	0.43
1:A:171:PHE:CE1	1:A:175:ASN:ND2	2.86	0.43
1:A:277:ARG:HB3	1:A:336:GLN:OE1	2.19	0.43
2:B:157:PRO:HG3	2:B:184:MET:HA	1.99	0.43
2:D:198:HIS:NE2	2:D:202:ILE:HD11	2.33	0.43
1:C:27:THR:O	1:C:31:ILE:HG12	2.18	0.43
1:A:451:LYS:O	1:A:471:ASN:N	2.51	0.43
1:C:492:GLU:HG2	1:C:530:LYS:HB2	2.01	0.43
2:D:11:LYS:HA	2:D:11:LYS:HD3	1.83	0.43
1:C:1:PRO:HB2	1:C:2:ILE:H	1.59	0.43
4:F:812:DT:H2''	4:F:813:DT:O5'	2.19	0.43
1:C:132:ILE:HB	1:C:142:ILE:HG22	2.00	0.43
1:A:325:LEU:HD11	1:A:383:TRP:CD2	2.53	0.43
1:A:395:LYS:HD2	1:A:414:TRP:CH2	2.54	0.43
1:A:74:LEU:HD22	3:T:705:DA:C2	2.54	0.42
4:P:819:DG:H2'	4:P:820:DC:C6	2.53	0.42
2:D:158:ALA:O	2:D:161:GLN:HB2	2.19	0.42
1:A:475:GLN:NE2	1:A:475:GLN:H	2.17	0.42
2:B:74:LEU:HD12	2:B:75:VAL:N	2.33	0.42
2:B:210:LEU:HD23	2:B:214:LEU:O	2.18	0.42
2:D:209:LEU:HD13	2:D:214:LEU:HD23	2.02	0.42
1:C:2:ILE:HD12	1:C:2:ILE:H	1.84	0.42
1:C:400:THR:O	1:C:404:GLU:HG2	2.20	0.42
1:C:325:LEU:HD23	1:C:325:LEU:HA	1.89	0.42
2:D:169:GLU:HB3	2:D:170:PRO:HD3	2.00	0.42
1:A:464:GLN:HE21	1:A:551:LEU:HD21	1.82	0.42
1:C:491:LEU:HA	1:C:491:LEU:HD23	1.71	0.42
1:C:58:THR:HG21	1:C:77:PHE:CE1	2.55	0.42
2:B:195:ILE:HG22	2:B:199:ARG:NE	2.33	0.42
2:D:5:ILE:O	2:D:119:PRO:HG2	2.19	0.42
2:D:28:GLU:HG3	2:D:135:ILE:HD11	2.02	0.42
2:D:350:LYS:HE2	2:D:378:GLU:OE1	2.19	0.42
1:C:39:THR:HA	1:C:42:GLU:OE2	2.18	0.42
2:B:34:LEU:HD23	2:B:34:LEU:HA	1.80	0.42
1:C:31:ILE:CG2	1:C:134:SER:HA	2.50	0.42
1:C:230:MET:O	4:F:821:DC:H5'	2.18	0.42
1:A:441:TYR:CD2	2:B:286:THR:HG23	2.55	0.42
2:D:120:LEU:HB3	2:D:147:ASN:O	2.20	0.42
2:D:200:THR:O	2:D:203:GLU:HB3	2.20	0.42
1:C:486:LEU:HB3	1:C:524:GLN:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:TRP:HB2	1:A:425:LEU:HD11	2.02	0.42
1:A:134:SER:O	1:A:135:ILE:HB	2.19	0.42
2:B:317:VAL:HG12	2:B:347:LYS:HD2	2.02	0.42
1:A:454:LYS:HB2	1:A:552:VAL:O	2.19	0.42
1:C:150:PRO:HG2	1:C:153:TRP:HB2	2.02	0.42
2:B:419:THR:HG22	2:B:419:THR:O	2.18	0.42
2:B:120:LEU:HD23	2:B:125:ARG:HG2	2.01	0.42
1:A:41:MET:HB2	1:A:47:ILE:HD11	2.02	0.41
2:B:167:ILE:HG23	2:B:212:TRP:CD1	2.55	0.41
1:C:249:LYS:HD2	1:C:249:LYS:HA	1.81	0.41
2:D:207:GLN:OE1	2:D:207:GLN:HA	2.20	0.41
1:C:135:ILE:O	1:C:136:ASN:HB2	2.20	0.41
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.56	0.41
1:C:10:VAL:HG12	1:C:11:LYS:N	2.35	0.41
1:C:326:ILE:O	1:C:341:ILE:HA	2.20	0.41
1:C:156:SER:HB2	1:C:157:PRO:HD3	2.01	0.41
4:P:822:ATM:O5'	4:P:822:ATM:H6	2.21	0.41
1:A:16:MET:CE	1:A:83:ARG:HG2	2.50	0.41
1:C:17:ASP:OD2	1:C:56:TYR:HE1	2.04	0.41
2:B:425:LEU:HD23	2:B:426:TRP:CE2	2.56	0.41
1:C:261:VAL:CG1	1:C:276:VAL:HG11	2.47	0.41
1:C:458:VAL:HG23	1:C:548:VAL:HB	2.01	0.41
2:D:24:TRP:HZ2	2:D:61:PHE:CD2	2.39	0.41
3:T:719:DG:H2"	3:T:720:DG:C8	2.55	0.41
2:D:10:VAL:HG13	2:D:87:PHE:CD1	2.55	0.41
2:B:210:LEU:HA	2:B:214:LEU:O	2.20	0.41
1:C:36:GLU:O	1:C:40:GLU:HG2	2.21	0.41
2:B:428:GLN:HA	2:B:428:GLN:OE1	2.21	0.41
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.61	0.41
1:C:266:TRP:O	1:C:269:GLN:HG2	2.20	0.41
1:A:270:ILE:HA	1:A:270:ILE:HD12	1.76	0.41
1:A:23:GLN:HE21	1:A:23:GLN:HB3	1.64	0.41
1:C:31:ILE:HG21	1:C:134:SER:HA	2.02	0.41
1:C:171:PHE:CE2	1:C:205:LEU:HD13	2.55	0.41
1:C:271:TYR:CE1	1:C:314:VAL:HG22	2.55	0.41
1:A:21:VAL:N	1:A:57:ASN:O	2.48	0.41
2:D:312:GLU:HB3	2:D:313:PRO:CD	2.48	0.41
2:B:56:TYR:CE2	2:B:126:LYS:HE2	2.50	0.41
2:D:168:LEU:CB	2:D:172:LYS:HE3	2.50	0.41
1:C:535:TRP:CD2	2:D:422:LEU:HD21	2.56	0.41
1:C:60:VAL:HG11	1:C:130:PHE:HD1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:357:MET:HB3	2:D:370:GLU:OE1	2.21	0.41
2:B:86:ASP:O	2:B:90:VAL:HB	2.21	0.41
4:F:815:DG:H2"	4:F:816:DG:OP2	2.21	0.41
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.21	0.41
2:D:73:LYS:HE3	2:D:146:TYR:OH	2.21	0.41
2:D:206:ARG:NH2	2:D:217:PRO:O	2.54	0.41
2:B:382:ILE:HG22	2:B:383:TRP:CE2	2.56	0.41
1:A:459:THR:CG2	1:A:460:ASN:N	2.84	0.41
1:A:326:ILE:O	1:A:341:ILE:HA	2.21	0.41
2:D:422:LEU:HA	2:D:422:LEU:HD12	1.77	0.40
1:C:130:PHE:HD2	1:C:130:PHE:N	2.18	0.40
1:C:54:ASN:HA	1:C:55:PRO:HD2	1.86	0.40
1:C:120:LEU:CG	1:C:121:ASP:H	2.34	0.40
2:B:379:SER:CB	2:B:387:PRO:HD3	2.51	0.40
2:B:50:ILE:HG13	2:B:51:GLY:N	2.35	0.40
1:A:89:GLU:OE1	1:A:89:GLU:HA	2.20	0.40
1:A:28:GLU:CD	1:A:28:GLU:H	2.24	0.40
1:C:395:LYS:HD2	1:C:414:TRP:CH2	2.56	0.40
2:D:56:TYR:CE2	2:D:127:TYR:CE1	3.10	0.40
1:C:475:GLN:HB3	1:C:501:TYR:CE2	2.56	0.40
2:B:53:GLU:HG2	2:B:54:ASN:N	2.35	0.40
2:B:297:GLU:OE1	2:B:297:GLU:HA	2.21	0.40
2:D:142:ILE:HG22	2:D:144:TYR:CE2	2.56	0.40
2:B:84:THR:HG22	2:B:84:THR:O	2.22	0.40
1:A:135:ILE:HG22	1:A:138:GLU:CB	2.50	0.40
2:D:336:GLN:HB2	2:D:336:GLN:HE21	1.79	0.40
2:D:197:GLN:O	2:D:201:LYS:HG2	2.22	0.40
2:B:28:GLU:HB2	2:B:135:ILE:HD11	2.03	0.40
1:A:553:SER:O	1:A:554:ALA:C	2.59	0.40
1:A:132:ILE:HD12	1:A:144:TYR:CD2	2.56	0.40
1:C:379:SER:CB	1:C:387:PRO:HD3	2.51	0.40
1:C:382:ILE:O	2:D:136:ASN:HB2	2.21	0.40
1:C:420:PRO:HA	1:C:421:PRO:C	2.40	0.40
2:D:257:ILE:O	2:D:261:VAL:HG23	2.22	0.40
2:B:78:ARG:HD3	2:B:411:ILE:O	2.21	0.40
2:D:376:THR:HG21	2:D:410:TRP:CZ3	2.56	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	553/556 (100%)	529 (96%)	23 (4%)	1 (0%)	52	80
1	C	552/556 (99%)	528 (96%)	24 (4%)	0	100	100
2	B	408/428 (95%)	399 (98%)	9 (2%)	0	100	100
2	D	408/428 (95%)	391 (96%)	17 (4%)	0	100	100
All	All	1921/1968 (98%)	1847 (96%)	73 (4%)	1 (0%)	56	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	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	495/497 (100%)	476 (96%)	19 (4%)	40	71
1	C	495/497 (100%)	475 (96%)	20 (4%)	38	69
2	B	374/390 (96%)	362 (97%)	12 (3%)	46	77
2	D	374/390 (96%)	366 (98%)	8 (2%)	61	87
All	All	1738/1774 (98%)	1679 (97%)	59 (3%)	44	75

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	3	SER
1	A	5	ILE
1	A	23	GLN
1	A	39	THR
1	A	63	ILE
1	A	67	ASP
1	A	90	VAL
1	A	105	SER
1	A	123	ASP
1	A	130	PHE
1	A	188	TYR
1	A	221	HIS
1	A	248	GLU
1	A	277	ARG
1	A	293	ILE
1	A	324	ASP
1	A	338	THR
1	A	523	GLU
2	B	72	ARG
2	B	113	ASP
2	B	115	TYR
2	B	163	SER
2	B	169	GLU
2	B	177	ASP
2	B	208	HIS
2	B	241	VAL
2	B	257	ILE
2	B	293	ILE
2	B	336	GLN
2	B	422	LEU
1	C	2	ILE
1	C	3	SER
1	C	5	ILE
1	C	7	THR
1	C	48	SER
1	C	50	ILE
1	C	53	GLU
1	C	123	ASP
1	C	130	PHE
1	C	199	ARG
1	C	218	ASP
1	C	221	HIS

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Mol	Chain	Res	Type
1	C	250	ASP
1	C	270	ILE
1	C	324	ASP
1	C	338	THR
1	C	357	MET
1	C	407	GLN
1	C	459	THR
1	C	498	ASN
2	D	74	LEU
2	D	113	ASP
2	D	134	SER
2	D	248	GLU
2	D	336	GLN
2	D	379	SER
2	D	423	VAL
2	D	424	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	407	GLN
1	A	464	GLN
1	A	487	GLN
2	B	278	GLN
2	B	336	GLN
1	C	222	GLN
1	C	367	GLN
1	C	407	GLN
1	C	464	GLN
1	C	547	GLN
2	D	348	ASN
2	D	361	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MRG	F	817	1,3,4	20,28,29	3.04	9 (45%)	25,39,42	1.94	7 (28%)
4	ATM	F	822	3,4	13,23,24	1.64	2 (15%)	17,32,35	1.88	4 (23%)
4	MRG	P	817	1,3,4	20,28,29	3.12	9 (45%)	25,39,42	2.07	9 (36%)
4	ATM	P	822	3,4	13,23,24	1.74	2 (15%)	17,32,35	2.22	4 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MRG	F	817	1,3,4	-	0/8/26/27	0/3/3/3
4	ATM	F	822	3,4	-	0/6/24/25	0/2/2/2
4	MRG	P	817	1,3,4	-	0/8/26/27	0/3/3/3
4	ATM	P	822	3,4	-	0/6/24/25	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	817	MRG	C2'-C3'	-3.35	1.43	1.52
4	F	817	MRG	C2'-C3'	-3.32	1.43	1.52
4	P	817	MRG	O3'-C3'	-3.17	1.36	1.43
4	F	817	MRG	O4'-C4'	-2.70	1.38	1.45
4	P	817	MRG	O4'-C4'	-2.64	1.38	1.45
4	F	817	MRG	O3'-C3'	-2.39	1.38	1.43
4	F	817	MRG	C2-N1	2.40	1.43	1.34
4	P	817	MRG	C2-N3	2.46	1.43	1.34
4	F	817	MRG	C2-N3	2.52	1.43	1.34
4	P	817	MRG	C2-N1	2.56	1.43	1.34
4	F	822	ATM	C6-N1	3.50	1.40	1.35
4	F	817	MRG	C6-C5	3.83	1.48	1.41
4	P	817	MRG	C6-C5	3.86	1.49	1.41
4	P	822	ATM	C4-N3	3.99	1.40	1.33
4	P	822	ATM	C6-N1	4.15	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	822	ATM	C4-N3	4.18	1.40	1.33
4	F	817	MRG	C6-N1	4.62	1.41	1.33
4	P	817	MRG	C6-N1	5.05	1.42	1.33
4	F	817	MRG	C4-N3	5.59	1.44	1.35
4	P	817	MRG	C4-N3	5.86	1.44	1.35
4	P	817	MRG	C2-N2	8.46	1.48	1.34
4	F	817	MRG	C2-N2	8.60	1.48	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	822	ATM	C2'-C1'-N1	-5.76	100.15	114.16
4	F	822	ATM	C5-C4-N3	-4.79	119.80	125.14
4	P	817	MRG	N3-C2-N1	-4.03	120.03	126.22
4	F	817	MRG	N3-C2-N1	-3.95	120.14	126.22
4	P	822	ATM	C5-C4-N3	-3.56	121.17	125.14
4	P	817	MRG	C5-C6-N1	-3.42	118.92	123.59
4	F	817	MRG	C5-C6-N1	-2.80	119.77	123.59
4	F	817	MRG	C4-C5-N7	-2.77	106.93	109.48
4	P	817	MRG	C1'-N9-C4	-2.63	122.70	127.16
4	P	817	MRG	C4-C5-N7	-2.43	107.25	109.48
4	P	822	ATM	C5'-C4'-C3'	-2.14	106.22	114.46
4	F	822	ATM	C2'-C1'-N1	-2.12	109.01	114.16
4	P	817	MRG	O5'-C5'-C4'	2.01	116.47	109.12
4	F	822	ATM	O4'-C1'-N1	2.32	111.73	107.72
4	F	817	MRG	C22-C21-N2	2.59	118.46	111.46
4	P	817	MRG	C22-C21-N2	3.05	119.71	111.46
4	F	817	MRG	C6-N1-C2	3.22	119.99	115.31
4	F	817	MRG	O4'-C1'-N9	3.25	113.34	107.72
4	P	817	MRG	C2-N3-C4	3.30	119.06	115.09
4	P	817	MRG	O4'-C1'-N9	3.49	113.76	107.72
4	P	817	MRG	C6-N1-C2	3.82	120.87	115.31
4	F	817	MRG	C2-N3-C4	3.95	119.85	115.09
4	F	822	ATM	C4-N3-C2	4.51	119.14	115.25
4	P	822	ATM	C4-N3-C2	4.84	119.43	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	817	MRG	4	0
4	F	822	ATM	2	0
4	P	817	MRG	1	0
4	P	822	ATM	4	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	555/556 (99%)	1.11	98 (17%) 2 1	36, 83, 138, 149	0
1	C	554/556 (99%)	1.06	93 (16%) 2 2	34, 81, 136, 148	0
2	B	412/428 (96%)	0.72	31 (7%) 17 15	34, 66, 118, 131	0
2	D	412/428 (96%)	0.80	45 (10%) 7 5	40, 69, 125, 132	0
3	E	24/27 (88%)	1.03	5 (20%) 1 1	67, 104, 156, 164	0
3	T	24/27 (88%)	1.28	5 (20%) 1 1	69, 106, 158, 161	0
4	F	18/21 (85%)	0.54	2 (11%) 7 5	60, 92, 141, 142	0
4	P	18/21 (85%)	0.51	3 (16%) 2 2	68, 90, 142, 144	0
All	All	2017/2064 (97%)	0.95	282 (13%) 4 3	34, 75, 133, 164	0

All (282) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	214	LEU	14.2
1	A	133	PRO	14.1
1	C	142	ILE	13.5
1	A	74	LEU	12.6
1	C	133	PRO	12.4
1	A	131	THR	12.3
3	T	702	DT	12.2
2	D	231	GLY	11.5
2	D	214	LEU	11.0
2	B	215	THR	10.1
1	A	140	PRO	9.4
1	A	135	ILE	9.0
1	A	128	THR	7.8
2	D	4	PRO	7.6
1	C	136	ASN	7.6
1	A	34	LEU	7.6

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Mol	Chain	Res	Type	RSRZ
1	C	287	LYS	7.5
1	C	140	PRO	7.4
2	D	94	ILE	7.1
1	A	72	ARG	7.0
1	C	132	ILE	7.0
1	C	293	ILE	6.9
1	A	26	LEU	6.9
2	B	88	TRP	6.9
1	A	132	ILE	6.8
1	C	138	GLU	6.7
1	A	52	PRO	6.7
1	A	129	ALA	6.6
1	A	134	SER	6.6
2	D	212	TRP	6.6
1	A	130	PHE	6.6
1	C	26	LEU	6.5
1	A	136	ASN	6.5
1	A	141	GLY	6.5
2	B	212	TRP	6.3
1	A	61	PHE	6.3
1	C	223	LYS	6.2
1	C	134	SER	6.2
1	C	135	ILE	6.2
1	C	61	PHE	6.2
1	C	24	TRP	6.0
1	C	144	TYR	6.0
1	C	34	LEU	6.0
1	C	252	TRP	5.9
1	A	66	LYS	5.8
1	A	549	ASP	5.7
1	C	25	PRO	5.7
1	A	19	PRO	5.6
1	C	129	ALA	5.6
1	A	144	TYR	5.5
1	A	59	PRO	5.5
3	T	725	DG	5.5
1	A	30	LYS	5.4
1	C	30	LYS	5.4
1	A	142	ILE	5.3
1	C	74	LEU	5.3
1	A	127	TYR	5.2
1	A	222	GLN	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	50	ILE	5.1
1	A	145	GLN	5.1
1	C	28	GLU	5.1
1	A	137	ASN	5.0
1	C	141	GLY	5.0
1	C	139	THR	4.9
3	E	702	DT	4.8
1	C	60	VAL	4.8
1	A	289	LEU	4.8
2	D	5	ILE	4.8
1	A	21	VAL	4.7
1	A	63	ILE	4.7
1	C	554	ALA	4.7
3	T	703	DG	4.7
2	D	95	PRO	4.6
1	A	29	GLU	4.6
1	A	550	LYS	4.5
2	B	295	LEU	4.5
1	A	75	VAL	4.5
2	B	428	GLN	4.4
2	B	89	GLU	4.4
1	C	71	TRP	4.3
1	A	286	THR	4.3
1	A	139	THR	4.3
1	C	254	VAL	4.3
1	A	70	LYS	4.3
2	D	216	THR	4.2
1	A	49	LYS	4.2
2	D	67	ASP	4.2
1	C	296	THR	4.2
1	A	285	GLY	4.1
2	B	5	ILE	4.1
1	A	146	TYR	4.1
4	P	803	DC	4.1
1	C	137	ASN	4.1
1	C	130	PHE	4.1
2	D	89	GLU	4.1
1	A	68	SER	4.1
1	C	69	THR	4.1
1	C	145	GLN	4.0
3	T	704	DG	4.0
1	A	62	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
2	D	232	TYR	4.0
1	C	78	ARG	3.9
1	A	223	LYS	3.9
2	D	90	VAL	3.9
1	C	27	THR	3.9
1	C	295	LEU	3.9
2	D	358	ARG	3.8
3	E	704	DG	3.8
1	A	23	GLN	3.8
3	E	725	DG	3.8
2	B	250	ASP	3.8
2	D	215	THR	3.8
1	C	21	VAL	3.8
1	A	56	TYR	3.7
2	D	357	MET	3.7
1	A	293	ILE	3.7
1	C	292	VAL	3.7
2	B	422	LEU	3.7
1	A	27	THR	3.6
1	A	28	GLU	3.6
1	A	71	TRP	3.6
1	C	448	ARG	3.6
2	B	232	TYR	3.5
1	C	143	ARG	3.5
1	A	77	PHE	3.5
2	D	88	TRP	3.5
2	D	360	ALA	3.5
2	D	177	ASP	3.5
1	A	32	LYS	3.5
1	A	553	SER	3.5
1	A	33	ALA	3.5
1	C	303	LEU	3.5
2	D	354	TYR	3.5
1	C	49	LYS	3.5
1	A	54	ASN	3.5
1	A	124	PHE	3.5
2	D	124	PHE	3.5
2	B	213	GLY	3.5
1	C	109	LEU	3.4
1	A	448	ARG	3.4
2	D	213	GLY	3.4
2	B	301	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	69	THR	3.4
2	D	92	LEU	3.3
1	A	287	LYS	3.3
1	C	257	ILE	3.3
2	B	4	PRO	3.3
1	C	58	THR	3.3
1	C	198	HIS	3.3
1	A	60	VAL	3.2
1	A	67	ASP	3.2
1	C	63	ILE	3.2
1	C	75	VAL	3.2
1	A	25	PRO	3.2
1	A	31	ILE	3.1
1	C	301	LEU	3.1
1	A	73	LYS	3.1
1	A	288	ALA	3.1
2	D	7	THR	3.1
1	A	37	ILE	3.1
2	B	92	LEU	3.1
2	B	209	LEU	3.1
2	D	168	LEU	3.1
1	C	22	LYS	3.1
4	F	804	DA	3.0
1	A	36	GLU	3.0
2	D	66	LYS	3.0
1	A	24	TRP	3.0
4	F	803	DC	3.0
2	D	178	ILE	2.9
3	E	703	DG	2.9
2	D	8	VAL	2.9
4	P	804	DA	2.9
2	B	204	GLU	2.9
2	D	361	HIS	2.9
1	A	551	LEU	2.9
1	C	66	LYS	2.9
1	C	222	GLN	2.9
1	C	131	THR	2.9
1	A	544	GLY	2.8
1	A	39	THR	2.8
1	C	247	PRO	2.8
2	B	281	LYS	2.8
2	D	428	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	70	LYS	2.8
1	A	546	GLU	2.8
1	C	283	LEU	2.8
2	B	282	LEU	2.8
1	C	128	THR	2.8
3	T	724	DT	2.8
1	C	224	GLU	2.8
1	A	78	ARG	2.7
1	C	246	LEU	2.7
1	C	37	ILE	2.7
2	B	284	ARG	2.7
1	A	200	THR	2.7
1	A	18	GLY	2.6
1	C	294	PRO	2.6
2	B	87	PHE	2.6
1	A	138	GLU	2.6
1	A	38	CYS	2.6
1	C	553	SER	2.6
2	D	209	LEU	2.6
2	B	277	ARG	2.6
1	C	50	ILE	2.6
1	C	312	GLU	2.5
1	A	261	VAL	2.5
1	A	234	LEU	2.5
2	D	187	LEU	2.5
2	B	211	ARG	2.5
1	C	311	LYS	2.5
3	E	724	DT	2.5
1	C	281	LYS	2.5
2	B	154	LYS	2.5
2	D	118	VAL	2.5
1	C	226	PRO	2.5
1	A	143	ARG	2.5
1	C	23	GLN	2.5
1	C	19	PRO	2.5
2	D	422	LEU	2.4
1	A	298	GLU	2.4
1	C	36	GLU	2.4
1	C	33	ALA	2.4
2	B	299	ALA	2.4
1	A	105	SER	2.4
1	A	254	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	552	VAL	2.4
2	B	90	VAL	2.4
1	A	194	GLU	2.4
1	C	54	ASN	2.4
1	C	17	ASP	2.4
1	C	73	LYS	2.4
1	A	149	LEU	2.4
1	C	308	GLU	2.4
2	D	119	PRO	2.4
1	C	280	SER	2.3
2	B	173	LYS	2.3
2	D	356	ARG	2.3
1	A	148	VAL	2.3
2	D	173	LYS	2.3
1	C	237	ASP	2.3
2	D	211	ARG	2.3
1	C	57	ASN	2.3
1	A	284	ARG	2.3
1	C	251	SER	2.3
1	C	300	GLU	2.3
1	A	83	ARG	2.3
1	C	124	PHE	2.2
1	C	291	GLU	2.2
1	C	228	LEU	2.2
1	A	102	LYS	2.2
1	C	299	ALA	2.2
1	C	297	GLU	2.2
1	A	193	LEU	2.2
1	A	543	GLY	2.2
1	A	154	LYS	2.2
1	A	292	VAL	2.2
1	C	260	LEU	2.2
2	D	202	ILE	2.2
1	C	310	LEU	2.1
2	B	159	ILE	2.1
1	C	298	GLU	2.1
1	A	283	LEU	2.1
2	B	168	LEU	2.1
1	A	65	LYS	2.1
1	C	236	PRO	2.1
2	D	197	GLN	2.1
1	C	76	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	425	LEU	2.1
1	A	57	ASN	2.1
2	D	189	VAL	2.1
1	C	278	GLN	2.1
2	D	184	MET	2.1
2	D	284	ARG	2.1
4	P	805	DG	2.1
2	B	86	ASP	2.0
1	C	146	TYR	2.0
2	D	105	SER	2.0
2	D	172	LYS	2.0
2	D	426	TRP	2.0
1	A	227	PHE	2.0
1	C	315	HIS	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	MRG	F	817	26/27	0.91	0.14	-	84,99,117,127	0
4	ATM	F	822	22/23	0.93	0.18	-	71,78,87,95	0
4	MRG	P	817	26/27	0.90	0.18	-	88,102,117,121	0
4	ATM	P	822	22/23	0.94	0.16	-	71,82,95,95	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.