



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:38 PM UTC

PDB ID : 3WFQ / pdb_00003wfq
Title : tRNA processing enzyme complex 1
Authors : Yamashita, S.; Takeshita, D.; Tomita, K.
Deposited on : 2013-07-23
Resolution : 3.62 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

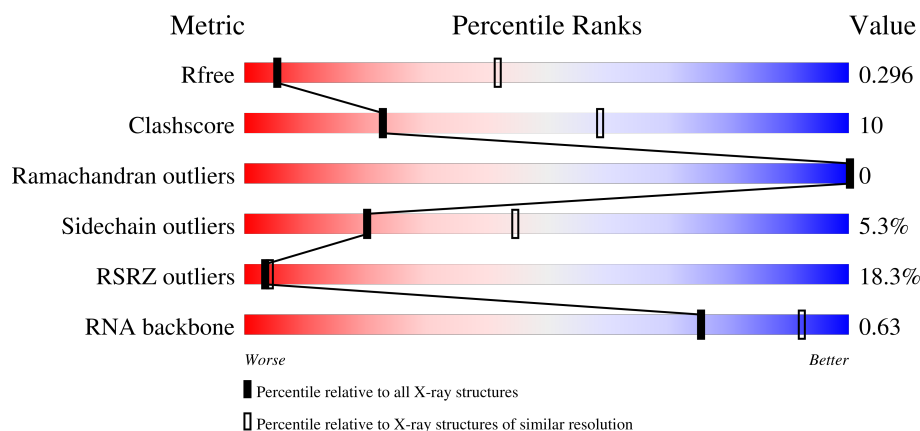
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.62 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}	180053	1062 (3.72-3.52)
Clashscore	190562	1092 (3.72-3.52)
Ramachandran outliers	187476	1057 (3.72-3.52)
Sidechain outliers	187428	1055 (3.72-3.52)
RSRZ outliers	180081	1060 (3.72-3.52)
RNA backbone	3983	1018 (4.18-3.06)

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 of 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	73	74% 63% 34% .
1	B	73	68% 64% 29% 7%
1	C	73	95% 68% 29% .
1	D	73	89% 66% 32% .

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Mol	Chain	Length	Quality of chain
2	E	512	4% 61% 23% • 14%
2	F	512	4% 59% 25% • 15%
2	G	512	7% 61% 24% • 14%
2	H	512	8% 60% 24% • 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20138 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 RNA chain called RNA (73-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	73	Total	C	N	O	P	0	0	0
			1545	687	276	509	73			
1	B	73	Total	C	N	O	P	0	0	0
			1545	687	276	509	73			
1	C	73	Total	C	N	O	P	0	0	0
			1545	687	276	509	73			
1	D	73	Total	C	N	O	P	0	0	0
			1545	687	276	509	73			

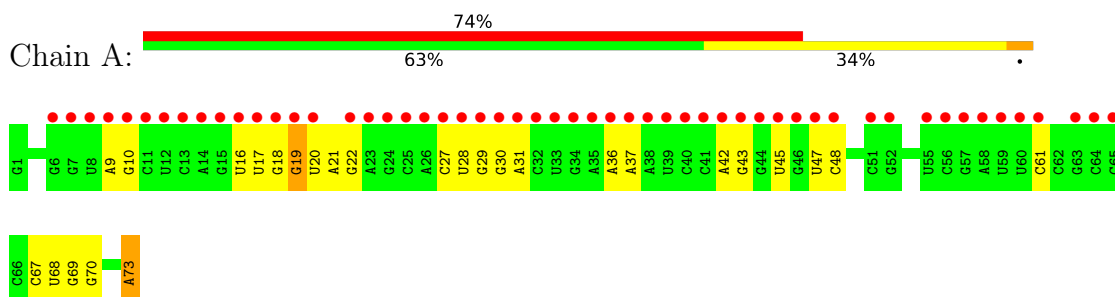
- Molecule 2 is a protein called Poly A polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	439	Total	C	N	O	S	0	0	0
			3489	2248	598	636	7			
2	F	436	Total	C	N	O	S	0	0	0
			3475	2240	595	633	7			
2	G	439	Total	C	N	O	S	0	0	0
			3491	2249	598	637	7			
2	H	441	Total	C	N	O	S	0	0	0
			3503	2256	601	639	7			

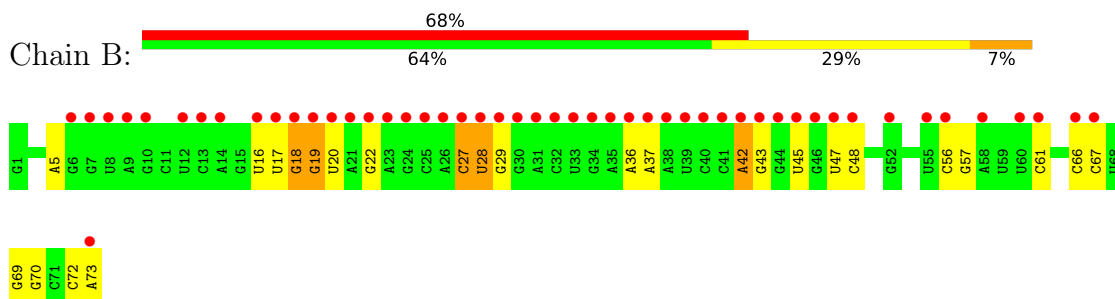
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

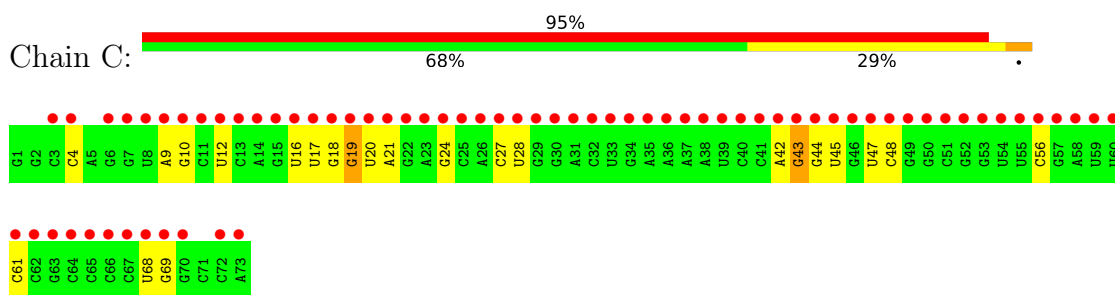
- Molecule 1: RNA (73-MER)



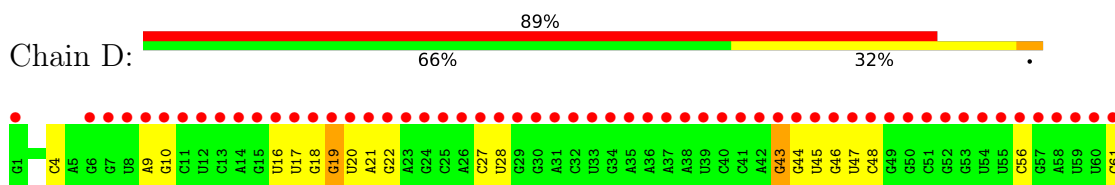
- Molecule 1: RNA (73-MER)

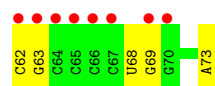


- Molecule 1: RNA (73-MER)

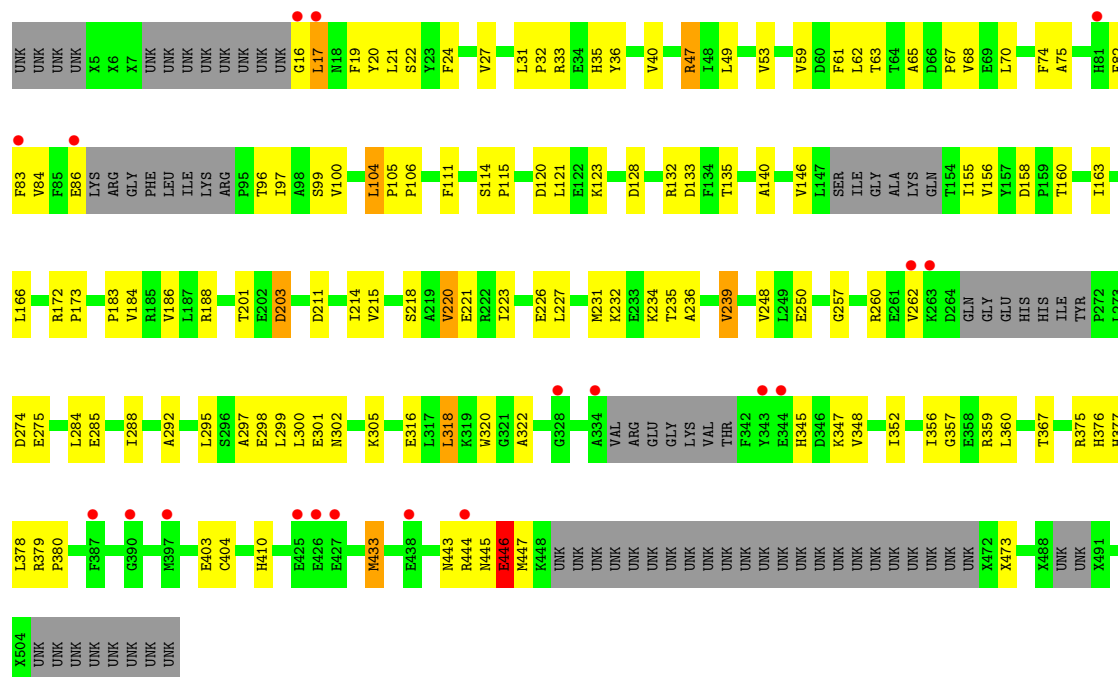


- Molecule 1: RNA (73-MER)

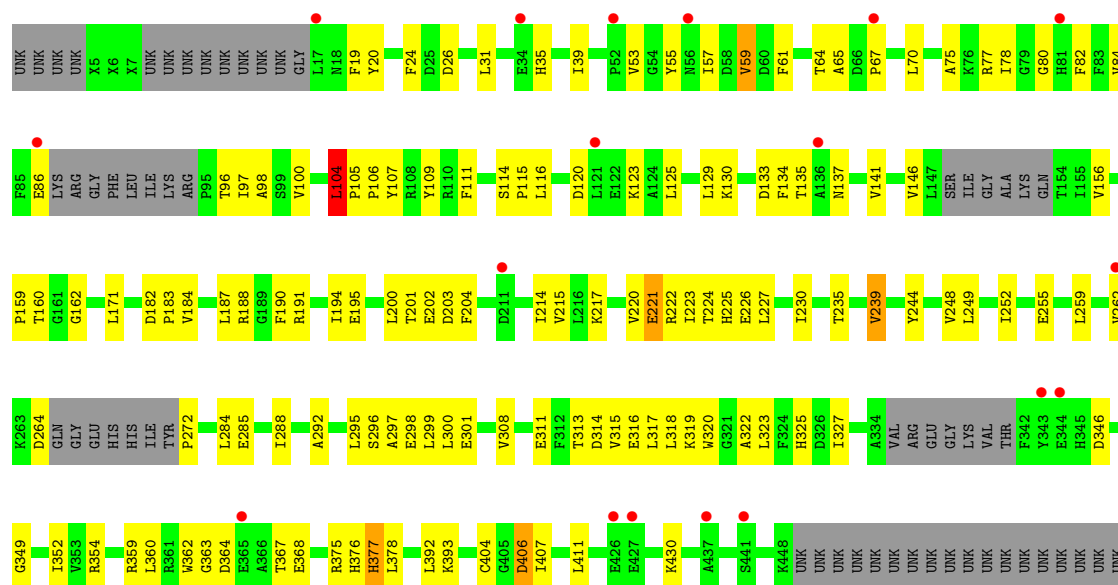




• Molecule 2: Poly A polymerase



• Molecule 2: Poly A polymerase



[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.97Å 154.03Å 158.35Å 90.00° 107.92° 90.00°	Depositor
Resolution (Å)	19.98 – 3.62 19.98 – 3.62	Depositor EDS
% Data completeness (in resolution range)	54.3 (19.98-3.62) 54.0 (19.98-3.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 3.67Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1389)	Depositor
R, R_{free}	0.222 , 0.289 0.231 , 0.296	Depositor DCC
R_{free} test set	1369 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	-11.0	Xtriage
Anisotropy	-1.846	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 126.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.057 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	20138	wwPDB-VP
Average B, all atoms (Å ²)	147.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.29	3/1726 (0.2%)	0.21	0/2688
1	B	0.30	4/1726 (0.2%)	0.21	0/2688
1	C	0.28	4/1726 (0.2%)	0.17	0/2688
1	D	0.29	3/1726 (0.2%)	0.17	0/2688
2	E	0.43	0/3389	0.83	3/4564 (0.1%)
2	F	0.40	0/3385	0.82	5/4559 (0.1%)
2	G	0.37	0/3391	0.77	0/4567
2	H	0.36	0/3398	0.76	4/4576 (0.1%)
All	All	0.36	14/20467 (0.1%)	0.64	12/29018 (0.0%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	43	G	C1'-N9	-6.16	1.38	1.48
1	B	28	U	C1'-N1	6.04	1.57	1.48
1	D	28	U	C1'-N1	5.99	1.57	1.48
1	C	43	G	C1'-N9	-5.94	1.39	1.48
1	A	28	U	C1'-N1	5.80	1.57	1.48
1	A	43	G	C1'-N9	-5.79	1.39	1.48
1	B	43	G	C1'-N9	-5.76	1.39	1.48
1	C	28	U	C1'-N1	5.76	1.57	1.48
1	B	27	C	C1'-N1	5.47	1.56	1.48
1	D	27	C	C1'-N1	5.44	1.56	1.48
1	A	27	C	C1'-N1	5.40	1.56	1.48
1	C	27	C	C1'-N1	5.11	1.56	1.48
1	B	42	A	C1'-N9	-5.08	1.40	1.48
1	C	42	A	C1'-N9	-5.01	1.40	1.48

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	220	VAL	N-CA-C	6.42	116.58	110.42
2	E	446	GLU	N-CA-C	-6.37	105.37	113.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	104	LEU	CA-C-N	-6.25	113.95	120.38
2	H	104	LEU	C-N-CA	-6.25	113.95	120.38
2	F	104	LEU	CA-C-N	-6.19	114.00	120.38
2	F	104	LEU	C-N-CA	-6.19	114.00	120.38
2	F	182	ASP	CA-C-N	5.87	126.28	119.47
2	F	182	ASP	C-N-CA	5.87	126.28	119.47
2	F	105	PRO	N-CA-C	5.64	117.58	110.70
2	E	105	PRO	N-CA-C	5.41	117.31	110.70
2	H	443	ASN	CA-C-N	5.14	127.12	120.44
2	H	443	ASN	C-N-CA	5.14	127.12	120.44

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	1545	0	781	9	0
1	B	1545	0	781	12	0
1	C	1545	0	781	9	0
1	D	1545	0	781	14	0
2	E	3489	0	3370	84	0
2	F	3475	0	3366	97	0
2	G	3491	0	3373	88	0
2	H	3503	0	3379	100	0
All	All	20138	0	16612	379	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 10.

All (379) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:19:PHE:O	2:E:146:VAL:HG13	1.43	1.15
2:F:221:GLU:O	2:F:224:THR:HG22	1.60	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:445:ASN:OD1	2:E:446:GLU:N	1.99	0.95
2:E:19:PHE:O	2:E:146:VAL:CG1	2.20	0.88
1:D:19:G:C5	2:H:473:UNK:CB	2.57	0.88
2:E:106:PRO:HG3	2:F:301:GLU:HA	1.56	0.85
2:H:296:SER:OG	2:H:299:LEU:HD13	1.77	0.84
2:G:297:ALA:HB1	2:H:104:LEU:HD11	1.60	0.82
2:G:86:GLU:HG3	2:G:96:THR:HG22	1.63	0.81
1:D:19:G:C6	2:H:473:UNK:HA	2.15	0.81
1:C:19:G:C6	2:G:473:UNK:HA	2.18	0.79
2:H:133:ASP:HB3	2:H:185:ARG:HD3	1.63	0.79
2:H:308:VAL:HG12	2:H:309:LEU:HD13	1.66	0.77
1:A:73:A:N3	1:A:73:A:H2'	2.01	0.74
2:F:221:GLU:C	2:F:224:THR:HG22	2.13	0.73
2:F:224:THR:HG1	2:F:362:TRP:CD1	2.06	0.72
2:F:130:LYS:HD3	2:F:159:PRO:HB2	1.70	0.72
2:F:221:GLU:O	2:F:224:THR:CG2	2.35	0.72
2:H:440:GLU:O	2:H:444:ARG:HB2	1.91	0.71
1:D:56:C:C4	2:H:476:UNK:CB	2.73	0.71
2:E:128:ASP:OD1	2:E:132:ARG:NH1	2.25	0.70
2:G:211:ASP:OD1	2:G:211:ASP:N	2.25	0.70
2:H:445:ASN:OD1	2:H:446:GLU:N	2.25	0.69
2:F:86:GLU:HG3	2:F:96:THR:HG22	1.74	0.69
2:G:194:ILE:HG13	2:G:239:VAL:HG22	1.74	0.69
2:H:250:GLU:OE2	2:H:260:ARG:NH2	2.25	0.69
1:C:19:G:O6	1:C:56:C:N4	2.25	0.69
2:F:224:THR:HG23	2:F:225:HIS:N	2.08	0.69
2:F:215:VAL:HG21	2:F:248:VAL:HG13	1.75	0.68
2:F:308:VAL:HG21	2:F:317:LEU:HD11	1.75	0.68
2:H:472:UNK:O	2:H:476:UNK:N	2.27	0.67
2:E:215:VAL:HG21	2:E:248:VAL:HG13	1.74	0.67
2:F:194:ILE:HG13	2:F:239:VAL:HG22	1.75	0.67
2:G:308:VAL:HG21	2:G:317:LEU:HD11	1.77	0.67
2:H:308:VAL:HG11	2:H:366:ALA:HB2	1.77	0.67
2:F:191:ARG:NH1	2:F:195:GLU:OE1	2.27	0.67
2:G:301:GLU:HA	2:H:106:PRO:HG3	1.77	0.67
2:E:17:LEU:N	2:E:17:LEU:HD22	2.11	0.66
2:G:108:ARG:HH22	2:G:110:ARG:HD2	1.61	0.65
2:F:191:ARG:NE	2:F:226:GLU:OE2	2.25	0.65
1:D:19:G:O6	1:D:56:C:N4	2.30	0.65
2:E:183:PRO:HB3	2:E:214:ILE:HG13	1.77	0.65
1:A:19:G:C4	2:E:473:UNK:CB	2.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:188:ARG:HG2	2:E:226:GLU:OE2	1.97	0.64
2:G:106:PRO:HG3	2:H:301:GLU:HA	1.79	0.64
2:H:399:ASN:O	2:H:403:GLU:HB2	1.97	0.64
2:E:104:LEU:HD11	2:F:297:ALA:HB1	1.80	0.64
2:F:296:SER:HB3	2:F:299:LEU:HD13	1.80	0.63
2:F:327:ILE:HG23	2:F:352:ILE:HD12	1.80	0.63
2:F:183:PRO:HB3	2:F:214:ILE:HG13	1.79	0.63
2:G:191:ARG:NH1	2:G:195:GLU:OE1	2.31	0.63
1:C:19:G:C5	2:G:473:UNK:CB	2.82	0.63
2:G:133:ASP:HB3	2:G:185:ARG:HD3	1.81	0.63
2:G:314:ASP:OD2	2:G:410:HIS:NE2	2.29	0.63
2:H:39:ILE:HD12	2:H:146:VAL:HG21	1.81	0.62
2:G:183:PRO:HB3	2:G:214:ILE:HG13	1.81	0.62
2:F:120:ASP:HB3	2:F:123:LYS:HE3	1.81	0.62
2:E:183:PRO:HG2	2:E:218:SER:HB3	1.80	0.62
1:A:29:G:C2	1:A:42:A:C2	2.87	0.62
1:D:19:G:C4	2:H:473:UNK:CB	2.83	0.61
2:G:252:ILE:O	2:G:359:ARG:NH1	2.27	0.61
2:H:183:PRO:HG2	2:H:218:SER:HB3	1.82	0.61
1:B:19:G:O6	1:B:56:C:N4	2.32	0.61
2:G:133:ASP:OD2	2:G:188:ARG:NH1	2.34	0.60
2:H:40:VAL:HG13	2:H:140:ALA:HB2	1.84	0.60
2:H:194:ILE:HG13	2:H:239:VAL:HG22	1.84	0.60
2:G:215:VAL:HG21	2:G:248:VAL:HG13	1.83	0.60
2:E:33:ARG:HE	2:H:31:LEU:HD23	1.67	0.59
1:D:4:C:H42	1:D:69:G:H1	1.48	0.59
2:G:284:LEU:HD22	2:G:322:ALA:HB2	1.84	0.59
2:H:350:ALA:HB2	2:H:375:ARG:HB2	1.83	0.59
2:E:172:ARG:HG3	2:E:201:THR:HG21	1.83	0.59
2:G:296:SER:OG	2:G:440:GLU:OE1	2.20	0.59
2:E:120:ASP:HB3	2:E:123:LYS:HE3	1.84	0.59
2:F:375:ARG:HG3	2:F:376:HIS:HD2	1.67	0.59
2:F:406:ASP:OD1	2:F:406:ASP:N	2.35	0.59
1:B:27:C:H2'	1:B:28:U:H6	1.68	0.58
2:G:183:PRO:HG2	2:G:218:SER:HB3	1.85	0.58
2:E:284:LEU:HD22	2:E:322:ALA:HB2	1.84	0.58
2:G:353:VAL:HG21	2:G:374:VAL:HG21	1.85	0.58
2:F:264:ASP:HB3	2:F:272:PRO:N	2.19	0.58
2:E:61:PHE:HE2	2:E:111:PHE:HD2	1.52	0.58
1:B:27:C:H2'	1:B:28:U:C6	2.38	0.58
2:E:16:GLY:O	2:E:20:TYR:HB2	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:35:HIS:CG	2:E:65:ALA:HB2	2.38	0.58
2:E:133:ASP:OD1	2:E:133:ASP:N	2.37	0.58
2:F:377:HIS:HA	2:F:411:LEU:HD11	1.86	0.58
2:E:67:PRO:HG2	2:E:115:PRO:HG3	1.86	0.57
2:E:83:PHE:HB3	2:E:99:SER:HB3	1.86	0.57
2:E:257:GLY:O	2:E:260:ARG:HG2	2.04	0.57
2:G:474:UNK:O	2:G:477:UNK:CB	2.51	0.57
2:H:215:VAL:HG21	2:H:248:VAL:HG13	1.86	0.57
2:E:359:ARG:HG2	2:E:360:LEU:HD12	1.86	0.57
2:G:120:ASP:HB3	2:G:123:LYS:HB3	1.85	0.57
2:E:433:MET:HE3	2:F:20:TYR:CE2	2.40	0.57
2:F:224:THR:HG1	2:F:362:TRP:HD1	1.49	0.57
2:F:224:THR:CG2	2:F:225:HIS:N	2.67	0.57
2:E:347:LYS:HG2	2:E:375:ARG:NE	2.20	0.56
1:B:69:G:H2'	1:B:70:G:H8	1.71	0.56
2:G:354:ARG:NH1	2:G:368:GLU:OE1	2.39	0.56
2:E:298:GLU:HG2	2:E:299:LEU:HD12	1.87	0.56
2:G:284:LEU:HD21	2:G:318:LEU:HD22	1.88	0.56
2:F:57:ILE:HD12	2:F:109:TYR:CE2	2.41	0.56
2:G:237:HIS:ND1	2:G:285:GLU:OE1	2.34	0.56
1:D:19:G:C6	2:H:473:UNK:CA	2.88	0.55
2:F:404:CYS:HB2	2:F:407:ILE:HG12	1.88	0.55
2:F:31:LEU:HA	2:F:70:LEU:HD11	1.88	0.55
2:H:184:VAL:HG23	2:H:223:ILE:HD13	1.87	0.55
2:E:301:GLU:HA	2:F:106:PRO:HG3	1.87	0.55
2:G:474:UNK:O	2:G:477:UNK:N	2.40	0.55
2:F:120:ASP:HB3	2:F:123:LYS:HB3	1.89	0.55
2:H:36:TYR:HD2	2:H:121:LEU:HD22	1.72	0.55
2:H:120:ASP:HB3	2:H:123:LYS:HE3	1.89	0.55
2:E:186:VAL:HG11	2:E:215:VAL:HG22	1.88	0.55
2:F:75:ALA:HB1	2:F:80:GLY:O	2.07	0.55
2:H:67:PRO:HG2	2:H:115:PRO:HG3	1.88	0.54
2:H:57:ILE:HD12	2:H:109:TYR:CE1	2.42	0.54
2:G:120:ASP:HB3	2:G:123:LYS:HE3	1.89	0.54
2:E:68:VAL:HG13	2:E:82:PHE:HZ	1.73	0.54
2:F:61:PHE:HE2	2:F:111:PHE:HD2	1.55	0.54
2:F:327:ILE:HG22	2:F:349:GLY:HA2	1.90	0.54
2:H:201:THR:OG1	2:H:202:GLU:N	2.40	0.54
2:H:377:HIS:HA	2:H:411:LEU:HD11	1.90	0.54
2:G:77:ARG:O	2:H:444:ARG:CZ	2.55	0.54
2:F:284:LEU:O	2:F:288:ILE:HG13	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:24:PHE:HB3	2:G:147:LEU:HD21	1.91	0.53
2:H:353:VAL:HG21	2:H:374:VAL:HG21	1.89	0.53
2:G:441:SER:O	2:G:445:ASN:ND2	2.42	0.53
2:F:221:GLU:HA	2:F:224:THR:HG22	1.91	0.53
2:G:327:ILE:HG23	2:G:352:ILE:HD12	1.90	0.53
2:H:227:LEU:HB3	2:H:320:TRP:HZ2	1.74	0.53
2:H:308:VAL:O	2:H:309:LEU:HB2	2.07	0.52
2:G:224:THR:OG1	2:G:360:LEU:O	2.24	0.52
2:H:314:ASP:OD2	2:H:410:HIS:NE2	2.38	0.52
2:H:141:VAL:HG12	2:H:156:VAL:HG12	1.91	0.52
2:F:215:VAL:HG11	2:F:252:ILE:HD11	1.91	0.52
2:G:350:ALA:HB2	2:G:375:ARG:HB2	1.90	0.52
2:H:120:ASP:HB3	2:H:123:LYS:HB3	1.92	0.52
2:F:104:LEU:HD23	2:F:106:PRO:HD2	1.90	0.52
2:H:233:GLU:O	2:H:319:LYS:NZ	2.43	0.52
2:F:125:LEU:O	2:F:129:LEU:HG	2.09	0.51
2:E:227:LEU:HB3	2:E:320:TRP:HZ2	1.73	0.51
1:B:18:G:O2'	1:B:57:G:N2	2.43	0.51
2:E:302:ASN:HA	2:E:305:LYS:HD2	1.92	0.51
2:G:363:GLY:O	2:G:367:THR:HG22	2.11	0.51
2:F:221:GLU:CD	2:F:221:GLU:H	2.18	0.51
2:G:182:ASP:OD2	2:G:222:ARG:NH2	2.43	0.51
2:G:433:MET:HE3	2:H:20:TYR:CZ	2.46	0.51
2:F:224:THR:CG2	2:F:225:HIS:H	2.24	0.51
2:G:203:ASP:OD1	2:G:203:ASP:N	2.40	0.51
2:H:225:HIS:NE2	2:H:311:GLU:OE2	2.44	0.51
2:E:104:LEU:HD23	2:E:106:PRO:HD2	1.93	0.50
2:H:49:LEU:HD21	2:H:166:LEU:HD22	1.93	0.50
2:E:292:ALA:HA	2:E:300:LEU:HD11	1.92	0.50
2:F:200:LEU:HD13	2:F:204:PHE:CD2	2.46	0.50
2:F:227:LEU:HD12	2:F:320:TRP:HH2	1.77	0.50
2:F:292:ALA:HA	2:F:300:LEU:HD11	1.93	0.50
2:E:49:LEU:HD21	2:E:166:LEU:HD22	1.94	0.50
2:F:141:VAL:HG12	2:F:156:VAL:HG12	1.94	0.50
2:G:318:LEU:HG	2:G:410:HIS:HB3	1.93	0.50
2:F:187:LEU:HD11	2:F:223:ILE:HG23	1.93	0.50
2:G:397:MET:HB3	2:G:442:PHE:CD2	2.46	0.50
2:E:284:LEU:HD21	2:E:318:LEU:HD22	1.94	0.50
2:E:352:ILE:O	2:E:356:ILE:HG13	2.12	0.49
1:C:68:U:H2'	1:C:69:G:C8	2.47	0.49
2:H:284:LEU:HD21	2:H:318:LEU:HD22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:354:ARG:NH1	2:H:368:GLU:OE1	2.45	0.49
2:F:134:PHE:O	2:F:137:ASN:N	2.45	0.49
2:H:211:ASP:N	2:H:211:ASP:OD1	2.46	0.49
2:F:57:ILE:HD12	2:F:109:TYR:HE2	1.77	0.49
2:E:16:GLY:C	2:E:17:LEU:HD13	2.38	0.49
2:H:183:PRO:HG3	2:H:217:LYS:HE3	1.94	0.49
2:E:27:VAL:HG23	2:E:74:PHE:CE1	2.48	0.49
2:H:183:PRO:HB3	2:H:214:ILE:HG13	1.95	0.49
2:H:285:GLU:HG2	2:H:319:LYS:HE2	1.94	0.49
2:F:171:LEU:HB3	2:F:200:LEU:HD23	1.95	0.48
2:H:128:ASP:OD1	2:H:132:ARG:NH1	2.46	0.48
2:E:63:THR:HG21	2:E:70:LEU:HD22	1.95	0.48
2:G:134:PHE:HA	2:G:173:PRO:HA	1.95	0.48
2:E:203:ASP:OD1	2:E:203:ASP:N	2.44	0.48
2:F:346:ASP:OD1	2:F:346:ASP:N	2.42	0.48
2:G:104:LEU:HD11	2:H:297:ALA:HB1	1.95	0.48
2:G:128:ASP:OD1	2:G:132:ARG:NH1	2.46	0.48
2:G:210:GLU:HB3	2:G:211:ASP:OD1	2.13	0.48
2:G:135:THR:HB	2:G:162:GLY:HA2	1.95	0.48
2:G:372:LYS:HG2	2:G:407:ILE:HD13	1.95	0.48
2:E:158:ASP:N	2:E:158:ASP:OD1	2.46	0.48
2:F:135:THR:HB	2:F:162:GLY:HA2	1.94	0.48
2:G:39:ILE:HG12	2:G:61:PHE:CE1	2.49	0.48
2:G:215:VAL:HG11	2:G:252:ILE:HD11	1.96	0.48
2:E:156:VAL:HG21	2:E:163:ILE:HD11	1.95	0.48
2:G:327:ILE:HG22	2:G:349:GLY:HA2	1.95	0.48
1:D:68:U:H2'	1:D:69:G:C8	2.48	0.48
2:E:40:VAL:HG13	2:E:140:ALA:HB2	1.94	0.48
2:H:244:TYR:HB2	2:H:249:LEU:HD23	1.96	0.48
2:H:364:ASP:HA	2:H:367:THR:HG22	1.95	0.48
1:D:68:U:H2'	1:D:69:G:H8	1.79	0.47
2:E:83:PHE:CD2	2:E:99:SER:HB3	2.49	0.47
2:G:201:THR:OG1	2:G:202:GLU:N	2.47	0.47
2:H:308:VAL:HG12	2:H:309:LEU:CD1	2.41	0.47
1:A:69:G:H2'	1:A:70:G:H8	1.79	0.47
2:E:345:HIS:HA	2:E:348:VAL:HB	1.96	0.47
2:F:135:THR:HG22	2:F:160:THR:HB	1.95	0.47
2:E:211:ASP:OD1	2:E:211:ASP:N	2.46	0.47
2:G:20:TYR:CZ	2:H:433:MET:HE3	2.49	0.47
2:E:47:ARG:HD3	2:E:47:ARG:HA	1.58	0.47
2:F:244:TYR:HD1	2:F:249:LEU:HD23	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:C:H42	1:C:69:G:H1	1.62	0.47
2:F:194:ILE:HG13	2:F:239:VAL:CG2	2.43	0.47
2:F:259:LEU:HD21	2:F:327:ILE:HD12	1.97	0.47
2:F:314:ASP:OD1	2:F:314:ASP:N	2.43	0.47
2:F:354:ARG:NH1	2:F:368:GLU:OE1	2.47	0.47
2:H:284:LEU:HD22	2:H:322:ALA:HB2	1.96	0.47
1:A:36:A:H2'	1:A:37:A:C8	2.49	0.47
2:H:472:UNK:O	2:H:476:UNK:CB	2.63	0.47
2:F:39:ILE:HG12	2:F:61:PHE:CE1	2.49	0.47
2:F:55:TYR:HA	2:F:107:TYR:CD1	2.50	0.47
2:G:352:ILE:O	2:G:356:ILE:HG13	2.14	0.47
2:H:277:THR:HG22	2:H:325:HIS:CE1	2.50	0.47
2:G:326:ASP:HB3	2:G:329:LYS:HG3	1.97	0.47
2:H:86:GLU:HG3	2:H:96:THR:HG22	1.96	0.47
2:H:104:LEU:HD23	2:H:106:PRO:HD2	1.95	0.47
2:E:135:THR:HG22	2:E:160:THR:HB	1.96	0.47
2:E:250:GLU:OE2	2:E:260:ARG:NH2	2.48	0.47
2:G:68:VAL:HG22	2:G:84:VAL:HG11	1.97	0.47
2:H:302:ASN:HA	2:H:305:LYS:HD2	1.97	0.47
1:D:62:C:H2'	1:D:63:G:H8	1.80	0.46
2:F:64:THR:HA	2:F:116:LEU:O	2.15	0.46
2:G:380:PRO:HG2	2:G:415:SER:HB3	1.97	0.46
2:H:308:VAL:CG1	2:H:366:ALA:HB2	2.45	0.46
1:A:9:A:O2'	1:A:10:G:N7	2.48	0.46
2:F:39:ILE:HD12	2:F:146:VAL:HG21	1.97	0.46
2:F:190:PHE:O	2:F:194:ILE:HG12	2.15	0.46
2:G:255:GLU:OE1	2:G:255:GLU:N	2.33	0.46
2:E:318:LEU:HG	2:E:410:HIS:HB3	1.97	0.46
2:E:24:PHE:CD2	2:E:146:VAL:HG11	2.50	0.46
2:E:33:ARG:NE	2:H:31:LEU:HD23	2.28	0.46
2:H:288:ILE:HD11	2:H:318:LEU:HD13	1.97	0.46
2:G:259:LEU:HD21	2:G:327:ILE:HD12	1.97	0.46
2:H:200:LEU:HD13	2:H:204:PHE:CD2	2.51	0.46
2:F:221:GLU:CA	2:F:224:THR:HG22	2.45	0.46
2:G:401:TRP:CE2	2:G:443:ASN:HB2	2.51	0.46
2:G:406:ASP:OD1	2:G:406:ASP:N	2.47	0.46
1:B:69:G:H2'	1:B:70:G:C8	2.50	0.46
1:A:29:G:N3	1:A:42:A:C2	2.84	0.45
2:F:201:THR:OG1	2:F:202:GLU:N	2.49	0.45
2:H:274:ASP:OD1	2:H:275:GLU:N	2.50	0.45
2:H:221:GLU:CD	2:H:221:GLU:H	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:346:ASP:OD2	2:H:375:ARG:NH1	2.49	0.45
2:E:21:LEU:HD12	2:E:22:SER:H	1.81	0.45
2:G:133:ASP:OD1	2:G:133:ASP:N	2.48	0.45
2:H:225:HIS:CE1	2:H:229:LYS:HD2	2.51	0.45
2:H:298:GLU:HG2	2:H:299:LEU:HD12	1.98	0.45
2:G:404:CYS:HB2	2:G:407:ILE:HG12	1.99	0.45
2:E:234:LYS:HB2	2:E:234:LYS:HE3	1.77	0.45
2:F:225:HIS:NE2	2:F:311:GLU:OE2	2.49	0.45
2:F:407:ILE:HD11	2:F:411:LEU:HD22	1.98	0.45
1:C:12:U:O2	1:C:24:G:N2	2.50	0.45
2:F:67:PRO:HG2	2:F:115:PRO:HG3	1.99	0.45
2:F:255:GLU:OE1	2:F:359:ARG:NH2	2.49	0.45
2:H:99:SER:OG	2:H:112:ASP:OD1	2.26	0.45
2:H:231:MET:HG3	2:H:320:TRP:NE1	2.32	0.45
2:E:97:ILE:HG22	2:E:115:PRO:HD3	1.98	0.45
2:E:297:ALA:HB1	2:F:104:LEU:HD11	1.98	0.45
2:F:97:ILE:HG22	2:F:115:PRO:HD3	1.99	0.45
2:G:430:LYS:HZ2	2:H:147:LEU:C	2.25	0.45
2:H:186:VAL:HG11	2:H:215:VAL:HG22	1.98	0.45
2:H:172:ARG:HG3	2:H:201:THR:HG21	1.99	0.45
2:H:308:VAL:CG1	2:H:309:LEU:HD13	2.42	0.45
2:F:191:ARG:HB2	2:F:230:ILE:HG12	1.98	0.45
2:F:200:LEU:HD23	2:F:200:LEU:HA	1.76	0.45
2:F:285:GLU:HG2	2:F:319:LYS:HE2	1.98	0.45
2:G:43:TRP:CD1	2:G:59:VAL:HG13	2.52	0.45
1:B:72:C:OP1	2:F:222:ARG:HD2	2.17	0.44
2:E:75:ALA:HB2	2:E:100:VAL:HG22	1.98	0.44
2:E:379:ARG:NH1	2:E:403:GLU:OE1	2.42	0.44
2:F:24:PHE:HD2	2:F:146:VAL:HG11	1.82	0.44
2:F:184:VAL:HG23	2:F:223:ILE:HD13	1.99	0.44
2:G:30:VAL:HG12	2:G:70:LEU:HD12	1.99	0.44
2:H:255:GLU:HB3	2:H:327:ILE:HD11	1.99	0.44
2:E:17:LEU:HD22	2:E:17:LEU:H	1.80	0.44
2:H:135:THR:HG22	2:H:160:THR:HB	1.98	0.44
2:H:256:ILE:HD11	2:H:324:PHE:HE1	1.83	0.44
1:C:19:G:C4	2:G:473:UNK:CB	3.00	0.44
2:F:313:THR:N	2:F:316:GLU:OE1	2.50	0.44
2:G:109:TYR:CE2	2:H:297:ALA:HB2	2.52	0.44
1:B:5:A:OP1	2:F:364:ASP:HB2	2.17	0.44
2:G:346:ASP:OD1	2:G:346:ASP:N	2.50	0.44
2:E:444:ARG:NH1	2:F:78:ILE:HA	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:357:GLY:HA3	2:E:367:THR:OG1	2.17	0.44
2:G:36:TYR:HD2	2:G:121:LEU:HD22	1.82	0.44
1:A:67:C:H2'	1:A:68:U:H6	1.82	0.44
2:F:133:ASP:OD2	2:F:188:ARG:NH1	2.51	0.43
2:F:363:GLY:O	2:F:367:THR:HG22	2.18	0.43
1:C:19:G:C5	2:G:473:UNK:HA	2.53	0.43
2:G:104:LEU:HD21	2:H:297:ALA:HB1	2.01	0.43
2:F:24:PHE:CE1	2:F:59:VAL:HG11	2.54	0.43
2:H:296:SER:OG	2:H:299:LEU:CD1	2.57	0.43
2:E:347:LYS:HE2	2:E:375:ARG:NH2	2.34	0.43
2:H:75:ALA:HB1	2:H:80:GLY:O	2.18	0.43
2:H:114:SER:HA	2:H:115:PRO:HD3	1.86	0.43
1:B:27:C:C2	1:B:28:U:C5	3.06	0.43
2:G:156:VAL:HG21	2:G:163:ILE:HD11	2.00	0.43
2:H:327:ILE:HG22	2:H:349:GLY:HA2	2.01	0.43
1:C:9:A:O2'	1:C:10:G:N7	2.52	0.43
2:E:31:LEU:HA	2:E:32:PRO:HD3	1.85	0.43
2:G:38:PHE:HE1	2:G:121:LEU:HD11	1.83	0.43
1:D:9:A:O2'	1:D:10:G:N7	2.52	0.43
2:E:183:PRO:HG2	2:E:218:SER:CB	2.48	0.43
2:E:223:ILE:O	2:E:227:LEU:HD23	2.19	0.43
2:E:232:LYS:HA	2:E:316:GLU:OE2	2.19	0.43
2:F:24:PHE:CD2	2:F:146:VAL:HG11	2.54	0.43
2:H:277:THR:HA	2:H:325:HIS:HE1	1.84	0.43
2:E:274:ASP:OD1	2:E:275:GLU:N	2.52	0.42
2:G:182:ASP:HA	2:G:183:PRO:HD2	1.90	0.42
2:G:433:MET:HE3	2:H:20:TYR:CE2	2.54	0.42
2:E:379:ARG:HB3	2:E:380:PRO:HD3	2.00	0.42
2:H:133:ASP:OD1	2:H:133:ASP:N	2.40	0.42
1:B:66:C:H2'	1:B:67:C:C6	2.54	0.42
2:E:236:ALA:HB3	2:E:285:GLU:OE2	2.19	0.42
2:F:392:LEU:C	2:F:393:LYS:HD2	2.44	0.42
1:B:29:G:C2	1:B:42:A:C2	3.08	0.42
2:F:19:PHE:CE2	2:F:141:VAL:HG11	2.54	0.42
2:G:45:ARG:HG3	2:G:136:ALA:HB1	2.02	0.42
2:G:64:THR:HA	2:G:116:LEU:O	2.20	0.42
2:E:236:ALA:HA	2:E:239:VAL:HG23	2.00	0.42
2:G:141:VAL:HG12	2:G:156:VAL:HG12	2.01	0.42
2:E:445:ASN:C	2:E:447:MET:N	2.74	0.42
2:G:448:LYS:HD3	2:G:448:LYS:HA	1.87	0.42
2:H:135:THR:HB	2:H:162:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:408:ALA:HB3	2:H:409:PRO:HD3	2.02	0.42
2:E:31:LEU:HD12	2:E:32:PRO:HD2	2.01	0.42
2:G:224:THR:HG23	2:G:362:TRP:CD1	2.55	0.42
2:E:318:LEU:HD11	2:E:410:HIS:HA	2.01	0.42
2:G:274:ASP:OD1	2:G:275:GLU:N	2.47	0.42
2:G:370:VAL:O	2:G:374:VAL:HG23	2.20	0.42
2:H:206:GLU:O	2:H:210:GLU:HG2	2.20	0.42
2:G:158:ASP:N	2:G:158:ASP:OD1	2.53	0.42
2:H:346:ASP:OD1	2:H:346:ASP:N	2.47	0.42
2:E:443:ASN:O	2:E:444:ARG:C	2.62	0.42
2:G:40:VAL:HG13	2:G:140:ALA:HB2	2.02	0.42
1:D:4:C:N4	1:D:69:G:H1	2.17	0.41
2:E:172:ARG:HA	2:E:173:PRO:HD2	1.94	0.41
2:F:75:ALA:HB2	2:F:100:VAL:HG22	2.01	0.41
1:B:36:A:H2'	1:B:37:A:C8	2.55	0.41
1:D:19:G:C6	2:H:473:UNK:CB	3.01	0.41
2:E:288:ILE:HD11	2:E:318:LEU:HD13	2.02	0.41
2:F:35:HIS:CG	2:F:65:ALA:HB2	2.55	0.41
2:G:148:SER:O	2:H:430:LYS:HG3	2.20	0.41
2:G:201:THR:OG1	2:G:203:ASP:OD1	2.22	0.41
2:H:404:CYS:O	2:H:404:CYS:SG	2.78	0.41
2:H:43:TRP:CD1	2:H:59:VAL:HG22	2.55	0.41
2:H:359:ARG:HG2	2:H:360:LEU:HD12	2.03	0.41
1:D:73:A:OP1	2:H:222:ARG:HD2	2.19	0.41
2:E:62:LEU:HD23	2:E:114:SER:HB2	2.02	0.41
2:F:59:VAL:HG21	2:F:111:PHE:CE2	2.55	0.41
2:F:171:LEU:HD23	2:F:200:LEU:HD21	2.03	0.41
2:E:231:MET:HG3	2:E:320:TRP:NE1	2.35	0.41
2:E:375:ARG:HG3	2:E:376:HIS:HD2	1.85	0.41
2:F:82:PHE:HE1	2:F:98:ALA:HB1	1.85	0.41
2:F:114:SER:HA	2:F:115:PRO:HD3	1.89	0.41
2:F:284:LEU:HD22	2:F:322:ALA:HB2	2.02	0.41
2:G:226:GLU:O	2:G:230:ILE:HG13	2.21	0.41
2:G:375:ARG:HG3	2:G:376:HIS:HD2	1.86	0.41
2:G:476:UNK:O	2:G:477:UNK:C	2.68	0.41
2:H:134:PHE:HA	2:H:173:PRO:HA	2.02	0.41
2:E:404:CYS:SG	2:E:404:CYS:O	2.79	0.41
1:A:30:G:H2'	1:A:31:A:H8	1.86	0.40
2:E:86:GLU:HG3	2:E:96:THR:HG22	2.03	0.40
2:E:184:VAL:HG23	2:E:223:ILE:HD13	2.03	0.40
2:H:183:PRO:HG3	2:H:217:LYS:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:26:ASP:OD1	2:F:77:ARG:NH2	2.41	0.40
2:F:24:PHE:HE1	2:F:59:VAL:HG11	1.87	0.40
2:H:204:PHE:O	2:H:208:VAL:HG23	2.20	0.40
2:E:36:TYR:HD2	2:E:121:LEU:HD22	1.87	0.40
2:F:183:PRO:HG3	2:F:217:LYS:HB3	2.04	0.40
2:F:288:ILE:HD13	2:F:315:VAL:HG13	2.04	0.40
2:F:327:ILE:CG2	2:F:349:GLY:HA2	2.51	0.40
2:F:221:GLU:HA	2:F:224:THR:CG2	2.51	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	
2	E	395/512 (77%)	390 (99%)	5 (1%)	0	100	100
2	F	394/512 (77%)	389 (99%)	5 (1%)	0	100	100
2	G	395/512 (77%)	390 (99%)	5 (1%)	0	100	100
2	H	396/512 (77%)	392 (99%)	4 (1%)	0	100	100
All	All	1580/2048 (77%)	1561 (99%)	19 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	E	352/375 (94%)	333 (95%)	19 (5%)	20	44
2	F	352/375 (94%)	332 (94%)	20 (6%)	18	43
2	G	353/375 (94%)	338 (96%)	15 (4%)	26	49
2	H	353/375 (94%)	332 (94%)	21 (6%)	18	43
All	All	1410/1500 (94%)	1335 (95%)	75 (5%)	20	45

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	17	LEU
2	E	47	ARG
2	E	53	VAL
2	E	59	VAL
2	E	84	VAL
2	E	104	LEU
2	E	155	ILE
2	E	203	ASP
2	E	220	VAL
2	E	221	GLU
2	E	235	THR
2	E	239	VAL
2	E	262	VAL
2	E	295	LEU
2	E	318	LEU
2	E	377	HIS
2	E	378	LEU
2	E	433	MET
2	E	446	GLU
2	F	53	VAL
2	F	59	VAL
2	F	84	VAL
2	F	104	LEU
2	F	203	ASP
2	F	220	VAL
2	F	221	GLU
2	F	235	THR
2	F	239	VAL
2	F	262	VAL
2	F	295	LEU
2	F	298	GLU
2	F	318	LEU
2	F	323	LEU

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Mol	Chain	Res	Type
2	F	325	HIS
2	F	360	LEU
2	F	377	HIS
2	F	378	LEU
2	F	406	ASP
2	F	430	LYS
2	G	40	VAL
2	G	47	ARG
2	G	53	VAL
2	G	59	VAL
2	G	104	LEU
2	G	203	ASP
2	G	211	ASP
2	G	221	GLU
2	G	239	VAL
2	G	288	ILE
2	G	295	LEU
2	G	318	LEU
2	G	323	LEU
2	G	342	PHE
2	G	377	HIS
2	H	34	GLU
2	H	40	VAL
2	H	47	ARG
2	H	53	VAL
2	H	59	VAL
2	H	104	LEU
2	H	133	ASP
2	H	153	GLN
2	H	155	ILE
2	H	220	VAL
2	H	221	GLU
2	H	227	LEU
2	H	239	VAL
2	H	295	LEU
2	H	318	LEU
2	H	323	LEU
2	H	377	HIS
2	H	378	LEU
2	H	403	GLU
2	H	433	MET
2	H	446	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	E	225	HIS
2	E	276	HIS
2	F	73	ASN
2	F	103	HIS
2	F	345	HIS
2	F	443	ASN
2	G	178	ASN
2	G	345	HIS
2	H	73	ASN
2	H	345	HIS
2	H	443	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	72/73 (98%)	12 (16%)	1 (1%)
1	B	72/73 (98%)	11 (15%)	1 (1%)
1	C	72/73 (98%)	12 (16%)	1 (1%)
1	D	72/73 (98%)	14 (19%)	1 (1%)
All	All	288/292 (98%)	49 (17%)	4 (1%)

All (49) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	U
1	A	17	U
1	A	18	G
1	A	19	G
1	A	20	U
1	A	21	A
1	A	22	G
1	A	45	U
1	A	47	U
1	A	48	C
1	A	61	C
1	A	73	A
1	B	16	U
1	B	17	U
1	B	18	G
1	B	19	G

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Mol	Chain	Res	Type
1	B	20	U
1	B	22	G
1	B	45	U
1	B	47	U
1	B	48	C
1	B	61	C
1	B	73	A
1	C	16	U
1	C	17	U
1	C	18	G
1	C	19	G
1	C	20	U
1	C	21	A
1	C	43	G
1	C	44	G
1	C	45	U
1	C	47	U
1	C	48	C
1	C	61	C
1	D	16	U
1	D	17	U
1	D	18	G
1	D	19	G
1	D	20	U
1	D	21	A
1	D	22	G
1	D	43	G
1	D	44	G
1	D	45	U
1	D	46	G
1	D	47	U
1	D	48	C
1	D	61	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	19	G
1	B	19	G
1	C	19	G
1	D	19	G

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 oligosaccharides 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	73/73 (100%)	3.28	54 (73%) 0 0	73, 208, 316, 362	0
1	B	73/73 (100%)	3.40	50 (68%) 0 0	90, 194, 309, 335	0
1	C	73/73 (100%)	3.65	69 (94%) 0 0	134, 268, 311, 348	0
1	D	73/73 (100%)	4.17	65 (89%) 0 0	119, 301, 368, 411	0
2	E	405/512 (79%)	0.37	19 (4%) 36 22	32, 70, 130, 164	0
2	F	404/512 (78%)	0.43	18 (4%) 38 23	35, 75, 120, 171	0
2	G	405/512 (79%)	0.80	34 (8%) 17 13	66, 126, 182, 216	0
2	H	406/512 (79%)	0.78	41 (10%) 12 11	70, 118, 201, 233	0
All	All	1912/2340 (81%)	1.06	350 (18%) 3 4	32, 105, 282, 411	0

All (350) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	36	A	7.5
1	D	13	C	7.1
1	D	32	C	6.9
1	B	45	U	6.6
1	A	30	G	6.6
1	B	44	G	6.6
1	D	58	A	6.6
1	D	18	G	6.5
1	A	13	C	6.5
1	B	46	G	6.4
1	A	12	U	6.4
1	D	26	A	6.2
1	D	40	C	6.2
1	A	44	G	6.1
1	D	44	G	6.1
1	D	37	A	6.1

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Mol	Chain	Res	Type	RSRZ
1	B	13	C	6.0
1	A	15	G	6.0
1	D	27	C	6.0
1	B	43	G	6.0
1	B	21	A	6.0
1	C	16	U	5.9
2	H	17	LEU	5.9
1	C	28	U	5.9
1	B	30	G	5.8
1	D	55	U	5.8
1	D	52	G	5.7
1	A	36	A	5.6
1	B	9	A	5.6
1	C	6	G	5.5
1	D	34	G	5.5
1	A	46	G	5.5
1	C	9	A	5.5
1	D	19	G	5.4
1	C	51	C	5.4
1	C	39	U	5.4
1	D	9	A	5.4
1	D	31	A	5.4
1	C	32	C	5.4
1	C	58	A	5.2
1	D	23	A	5.2
1	C	60	U	5.2
1	D	30	G	5.2
1	B	37	A	5.2
1	D	20	U	5.2
2	E	16	GLY	5.2
1	A	32	C	5.1
1	C	53	G	5.1
1	A	31	A	5.1
1	C	36	A	5.1
1	B	26	A	5.0
1	D	42	A	5.0
1	D	10	G	5.0
1	B	12	U	5.0
1	B	16	U	5.0
1	D	51	C	5.0
1	A	14	A	5.0
1	B	17	U	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	20	U	4.9
1	C	21	A	4.9
1	C	73	A	4.8
1	D	54	U	4.8
2	H	263	LYS	4.8
1	B	34	G	4.8
1	C	52	G	4.8
1	A	23	A	4.7
2	G	17	LEU	4.7
1	B	18	G	4.7
1	C	7	G	4.7
1	D	6	G	4.7
1	D	24	G	4.7
1	C	44	G	4.6
1	A	47	U	4.6
1	D	65	C	4.6
1	A	43	G	4.6
1	A	63	G	4.6
1	B	10	G	4.6
1	C	59	U	4.6
1	D	59	U	4.6
1	D	22	G	4.6
1	D	48	C	4.6
1	D	50	G	4.5
1	A	11	C	4.5
1	D	25	C	4.5
1	C	22	G	4.5
1	D	46	G	4.5
2	H	390	GLY	4.5
1	D	14	A	4.5
1	D	63	G	4.4
1	A	26	A	4.4
1	D	21	A	4.4
1	D	43	G	4.4
2	H	402	ARG	4.4
1	C	20	U	4.4
1	D	8	U	4.4
1	D	15	G	4.4
1	A	35	A	4.4
1	D	38	A	4.4
1	B	27	C	4.3
1	B	40	C	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	48	C	4.3
1	B	33	U	4.3
1	A	38	A	4.3
1	A	39	U	4.3
1	C	23	A	4.3
1	B	38	A	4.2
1	A	16	U	4.2
1	D	11	C	4.2
1	C	25	C	4.2
1	A	59	U	4.2
1	C	67	C	4.2
1	A	7	G	4.1
1	B	24	G	4.1
1	C	8	U	4.0
1	C	42	A	4.0
1	D	33	U	4.0
1	D	45	U	4.0
1	A	9	A	4.0
1	B	23	A	4.0
1	C	13	C	4.0
1	C	54	U	4.0
1	D	39	U	4.0
1	B	31	A	4.0
1	C	63	G	4.0
1	B	47	U	4.0
1	C	48	C	3.9
2	G	343	TYR	3.9
1	A	17	U	3.9
1	A	34	G	3.9
1	D	60	U	3.9
1	D	36	A	3.9
1	A	22	G	3.9
1	A	24	G	3.9
1	D	57	G	3.9
1	D	17	U	3.9
1	C	18	G	3.9
1	D	41	C	3.9
1	A	45	U	3.8
1	B	39	U	3.8
1	C	43	G	3.8
1	C	50	G	3.8
1	D	53	G	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	40	C	3.8
1	B	8	U	3.8
1	C	33	U	3.8
2	E	334	ALA	3.8
1	A	10	G	3.8
1	C	62	C	3.8
1	B	20	U	3.8
1	B	19	G	3.8
1	C	29	G	3.8
1	C	61	C	3.8
1	B	60	U	3.7
1	A	33	U	3.7
1	C	15	G	3.7
1	C	26	A	3.7
1	D	7	G	3.7
1	B	73	A	3.6
1	B	7	G	3.6
1	C	46	G	3.6
1	A	25	C	3.6
2	G	332	THR	3.6
1	C	34	G	3.6
1	D	28	U	3.6
1	C	49	G	3.5
1	D	29	G	3.5
1	A	8	U	3.5
1	B	6	G	3.5
1	A	65	C	3.5
1	D	47	U	3.4
1	A	19	G	3.4
1	D	49	G	3.4
1	A	37	A	3.4
1	B	29	G	3.4
1	D	69	G	3.4
1	D	12	U	3.4
1	D	16	U	3.4
1	C	38	A	3.4
2	H	387	PHE	3.4
1	C	57	G	3.4
1	C	27	C	3.4
1	B	52	G	3.3
1	D	1	G	3.3
2	H	343	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	45	U	3.3
1	C	11	C	3.3
1	D	64	C	3.3
1	B	42	A	3.3
1	B	58	A	3.3
2	E	86	GLU	3.3
1	A	56	C	3.3
1	C	31	A	3.3
2	G	25	ASP	3.3
2	H	165	ASP	3.3
1	D	56	C	3.2
2	H	310	GLY	3.2
1	B	32	C	3.2
1	C	19	G	3.2
2	H	26	ASP	3.2
2	F	34	GLU	3.2
1	A	58	A	3.1
1	B	35	A	3.1
1	C	41	C	3.1
1	D	35	A	3.1
2	E	263	LYS	3.1
1	A	41	C	3.1
1	D	62	C	3.1
1	C	24	G	3.1
1	A	40	C	3.1
1	D	66	C	3.1
2	E	262	VAL	3.1
1	B	14	A	3.1
2	G	160	THR	3.1
1	B	55	U	3.0
1	A	6	G	3.0
1	A	18	G	3.0
1	A	29	G	3.0
1	B	22	G	3.0
1	B	41	C	3.0
1	C	56	C	3.0
1	A	55	U	3.0
1	C	17	U	3.0
2	F	343	TYR	3.0
1	C	10	G	3.0
2	G	329	LYS	3.0
2	H	264	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	27	C	3.0
1	C	65	C	3.0
1	D	61	C	3.0
2	F	81	HIS	3.0
2	H	427	GLU	3.0
2	E	438	GLU	2.9
2	F	86	GLU	2.9
1	B	66	C	2.9
2	H	426	GLU	2.9
1	B	67	C	2.9
1	C	68	U	2.9
2	G	155	ILE	2.9
2	E	81	HIS	2.9
2	H	334	ALA	2.9
2	G	330	PRO	2.9
2	G	437	ALA	2.8
1	D	67	C	2.8
1	D	70	G	2.8
1	C	55	U	2.8
2	G	441	SER	2.8
2	H	329	LYS	2.8
2	H	388	LYS	2.8
1	B	28	U	2.8
2	G	333	PHE	2.8
2	G	81	HIS	2.7
1	B	56	C	2.7
2	G	386	ALA	2.7
2	H	95	PRO	2.7
2	H	292	ALA	2.7
2	H	363	GLY	2.7
1	C	3	C	2.7
1	C	69	G	2.7
2	G	37	CYS	2.7
2	E	427	GLU	2.7
2	H	293	LYS	2.7
1	C	64	C	2.7
2	H	328	GLY	2.7
2	H	396	GLY	2.7
2	E	426	GLU	2.7
2	F	52	PRO	2.6
2	E	328	GLY	2.6
2	E	390	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
2	H	16	GLY	2.6
1	A	60	U	2.6
2	G	72	LYS	2.6
1	C	14	A	2.6
2	G	169	GLY	2.6
2	H	170	LEU	2.5
1	C	30	G	2.5
1	A	64	C	2.5
2	F	437	ALA	2.5
1	A	51	C	2.5
1	A	28	U	2.5
2	E	17	LEU	2.5
2	H	403	GLU	2.5
2	F	427	GLU	2.5
2	G	58	ASP	2.5
2	G	157	TYR	2.5
2	E	425	GLU	2.4
2	F	344	GLU	2.4
2	G	344	GLU	2.4
1	A	61	C	2.4
1	C	47	U	2.4
1	A	42	A	2.4
2	H	444	ARG	2.4
2	H	418	ASP	2.4
2	E	387	PHE	2.4
2	H	262	VAL	2.4
2	G	326	ASP	2.4
1	C	12	U	2.4
1	C	37	A	2.3
2	G	96	THR	2.3
1	A	57	G	2.3
2	G	119	LYS	2.3
1	C	35	A	2.3
2	G	405	GLY	2.3
2	H	361	ARG	2.3
2	F	211	ASP	2.3
1	B	25	C	2.3
1	B	61	C	2.3
2	F	67	PRO	2.3
2	G	42	GLY	2.3
1	A	48	C	2.3
2	G	159	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	H	330	PRO	2.2
2	H	397	MET	2.2
2	G	68	VAL	2.2
2	F	17	LEU	2.2
2	H	211	ASP	2.2
1	A	52	G	2.2
2	E	444	ARG	2.2
1	C	4	C	2.2
2	H	326	ASP	2.2
2	G	71	ALA	2.2
1	C	70	G	2.2
2	G	162	GLY	2.2
2	H	405	GLY	2.2
2	F	441	SER	2.1
2	H	358	GLU	2.1
2	F	121	LEU	2.1
1	C	66	C	2.1
2	G	36	TYR	2.1
2	F	426	GLU	2.1
2	H	438	GLU	2.1
2	G	67	PRO	2.1
2	F	136	ALA	2.1
1	C	72	C	2.1
2	H	272	PRO	2.1
2	H	386	ALA	2.1
2	F	56	ASN	2.1
2	F	262	VAL	2.1
2	E	344	GLU	2.0
2	G	117	LYS	2.0
2	G	365	GLU	2.0
2	H	399	ASN	2.0
2	E	343	TYR	2.0
2	G	33	ARG	2.0
2	F	365	GLU	2.0
2	H	434	GLU	2.0
2	E	83	PHE	2.0
2	E	397	MET	2.0
2	H	425	GLU	2.0
2	G	66	ASP	2.0
2	H	348	VAL	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 oligosaccharides 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.