



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:20 pm BST

PDB ID : 4OL8
Title : Ty3 reverse transcriptase bound to DNA/RNA
Authors : Nowak, E.; Miller, J.T.; Bona, M.K.; Studnicka, J.; Szczepanowski, R.H.;
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Deposited on : 2014-01-23
Resolution : 3.10 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

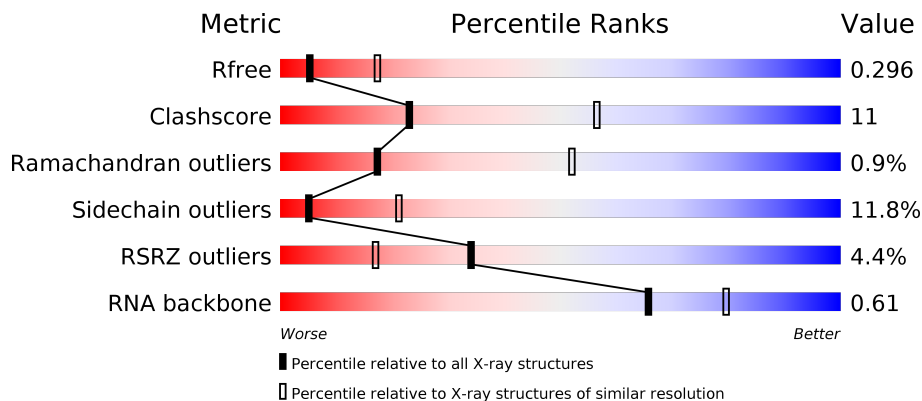
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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





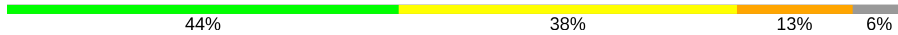

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	478	 2% 54% 24% 18%
1	B	478	 % 63% 27% 5% 5%
1	E	478	 8% 49% 27% 20%
1	F	478	 5% 69% 18% 11%

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Mol	Chain	Length	Quality of chain
2	C	18	
2	G	18	
3	D	16	
3	H	16	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 14105 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	390	3004	1938	504	552	5	5	0	0	0
1	B	452	3547	2291	604	639	8	5	0	0	0
1	F	427	3310	2129	561	608	7	5	0	0	0
1	E	381	2873	1839	484	540	5	5	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q99315
A	0	PRO	-	EXPRESSION TAG	UNP Q99315
A	426	ASN	ASP	ENGINEERED MUTATION	UNP Q99315
B	-1	GLY	-	EXPRESSION TAG	UNP Q99315
B	0	PRO	-	EXPRESSION TAG	UNP Q99315
B	426	ASN	ASP	ENGINEERED MUTATION	UNP Q99315
F	-1	GLY	-	EXPRESSION TAG	UNP Q99315
F	0	PRO	-	EXPRESSION TAG	UNP Q99315
F	426	ASN	ASP	ENGINEERED MUTATION	UNP Q99315
E	-1	GLY	-	EXPRESSION TAG	UNP Q99315
E	0	PRO	-	EXPRESSION TAG	UNP Q99315
E	426	ASN	ASP	ENGINEERED MUTATION	UNP Q99315

- Molecule 2 is a RNA chain called 5'-R>(*CP*UP*GP*AP*GP*AP*GP*AP*GP*AP*GP*G P*AP*AP*GP*AP*UP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	17	378	168	79	114	17	0	0	0

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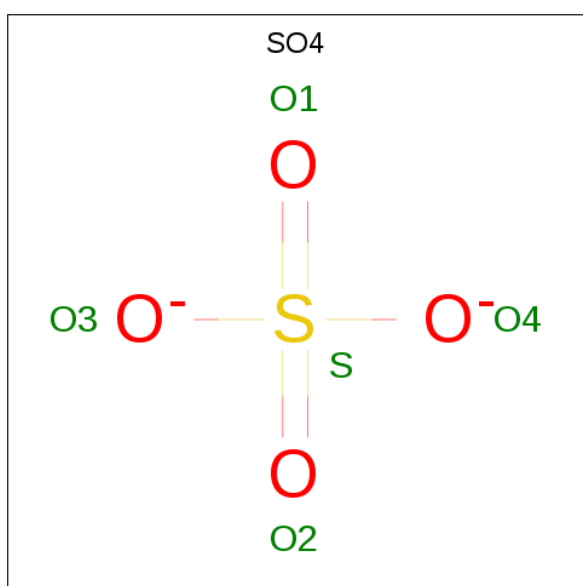
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	G	17	378	168	79	114	17	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	D	15	294	143	40	96	15	0	0	0
3	H	16	310	152	43	100	15	0	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	B	1	5	4	1	0	0
4	B	1	5	4	1	0	0

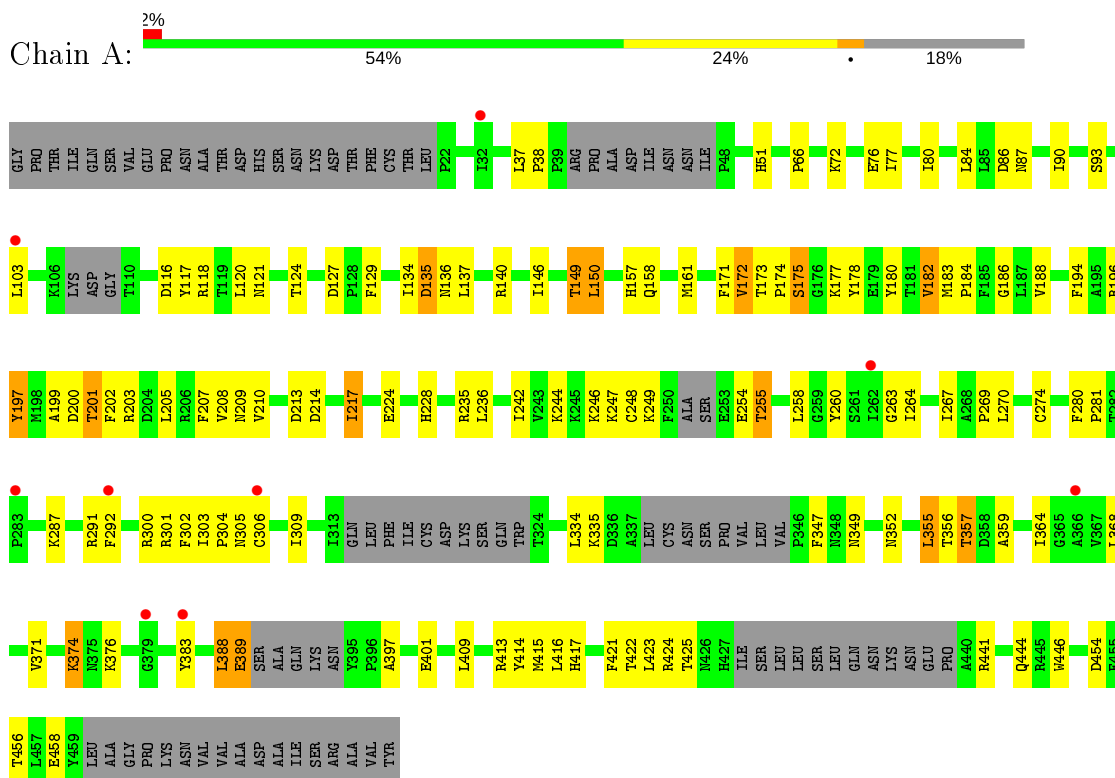
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total 1 O 1	0	0

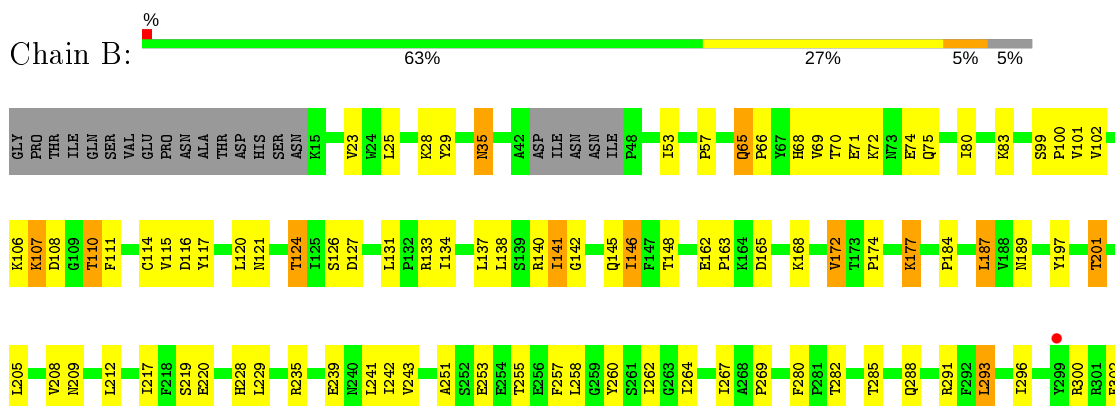
3 Residue-property plots [i](#)

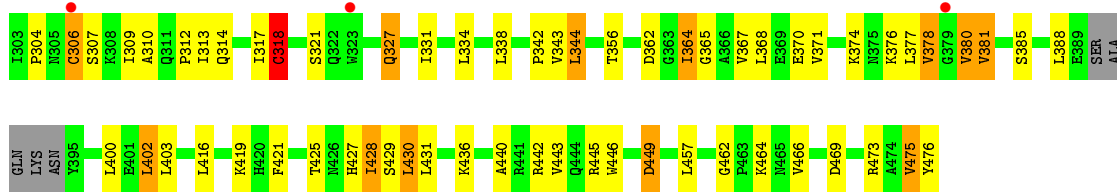
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: Reverse transcriptase/ribonuclease H

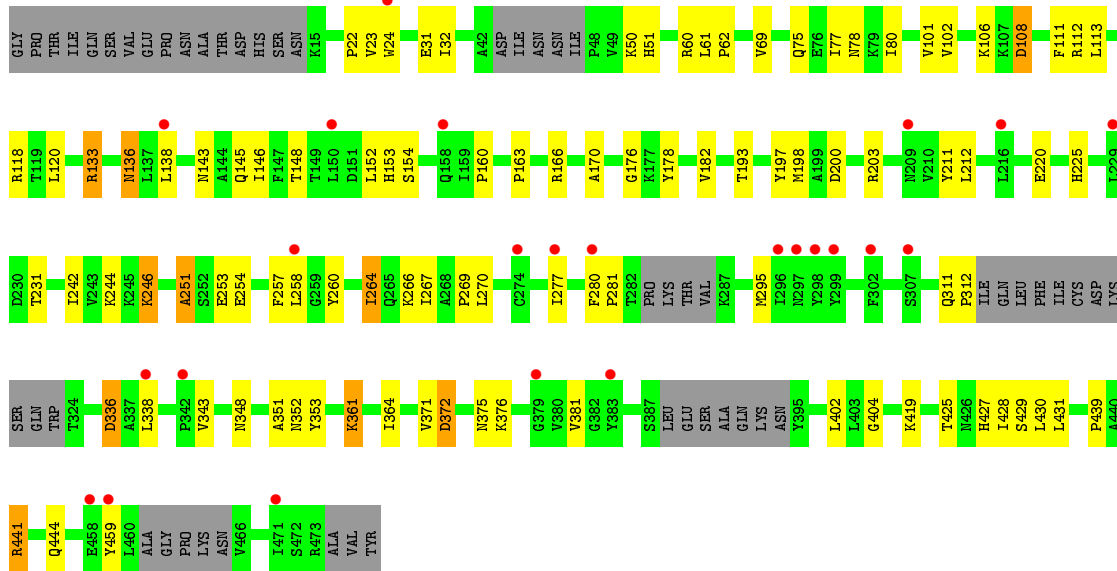


- Molecule 1: Reverse transcriptase/ribonuclease H

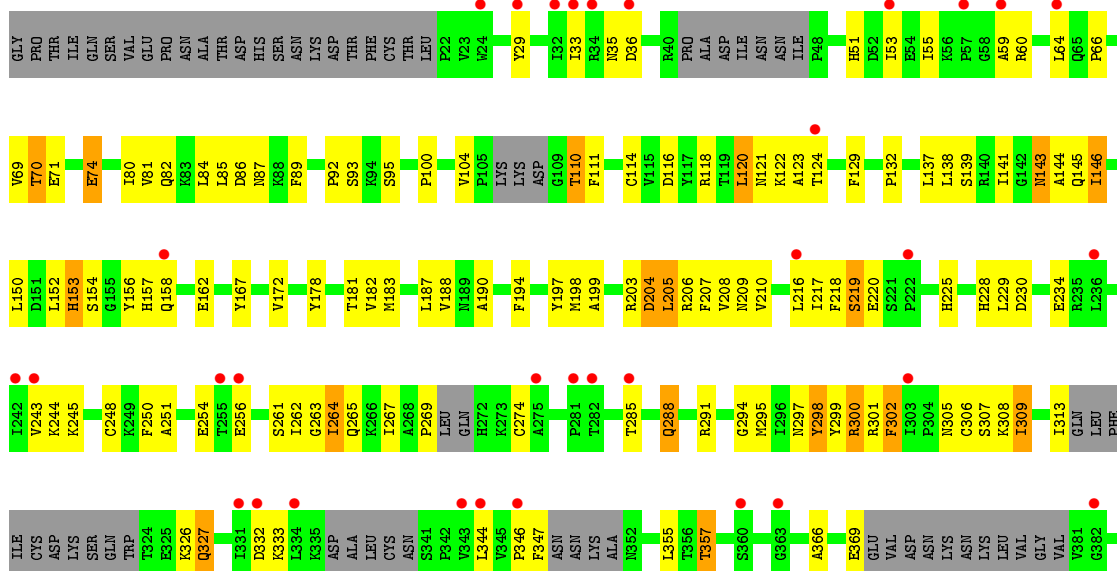


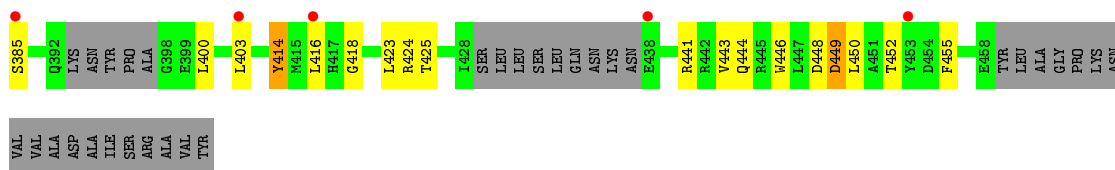


• Molecule 1: Reverse transcriptase/ribonuclease H



• Molecule 1: Reverse transcriptase/ribonuclease H





VAL
VAL
ALA
ASP
ALA
ILE
SER
ARG
ALA
VAL
TYR

- Molecule 2: 5'-R(*CP*UP*GP*AP*GP*AP*GP*AP*GP*AP*GP*GP*AP*AP*GP*AP*UP*G)-3'

Chain C: 72% 22% 6%

C
D2
G3
A4
G5
G11
G18

- Molecule 2: 5'-R(*CP*UP*GP*AP*GP*AP*GP*AP*GP*AP*GP*GP*AP*AP*GP*AP*UP*G)-3'

Chain G: 61% 28% 6% 6%

C
D2
G3
A4
G5
G6
G7
A8
A16
U17
G18

- Molecule 3: 5'-D(*CP*AP*TP*CP*TP*TP*CP*CP*TP*CP*TP*CP*TP*CP*TP*C)-3'

Chain D: 44% 38% 13% 6%

DC
A33
T34
C35
T36
T37
C38
C39
T44
C45
T46
C47

- Molecule 3: 5'-D(*CP*AP*TP*CP*TP*TP*CP*CP*TP*CP*TP*CP*TP*CP*TP*C)-3'

Chain H: 50% 44% 6%

C32
A33
T34
T37
C38
C41
T44
C45
T46
C47

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	320.70Å 75.06Å 108.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.90 – 3.10 48.90 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.90-3.10) 99.6 (48.90-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 3.01Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.227 , 0.296 0.227 , 0.296	Depositor DCC
R_{free} test set	2665 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	78.5	Xtrriage
Anisotropy	0.243	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 98.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	14105	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.32	0/3069	0.54	0/4169
1	B	0.42	0/3629	0.60	0/4928
1	E	0.29	0/2933	0.51	0/3990
1	F	0.30	0/3382	0.49	0/4597
2	C	0.37	0/426	0.75	0/665
2	G	0.35	0/426	0.80	0/665
3	D	0.62	0/324	1.47	4/495 (0.8%)
3	H	0.60	0/342	1.35	3/523 (0.6%)
All	All	0.36	0/14531	0.63	7/20032 (0.0%)

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	B	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	35	DC	O4'-C4'-C3'	-8.14	101.11	106.00
3	H	41	DC	O4'-C4'-C3'	-6.58	101.87	104.50
3	D	36	DT	O4'-C4'-C3'	-5.88	102.15	104.50
3	H	44	DT	N3-C4-O4	5.66	123.30	119.90
3	H	44	DT	C5-C4-O4	-5.57	121.00	124.90
3	D	46	DT	N3-C4-O4	5.25	123.05	119.90
3	D	38	DC	O4'-C4'-C3'	-5.24	102.40	104.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	475	VAL	Peptide

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	3004	0	2838	85	0
1	B	3547	0	3500	84	0
1	E	2873	0	2637	88	0
1	F	3310	0	3193	50	0
2	C	378	0	186	2	0
2	G	378	0	186	6	0
3	D	294	0	173	6	0
3	H	310	0	185	8	0
4	B	10	0	0	1	0
5	B	1	0	0	0	0
All	All	14105	0	12898	307	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (307) 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:E:154:SER:HB3	1:E:157:HIS:HB2	1.57	0.86
1:F:50:LYS:HG2	1:F:160:PRO:HG2	1.67	0.76
1:B:205:LEU:HD21	1:B:235:ARG:HH12	1.51	0.75
1:A:349:ASN:HD21	1:B:72:LYS:HE3	1.50	0.75
1:E:153:HIS:HB3	1:E:244:LYS:HB2	1.68	0.73
1:E:141:ILE:HB	1:E:346:PRO:HB3	1.69	0.73
1:F:364:ILE:HG12	1:F:404:GLY:HA3	1.69	0.73
1:E:285:THR:H	1:E:288:GLN:HE22	1.35	0.72
1:A:199:ALA:O	1:A:203:ARG:HB2	1.92	0.69
1:B:376:LYS:HD2	1:B:377:LEU:H	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:16:A:H2	3:H:34:DT:H3	1.40	0.67
1:F:80:ILE:HD11	1:F:111:PHE:HB2	1.76	0.67
1:E:137:LEU:O	1:E:209:ASN:ND2	2.28	0.67
1:F:108:ASP:OD1	1:F:108:ASP:N	2.27	0.67
1:E:138:LEU:HD12	1:E:301:ARG:HH22	1.59	0.66
1:B:291:ARG:NH2	4:B:501:SO4:O2	2.29	0.66
1:F:348:ASN:HB3	1:F:351:ALA:HB2	1.76	0.66
1:A:161:MSE:HE3	1:A:184:PRO:HD2	1.76	0.66
1:E:357:THR:O	1:E:357:THR:OG1	2.13	0.65
1:A:388:LEU:HB2	1:A:389:GLU:HB2	1.78	0.64
1:B:219:SER:OG	1:B:228:HIS:ND1	2.29	0.64
3:H:45:DC:H4'	1:E:298:TYR:CD2	2.32	0.64
1:E:262:ILE:HG23	1:E:267:ILE:HG12	1.80	0.64
1:E:204:ASP:N	1:E:204:ASP:OD1	2.30	0.64
2:G:2:U:H1'	1:E:114:CYS:SG	2.38	0.63
1:B:370:GLU:HB3	1:B:378:VAL:HG22	1.81	0.63
1:A:77:ILE:HG13	1:A:103:LEU:HD12	1.81	0.63
1:E:449:ASP:N	1:E:449:ASP:OD1	2.28	0.62
1:A:140:ARG:NH1	1:B:71:GLU:OE1	2.32	0.62
1:A:359:ALA:N	1:A:401:GLU:OE2	2.32	0.62
1:A:200:ASP:OD1	1:A:203:ARG:NH2	2.26	0.62
1:B:107:LYS:HE3	1:B:107:LYS:H	1.63	0.62
1:B:436:LYS:NZ	3:D:38:DC:OP2	2.31	0.62
1:E:285:THR:N	1:E:288:GLN:HE22	1.97	0.62
1:E:144:ALA:HA	1:E:220:GLU:HA	1.80	0.62
1:B:300:ARG:HH22	1:B:307:SER:HB3	1.65	0.61
1:A:356:THR:HG22	1:A:424:ARG:HB2	1.81	0.61
1:A:129:PHE:CE2	1:A:196:ARG:HG3	2.36	0.60
1:B:425:THR:HG21	1:B:430:LEU:HD13	1.82	0.60
1:E:145:GLN:HG3	1:E:264:ILE:HD11	1.83	0.60
3:H:37:DT:H2'	3:H:38:DC:H6	1.66	0.60
1:B:462:GLY:HA2	1:B:464:LYS:H	1.67	0.60
1:B:102:VAL:HG23	1:B:114:CYS:HB3	1.84	0.60
1:A:134:ILE:HG23	1:A:258:LEU:HD13	1.83	0.60
1:B:126:SER:HA	1:B:189:ASN:OD1	2.03	0.59
1:A:444:GLN:HB3	1:B:428:ILE:HD12	1.84	0.59
1:E:264:ILE:HG23	1:E:265:GLN:H	1.66	0.59
1:A:397:ALA:O	1:A:401:GLU:N	2.35	0.59
1:E:297:ASN:O	1:E:300:ARG:HG2	2.03	0.59
1:B:312:PRO:O	1:B:327:GLN:NE2	2.36	0.59
1:F:75:GLN:OE1	1:E:206:ARG:NE	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:LYS:O	1:A:291:ARG:N	2.28	0.58
1:B:293:LEU:HD21	1:B:310:ALA:HB1	1.83	0.58
1:B:449:ASP:N	1:B:449:ASP:OD1	2.35	0.58
1:E:254:GLU:HA	1:E:263:GLY:HA2	1.85	0.58
1:E:256:GLU:HA	1:E:261:SER:HA	1.83	0.58
1:B:165:ASP:OD1	1:B:168:LYS:NZ	2.25	0.58
1:E:143:ASN:OD1	1:E:143:ASN:N	2.36	0.58
1:A:260:TYR:OH	1:A:301:ARG:NH2	2.37	0.58
1:F:133:ARG:HD3	1:F:136:ASN:HB3	1.86	0.57
1:F:353:TYR:HE1	1:F:381:VAL:HG21	1.68	0.57
1:A:300:ARG:NH1	1:A:306:CYS:SG	2.78	0.57
3:H:37:DT:H2'	3:H:38:DC:C6	2.39	0.57
1:E:219:SER:HB3	1:E:228:HIS:ND1	2.19	0.57
1:E:262:ILE:HG12	1:E:267:ILE:HG23	1.86	0.57
1:A:249:LYS:HD2	1:A:255:THR:HG23	1.86	0.56
1:F:146:ILE:HG21	1:F:225:HIS:HB2	1.87	0.56
1:F:260:TYR:CE1	1:F:269:PRO:HB3	2.40	0.56
3:D:45:DC:H2'	3:D:46:DT:C6	2.40	0.56
1:B:134:ILE:HG12	1:B:258:LEU:HD23	1.86	0.56
1:A:292:PHE:CE1	1:A:334:LEU:HD11	2.41	0.56
1:F:427:HIS:CE1	1:F:429:SER:HB3	2.41	0.56
1:B:74:GLU:HG3	1:B:174:PRO:HG2	1.88	0.56
1:E:150:LEU:HD12	1:E:243:VAL:HG11	1.87	0.55
1:E:156:TYR:CD2	1:E:183:MSE:HE3	2.41	0.55
1:B:148:THR:OG1	1:B:251:ALA:N	2.25	0.55
1:B:362:ASP:O	1:B:388:LEU:N	2.39	0.55
1:F:146:ILE:HD11	1:F:251:ALA:HB1	1.87	0.55
1:F:200:ASP:OD1	1:F:203:ARG:NH2	2.40	0.55
1:A:309:ILE:HD11	1:A:334:LEU:HD23	1.88	0.55
1:A:173:THR:HG23	1:A:175:SER:H	1.72	0.54
1:A:347:PHE:CD1	1:A:415:MSE:HE3	2.43	0.54
1:E:355:LEU:HD13	1:E:416:LEU:HD21	1.89	0.54
1:B:296:ILE:HG21	1:B:334:LEU:HD22	1.89	0.54
1:B:106:LYS:HD3	1:B:110:THR:HB	1.90	0.54
1:B:100:PRO:HG2	1:B:116:ASP:HB3	1.91	0.54
1:A:116:ASP:OD2	1:A:118:ARG:NH1	2.41	0.53
1:A:186:GLY:HA2	2:C:3:G:O4'	2.08	0.53
1:B:416:LEU:HD22	1:B:421:PHE:CD1	2.43	0.53
1:A:157:HIS:HA	1:A:182:VAL:HG13	1.90	0.53
1:E:66:PRO:HG3	1:E:172:VAL:HB	1.90	0.53
1:F:148:THR:OG1	1:F:225:HIS:NE2	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:31:GLU:HG3	1:F:32:ILE:HG23	1.89	0.53
1:A:136:ASN:O	1:A:140:ARG:HG3	2.09	0.53
1:F:77:ILE:HG23	1:F:113:LEU:HD21	1.90	0.53
1:F:260:TYR:HA	1:F:269:PRO:HA	1.90	0.53
1:A:196:ARG:O	1:A:199:ALA:N	2.42	0.53
1:B:314:GLN:O	1:B:318:CYS:HB2	2.08	0.53
1:E:297:ASN:HA	1:E:300:ARG:HD3	1.91	0.52
1:A:202:PHE:HB2	1:A:210:VAL:HG11	1.91	0.52
1:A:84:LEU:HB3	1:A:90:ILE:HG12	1.90	0.52
1:E:89:PHE:O	1:E:181:THR:OG1	2.27	0.52
1:B:131:LEU:HD21	1:B:212:LEU:HG	1.92	0.52
1:A:134:ILE:HD12	1:A:134:ILE:H	1.75	0.52
1:A:172:VAL:HG13	1:A:177:LYS:HG3	1.92	0.52
1:A:161:MSE:HE3	1:A:183:MSE:HA	1.91	0.52
1:B:262:ILE:HD13	1:B:267:ILE:HG13	1.91	0.52
1:A:127:ASP:OD2	1:A:196:ARG:NH1	2.42	0.52
1:A:90:ILE:HG22	1:A:180:TYR:HA	1.91	0.51
1:E:152:LEU:HD21	1:E:158:GLN:HB2	1.93	0.51
1:A:207:PHE:CD1	1:A:208:VAL:HG23	2.45	0.51
1:E:199:ALA:O	1:E:203:ARG:HB2	2.11	0.51
1:A:359:ALA:HB1	1:A:364:ILE:HA	1.93	0.51
1:F:163:PRO:HA	1:F:166:ARG:HD3	1.91	0.51
1:A:413:ARG:NH1	1:B:68:HIS:HB2	2.26	0.51
1:E:285:THR:H	1:E:288:GLN:NE2	2.07	0.51
1:E:82:GLN:HG3	1:E:85:LEU:HD12	1.91	0.50
1:F:106:LYS:HE3	1:F:112:ARG:HD3	1.93	0.50
1:A:303:ILE:HB	1:A:306:CYS:HB2	1.93	0.50
1:B:208:VAL:HG22	1:B:217:ILE:HG12	1.93	0.50
2:G:16:A:N1	3:H:34:DT:O4	2.45	0.50
1:A:356:THR:HG22	1:A:424:ARG:HD3	1.94	0.50
1:A:158:GLN:OE1	1:A:242:ILE:N	2.45	0.49
1:E:414:TYR:HD1	1:E:414:TYR:H	1.60	0.49
1:F:50:LYS:HD3	1:F:163:PRO:HD3	1.94	0.49
1:B:65:GLN:HG3	1:B:66:PRO:HD2	1.93	0.49
1:F:429:SER:HB2	1:E:448:ASP:OD2	2.12	0.49
1:A:254:GLU:HG3	1:A:263:GLY:HA2	1.92	0.49
1:B:110:THR:HG22	1:B:111:PHE:H	1.78	0.49
1:E:216:LEU:HG	1:E:217:ILE:N	2.27	0.49
1:E:423:LEU:HD13	1:E:424:ARG:N	2.28	0.48
1:A:149:THR:HG22	1:A:248:CYS:HB2	1.94	0.48
1:F:145:GLN:HA	1:F:264:ILE:HB	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:2:U:H5'	1:E:118:ARG:HH21	1.79	0.48
1:E:100:PRO:HG2	1:E:116:ASP:HB3	1.96	0.48
1:E:110:THR:OG1	1:E:111:PHE:N	2.45	0.48
1:F:277:ILE:HD13	1:F:295:MSE:HE1	1.95	0.48
1:B:184:PRO:HG2	1:B:187:LEU:HD22	1.94	0.48
1:B:53:ILE:HB	1:B:168:LYS:HD3	1.96	0.48
1:E:141:ILE:HA	1:E:218:PHE:CZ	2.49	0.48
3:H:32:DC:H2'	3:H:33:DA:C8	2.48	0.48
1:A:118:ARG:NH2	2:C:2:U:H5''	2.29	0.47
1:A:368:LEU:HD21	1:A:416:LEU:HD21	1.96	0.47
1:F:102:VAL:HG11	1:F:444:GLN:HB3	1.96	0.47
1:A:135:ASP:OD1	1:A:414:TYR:OH	2.30	0.47
1:B:338:LEU:HA	1:B:343:VAL:HG11	1.96	0.47
1:E:95:SER:HB2	1:E:167:TYR:HB2	1.96	0.47
1:F:352:ASN:HB2	1:F:371:VAL:O	2.14	0.47
1:A:117:TYR:O	1:A:121:ASN:ND2	2.47	0.47
1:A:292:PHE:HE1	1:A:334:LEU:HD11	1.78	0.47
1:B:28:LYS:HD3	1:B:29:TYR:CZ	2.50	0.47
1:E:309:ILE:HD11	1:E:333:LYS:HB2	1.97	0.47
1:A:304:PRO:HB3	1:A:383:TYR:CD2	2.49	0.47
1:B:235:ARG:O	1:B:239:GLU:HG2	2.14	0.47
1:F:372:ASP:OD1	1:F:372:ASP:N	2.45	0.47
1:A:357:THR:OG1	1:A:357:THR:O	2.31	0.47
1:B:306:CYS:HA	1:B:309:ILE:HG22	1.97	0.47
1:F:428:ILE:HG12	1:E:444:GLN:HB3	1.97	0.47
1:A:183:MSE:HE1	1:A:194:PHE:HB2	1.95	0.47
1:B:205:LEU:HD21	1:B:235:ARG:NH1	2.26	0.47
1:B:344:LEU:HD23	1:B:380:VAL:O	2.15	0.47
1:E:306:CYS:O	1:E:309:ILE:HG22	2.15	0.47
1:A:304:PRO:HB3	1:A:383:TYR:CE2	2.50	0.46
1:F:311:GLN:H	1:F:312:PRO:HD2	1.80	0.46
1:A:352:ASN:OD1	1:A:352:ASN:N	2.47	0.46
1:B:131:LEU:CD2	1:B:212:LEU:HG	2.46	0.46
1:E:146:ILE:HD11	1:E:229:LEU:HD21	1.96	0.46
1:F:428:ILE:HA	1:F:431:LEU:HB2	1.96	0.46
1:B:260:TYR:HA	1:B:269:PRO:HA	1.98	0.46
1:B:138:LEU:HD22	1:B:262:ILE:HD11	1.97	0.46
1:E:35:ASN:OD1	1:E:245:LYS:N	2.48	0.46
3:D:44:DT:H2'	3:D:45:DC:C6	2.51	0.46
1:A:417:HIS:O	1:B:70:THR:HG21	2.16	0.46
1:A:355:LEU:HB3	1:A:423:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:336:ASP:N	1:F:336:ASP:OD1	2.50	0.46
1:A:305:ASN:O	1:A:309:ILE:HG23	2.16	0.45
2:G:4:A:H2'	2:G:5:G:O4'	2.16	0.45
1:B:172:VAL:HG23	1:B:177:LYS:HG2	1.97	0.45
3:D:38:DC:H2'	3:D:39:DC:H6	1.81	0.45
1:E:64:LEU:HD12	1:E:100:PRO:HD3	1.97	0.45
1:E:55:ILE:HG12	1:E:124:THR:HG22	1.98	0.45
1:B:402:LEU:HD13	1:B:446:TRP:CD1	2.51	0.45
1:A:423:LEU:O	1:A:458:GLU:N	2.50	0.45
1:B:141:ILE:HG13	1:B:142:GLY:N	2.31	0.45
1:B:172:VAL:HG23	1:B:177:LYS:CG	2.47	0.45
1:F:280:PHE:HA	1:F:281:PRO:HD3	1.78	0.45
1:B:370:GLU:HG2	1:B:371:VAL:H	1.81	0.45
1:B:285:THR:HB	1:B:288:GLN:HG3	1.97	0.45
1:E:141:ILE:HA	1:E:218:PHE:CE1	2.52	0.45
1:F:338:LEU:HD23	1:F:343:VAL:HG11	1.97	0.45
1:A:197:TYR:O	1:A:201:THR:OG1	2.32	0.45
1:B:106:LYS:C	1:B:108:ASP:H	2.19	0.45
1:A:120:LEU:O	1:A:124:THR:HG23	2.16	0.45
1:F:78:ASN:ND2	1:E:203:ARG:HD3	2.31	0.44
1:A:173:THR:OG1	1:A:174:PRO:HD2	2.15	0.44
1:E:416:LEU:O	1:E:418:GLY:HA2	2.17	0.44
1:A:374:LYS:HB2	1:A:374:LYS:HE3	1.74	0.44
1:E:291:ARG:O	1:E:295:MSE:HG3	2.17	0.44
1:A:51:HIS:HB3	1:A:161:MSE:HE2	2.00	0.44
1:A:80:ILE:HG22	1:A:84:LEU:HD23	1.99	0.44
1:B:368:LEU:O	1:B:381:VAL:HG23	2.18	0.44
1:B:476:TYR:N	1:B:476:TYR:CD1	2.85	0.44
1:E:80:ILE:HD12	1:E:80:ILE:HA	1.86	0.44
1:E:141:ILE:HD13	1:E:218:PHE:CD2	2.52	0.44
1:F:22:PRO:HB2	1:F:24:TRP:CD1	2.53	0.44
1:F:270:LEU:H	1:F:270:LEU:HD12	1.83	0.44
1:E:313:ILE:HD13	1:E:327:GLN:HB2	1.99	0.44
1:B:197:TYR:CE2	1:B:241:LEU:HD11	2.53	0.44
1:E:187:LEU:HB2	1:E:190:ALA:HB2	2.00	0.44
1:E:132:PRO:HG2	1:E:210:VAL:O	2.18	0.44
1:E:205:LEU:HD12	1:E:207:PHE:CZ	2.52	0.44
1:B:121:ASN:HA	1:B:124:THR:HG23	1.98	0.43
1:F:244:LYS:HE2	1:F:244:LYS:HB3	1.76	0.43
1:A:173:THR:HG23	1:A:175:SER:N	2.33	0.43
1:A:376:LYS:HD3	1:A:376:LYS:HA	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:LYS:HE2	1:B:445:ARG:NH2	2.33	0.43
1:A:246:LYS:HZ3	1:A:246:LYS:HB3	1.82	0.43
1:E:207:PHE:CD1	1:E:208:VAL:HG23	2.53	0.43
1:F:253:GLU:HG3	1:F:254:GLU:HG2	2.01	0.43
1:A:66:PRO:HG3	1:A:172:VAL:HB	2.00	0.43
1:B:35:ASN:OD1	1:B:35:ASN:N	2.49	0.43
1:B:257:PHE:CE2	1:B:258:LEU:HD22	2.53	0.43
1:E:55:ILE:HG23	1:E:123:ALA:O	2.18	0.43
1:A:171:PHE:CE1	1:A:178:TYR:HB2	2.54	0.43
1:B:162:GLU:HA	1:B:163:PRO:HD2	1.80	0.43
1:B:197:TYR:O	1:B:201:THR:HG23	2.19	0.43
1:A:334:LEU:HD12	1:A:335:LYS:N	2.33	0.43
1:B:115:VAL:HG11	1:B:117:TYR:CZ	2.53	0.43
3:D:38:DC:H2'	3:D:39:DC:C6	2.54	0.43
1:A:213:ASP:N	1:A:213:ASP:OD1	2.44	0.43
1:A:224:GLU:HG2	1:A:228:HIS:CE1	2.54	0.43
1:B:146:ILE:HD12	1:B:146:ILE:H	1.84	0.43
1:B:140:ARG:NH1	1:B:209:ASN:OD1	2.52	0.43
1:F:138:LEU:HD13	1:F:267:ILE:HD13	2.01	0.43
1:F:257:PHE:CE2	1:F:258:LEU:HD22	2.54	0.43
3:H:45:DC:H4'	1:E:298:TYR:CG	2.54	0.43
1:A:280:PHE:HA	1:A:281:PRO:HD3	1.92	0.42
1:E:121:ASN:C	1:E:123:ALA:H	2.22	0.42
1:B:293:LEU:HD23	1:B:313:ILE:HG21	2.01	0.42
1:E:139:SER:HA	1:E:347:PHE:HB2	2.00	0.42
1:E:81:VAL:O	1:E:85:LEU:HG	2.19	0.42
1:B:440:ALA:O	1:B:443:VAL:HG12	2.20	0.42
1:B:473:ARG:HB3	1:B:473:ARG:NH1	2.35	0.42
1:E:357:THR:HA	1:E:366:ALA:HA	2.01	0.42
1:E:194:PHE:O	1:E:198:MSE:HG2	2.20	0.42
1:F:428:ILE:CD1	1:E:448:ASP:HB2	2.50	0.42
1:E:59:ALA:HB1	1:E:123:ALA:HB1	2.01	0.42
1:F:118:ARG:NH2	1:F:439:PRO:HD3	2.34	0.42
1:A:205:LEU:HD12	1:A:207:PHE:CZ	2.55	0.42
1:A:37:LEU:HA	1:A:38:PRO:HD2	1.87	0.42
1:E:208:VAL:HG22	1:E:217:ILE:HB	2.02	0.42
1:E:269:PRO:HD3	1:E:302:PHE:CE2	2.55	0.42
1:B:469:ASP:OD2	1:B:473:ARG:HG3	2.19	0.42
1:E:299:TYR:HB3	1:E:302:PHE:CD1	2.55	0.42
1:E:70:THR:O	1:E:74:GLU:HB3	2.19	0.42
1:A:309:ILE:HD11	1:A:334:LEU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:351:ALA:HB3	1:F:353:TYR:CE2	2.55	0.42
1:A:413:ARG:HH12	1:B:68:HIS:HB2	1.85	0.42
1:B:72:LYS:O	1:B:75:GLN:HB2	2.20	0.42
1:E:443:VAL:HA	1:E:446:TRP:CD1	2.54	0.42
1:A:409:LEU:HD21	1:A:421:PHE:HZ	1.84	0.41
1:F:441:ARG:HA	1:F:444:GLN:NE2	2.35	0.41
1:A:149:THR:O	1:A:150:LEU:HD13	2.20	0.41
1:B:138:LEU:HD13	1:B:267:ILE:HG21	2.02	0.41
1:B:313:ILE:HD11	1:B:331:ILE:HG12	2.02	0.41
1:E:400:LEU:O	1:E:403:LEU:HB2	2.20	0.41
1:F:170:ALA:HA	1:F:178:TYR:O	2.20	0.41
3:D:46:DT:H2'	3:D:47:DC:C6	2.55	0.41
1:E:146:ILE:HG12	1:E:225:HIS:CB	2.50	0.41
1:E:217:ILE:HD11	1:E:228:HIS:HB3	2.02	0.41
1:A:137:LEU:HD13	1:A:209:ASN:HB3	2.02	0.41
2:G:7:G:H2'	2:G:8:A:H8	1.86	0.41
3:H:44:DT:H4'	1:E:294:GLY:C	2.41	0.41
1:B:314:GLN:HA	1:B:317:ILE:HD12	2.01	0.41
1:F:361:LYS:HB3	1:F:361:LYS:NZ	2.36	0.41
1:B:302:PHE:O	1:B:342:PRO:HD2	2.21	0.41
1:F:61:LEU:HB3	1:F:62:PRO:HD2	2.02	0.41
1:F:176:GLY:HA2	1:E:129:PHE:CZ	2.56	0.41
1:F:51:HIS:HB2	1:F:193:THR:HG21	2.03	0.41
1:A:269:PRO:HD3	1:A:302:PHE:CZ	2.56	0.41
1:B:431:LEU:HA	1:B:457:LEU:HD13	2.02	0.41
1:F:160:PRO:HA	1:F:182:VAL:HA	2.03	0.41
1:A:149:THR:OG1	1:A:255:THR:HG21	2.21	0.41
1:B:107:LYS:H	1:B:107:LYS:CD	2.33	0.41
1:B:187:LEU:HA	1:B:187:LEU:HD12	1.79	0.41
1:B:374:LYS:O	1:B:376:LYS:N	2.53	0.41
1:B:80:ILE:HA	1:B:83:LYS:HE2	2.03	0.41
1:E:307:SER:N	1:E:385:SER:OG	2.53	0.41
1:B:107:LYS:H	1:B:107:LYS:CE	2.30	0.40
1:B:364:ILE:HG13	1:B:365:GLY:N	2.35	0.40
1:B:427:HIS:CE1	1:B:429:SER:HB2	2.56	0.40
1:E:51:HIS:HE2	1:E:53:ILE:HD11	1.85	0.40
1:A:205:LEU:HD21	1:A:235:ARG:NH2	2.36	0.40
1:A:244:LYS:HD2	1:A:247:LYS:CG	2.52	0.40
1:E:156:TYR:HD2	1:E:183:MSE:HE3	1.85	0.40
1:E:207:PHE:HB2	1:E:218:PHE:O	2.21	0.40
1:E:33:ILE:HG21	1:E:250:PHE:HZ	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:92:PRO:HA	1:E:178:TYR:CD1	2.56	0.40
1:A:76:GLU:HB3	1:A:103:LEU:HD11	2.03	0.40
1:A:208:VAL:HG22	1:A:217:ILE:HB	2.02	0.40
1:A:236:LEU:HA	1:A:236:LEU:HD23	1.96	0.40
1:E:120:LEU:HD23	1:E:120:LEU:HA	1.91	0.40
1:E:230:ASP:O	1:E:234:GLU:HG3	2.21	0.40
1:B:25:LEU:HA	1:B:25:LEU:HD23	1.87	0.40
1:E:29:TYR:HB3	1:E:33:ILE:HG12	2.04	0.40
1:A:371:VAL:HG22	1:A:376:LYS:O	2.21	0.40
1:F:246:LYS:HG3	1:F:246:LYS:H	1.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	374/478 (78%)	338 (90%)	36 (10%)	0	100	100
1	B	446/478 (93%)	398 (89%)	45 (10%)	3 (1%)	22	57
1	E	361/478 (76%)	307 (85%)	45 (12%)	9 (2%)	5	27
1	F	415/478 (87%)	376 (91%)	37 (9%)	2 (0%)	29	64
All	All	1596/1912 (84%)	1419 (89%)	163 (10%)	14 (1%)	17	52

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	205	LEU
1	E	264	ILE
1	E	251	ALA
1	B	318	CYS
1	F	372	ASP

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Mol	Chain	Res	Type
1	E	122	LYS
1	E	305	ASN
1	E	455	PHE
1	B	304	PRO
1	E	302	PHE
1	F	251	ALA
1	E	36	ASP
1	E	70	THR
1	B	57	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	304/426 (71%)	272 (90%)	32 (10%)	7	26
1	B	377/426 (88%)	325 (86%)	52 (14%)	3	16
1	E	286/426 (67%)	247 (86%)	39 (14%)	3	16
1	F	347/426 (82%)	315 (91%)	32 (9%)	9	33
All	All	1314/1704 (77%)	1159 (88%)	155 (12%)	5	21

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	LYS
1	A	86	ASP
1	A	87	ASN
1	A	93	SER
1	A	135	ASP
1	A	146	ILE
1	A	149	THR
1	A	150	LEU
1	A	172	VAL
1	A	175	SER
1	A	182	VAL
1	A	188	VAL

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Mol	Chain	Res	Type
1	A	197	TYR
1	A	201	THR
1	A	214	ASP
1	A	217	ILE
1	A	255	THR
1	A	264	ILE
1	A	267	ILE
1	A	270	LEU
1	A	274	CYS
1	A	355	LEU
1	A	357	THR
1	A	374	LYS
1	A	388	LEU
1	A	389	GLU
1	A	422	THR
1	A	425	THR
1	A	441	ARG
1	A	446	TRP
1	A	454	ASP
1	A	456	THR
1	B	23	VAL
1	B	35	ASN
1	B	65	GLN
1	B	69	VAL
1	B	99	SER
1	B	101	VAL
1	B	107	LYS
1	B	110	THR
1	B	120	LEU
1	B	124	THR
1	B	127	ASP
1	B	133	ARG
1	B	137	LEU
1	B	141	ILE
1	B	145	GLN
1	B	146	ILE
1	B	172	VAL
1	B	177	LYS
1	B	187	LEU
1	B	201	THR
1	B	220	GLU
1	B	229	LEU

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Mol	Chain	Res	Type
1	B	242	ILE
1	B	243	VAL
1	B	253	GLU
1	B	255	THR
1	B	264	ILE
1	B	280	PHE
1	B	282	THR
1	B	293	LEU
1	B	306	CYS
1	B	318	CYS
1	B	321	SER
1	B	327	GLN
1	B	344	LEU
1	B	356	THR
1	B	364	ILE
1	B	367	VAL
1	B	378	VAL
1	B	380	VAL
1	B	381	VAL
1	B	385	SER
1	B	400	LEU
1	B	402	LEU
1	B	403	LEU
1	B	419	LYS
1	B	428	ILE
1	B	430	LEU
1	B	442	ARG
1	B	449	ASP
1	B	466	VAL
1	B	475	VAL
1	F	23	VAL
1	F	60	ARG
1	F	69	VAL
1	F	101	VAL
1	F	108	ASP
1	F	120	LEU
1	F	133	ARG
1	F	136	ASN
1	F	143	ASN
1	F	152	LEU
1	F	153	HIS
1	F	154	SER

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Mol	Chain	Res	Type
1	F	197	TYR
1	F	198	MSE
1	F	211	TYR
1	F	212	LEU
1	F	220	GLU
1	F	231	THR
1	F	242	ILE
1	F	246	LYS
1	F	264	ILE
1	F	266	LYS
1	F	336	ASP
1	F	361	LYS
1	F	375	ASN
1	F	376	LYS
1	F	402	LEU
1	F	419	LYS
1	F	425	THR
1	F	430	LEU
1	F	441	ARG
1	F	459	TYR
1	E	60	ARG
1	E	69	VAL
1	E	71	GLU
1	E	74	GLU
1	E	84	LEU
1	E	86	ASP
1	E	87	ASN
1	E	93	SER
1	E	104	VAL
1	E	110	THR
1	E	120	LEU
1	E	143	ASN
1	E	146	ILE
1	E	153	HIS
1	E	162	GLU
1	E	182	VAL
1	E	188	VAL
1	E	197	TYR
1	E	204	ASP
1	E	219	SER
1	E	248	CYS
1	E	274	CYS

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Mol	Chain	Res	Type
1	E	288	GLN
1	E	298	TYR
1	E	300	ARG
1	E	308	LYS
1	E	309	ILE
1	E	326	LYS
1	E	327	GLN
1	E	332	ASP
1	E	344	LEU
1	E	357	THR
1	E	369	GLU
1	E	414	TYR
1	E	425	THR
1	E	441	ARG
1	E	449	ASP
1	E	450	LEU
1	E	452	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	349	ASN
1	E	288	GLN
1	E	327	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	16/18 (88%)	2 (12%)	0
2	G	16/18 (88%)	1 (6%)	0
All	All	32/36 (88%)	3 (9%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	5	G
2	C	11	G
2	G	5	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	SO4	B	501	-	4,4,4	0.12	0	6,6,6	0.14	0
4	SO4	B	502	-	4,4,4	0.14	0	6,6,6	0.07	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	385/478 (80%)	0.10	9 (2%) 60 39	81, 132, 173, 195	1 (0%)
1	B	447/478 (93%)	-0.22	4 (0%) 84 69	55, 87, 137, 174	2 (0%)
1	E	376/478 (78%)	0.50	38 (10%) 7 2	94, 158, 204, 236	0
1	F	422/478 (88%)	0.22	24 (5%) 23 11	75, 142, 197, 239	0
2	C	17/18 (94%)	-0.27	0 100 100	101, 147, 167, 189	0
2	G	17/18 (94%)	-0.18	0 100 100	120, 146, 202, 216	0
3	D	15/16 (93%)	-0.12	0 100 100	125, 147, 196, 224	0
3	H	16/16 (100%)	-0.36	0 100 100	126, 144, 216, 234	0
All	All	1695/1980 (85%)	0.12	75 (4%) 34 17	55, 132, 193, 239	3 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	438	GLU	6.8
1	E	242	ILE	5.8
1	F	299	TYR	5.4
1	E	29	TYR	4.7
1	F	274	CYS	4.4
1	E	346	PRO	4.3
1	E	32	ILE	4.2
1	E	281	PRO	3.9
1	F	138	LEU	3.8
1	E	36	ASP	3.7
1	F	379	GLY	3.6
1	F	209	ASN	3.5
1	F	280	PHE	3.5
1	E	64	LEU	3.5
1	F	229	LEU	3.5
1	E	332	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	F	302	PHE	3.4
1	E	158	GLN	3.4
1	F	277	ILE	3.4
1	E	33	ILE	3.3
1	B	306	CYS	3.3
1	F	150	LEU	3.3
1	A	383	TYR	3.3
1	E	24	TRP	3.3
1	F	158	GLN	3.3
1	E	416	LEU	3.1
1	A	366	ALA	3.1
1	E	57	PRO	3.1
1	F	298	TYR	3.1
1	E	222	PRO	3.0
1	F	458	GLU	2.9
1	E	360	SER	2.9
1	E	331	ILE	2.9
1	E	282	THR	2.8
1	B	299	TYR	2.8
1	E	285	THR	2.8
1	F	24	TRP	2.7
1	E	216	LEU	2.7
1	E	385	SER	2.6
1	F	296	ILE	2.6
1	F	383	TYR	2.6
1	E	34	ARG	2.6
1	A	32	ILE	2.6
1	F	258	LEU	2.6
1	E	363	GLY	2.6
1	E	334	LEU	2.6
1	F	297	ASN	2.5
1	E	255	THR	2.5
1	A	306	CYS	2.5
1	E	343	VAL	2.5
1	E	344	LEU	2.4
1	E	275	ALA	2.4
1	E	53	ILE	2.3
1	A	283	PRO	2.3
1	B	379	GLY	2.3
1	A	262	ILE	2.3
1	F	471	ILE	2.3
1	E	59	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	323	TRP	2.2
1	E	243	VAL	2.2
1	F	338	LEU	2.2
1	E	236	LEU	2.2
1	A	379	GLY	2.2
1	E	453	TYR	2.2
1	A	292	PHE	2.2
1	A	103	LEU	2.1
1	E	403	LEU	2.1
1	F	459	TYR	2.1
1	E	303	ILE	2.1
1	F	216	LEU	2.1
1	F	307	SER	2.1
1	F	342	PRO	2.1
1	E	382	GLY	2.0
1	E	124	THR	2.0
1	E	256	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	B-factors(Å ²)	Q<0.9
4	SO4	B	502	5/5	0.86	0.23	174,175,175,175	0
4	SO4	B	501	5/5	0.92	0.25	154,156,157,158	0

6.5 Other polymers [i](#)

There are no such residues in this entry.