



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:43 PM GMT

PDB ID : 4FWT
Title : Complex structure of viral RNA polymerase form III
Authors : Takeshita, D.; Tomita, K.
Deposited on : 2012-07-02
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
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

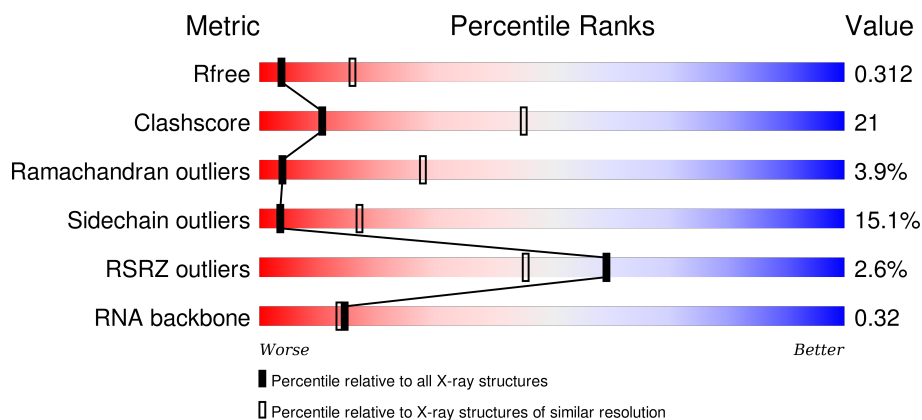
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)
RNA backbone	2183	1079 (3.70-2.70)

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	1289	
2	G	8	
3	T	8	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GTP	A	2501	-	-	X	-
5	CA	A	2503	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9582 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 Elongation factor Ts, Elongation factor Tu, LINKER, Q beta replicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1203	Total	C	N	O	S	0	0	0
			9287	5865	1605	1772	45			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	284	HIS	-	LINKER	UNP P0A6P3
A	1284	HIS	-	EXPRESSION TAG	UNP Q8LTE0
A	1285	HIS	-	EXPRESSION TAG	UNP Q8LTE0
A	1286	HIS	-	EXPRESSION TAG	UNP Q8LTE0
A	1287	HIS	-	EXPRESSION TAG	UNP Q8LTE0
A	1288	HIS	-	EXPRESSION TAG	UNP Q8LTE0
A	1289	HIS	-	EXPRESSION TAG	UNP Q8LTE0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	7	Total	C	N	O	P	0	0	1
			122	55	19	42	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	6	Total	C	N	O	P	0	0	0
			131	59	27	40	5			

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Ca	0	0
			2	2		

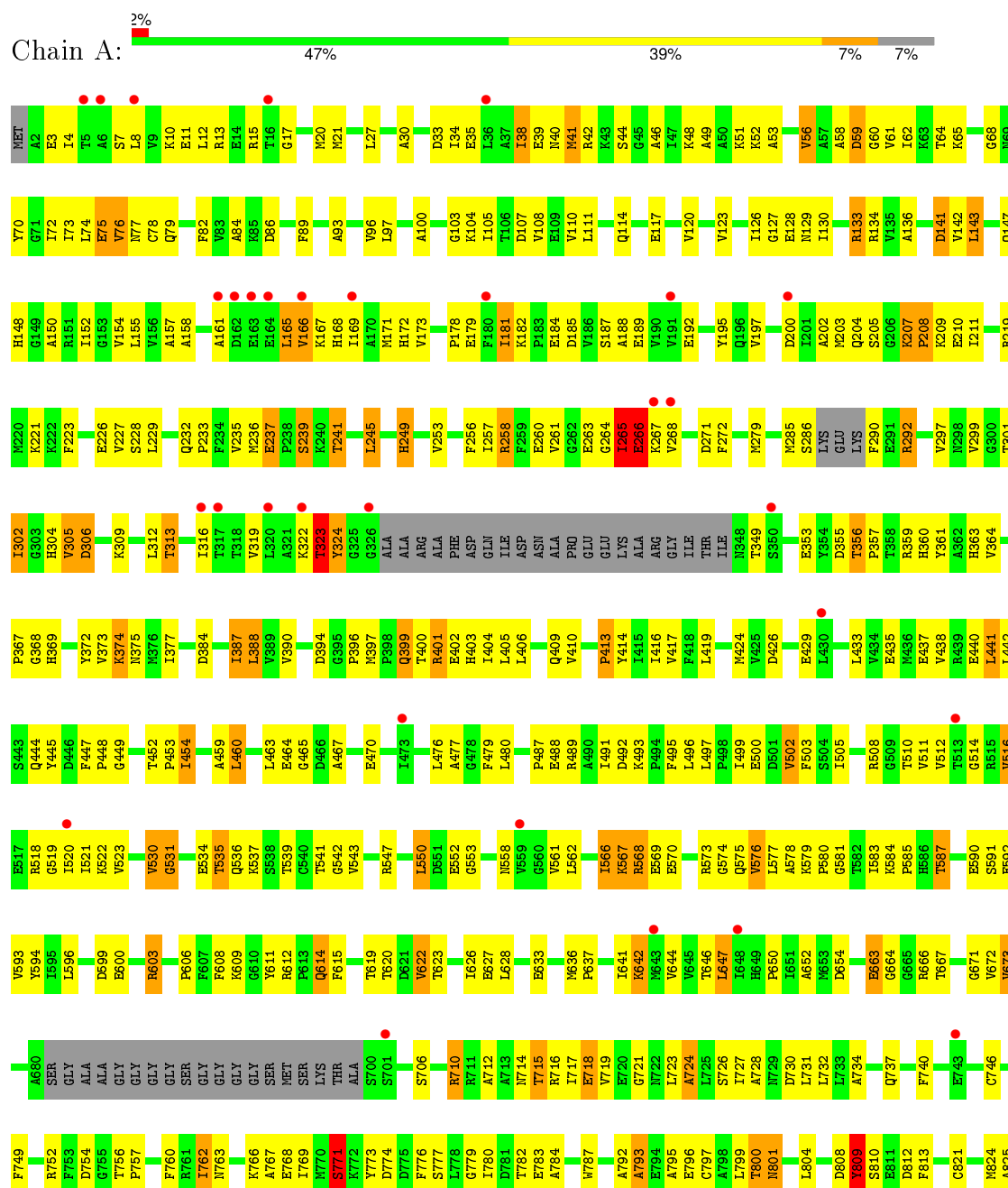
- Molecule 6 is water.

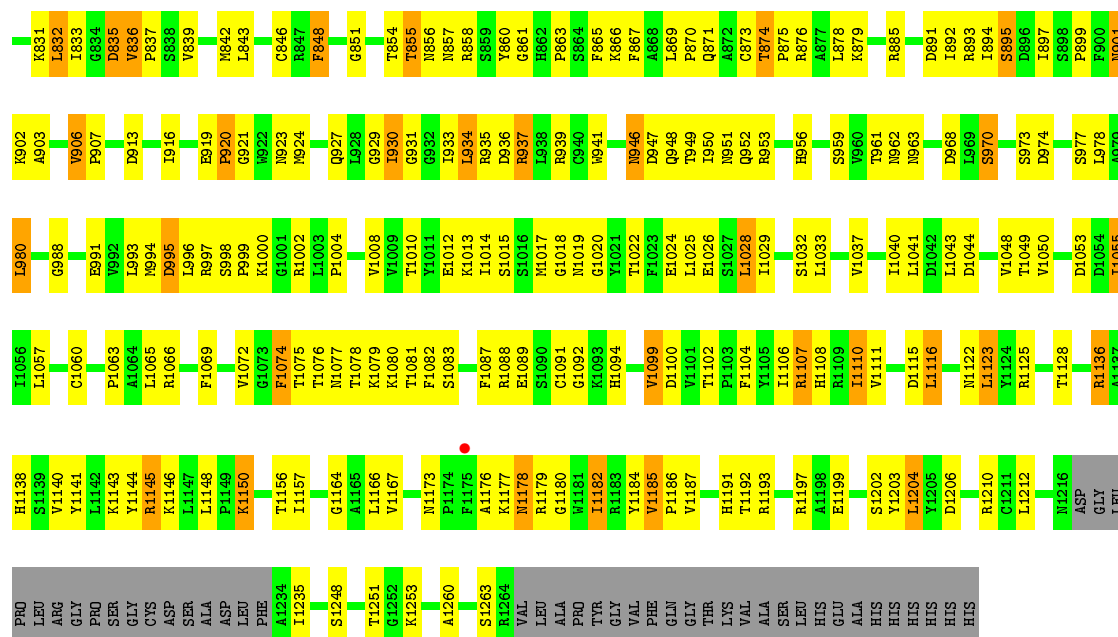
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	O	0	0
			8	8		

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: Elongation factor Ts, Elongation factor Tu, LINKER, Q beta replicase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	137.51Å 255.05Å 100.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 46.57 – 3.10	Depositor EDS
% Data completeness (in resolution range)	90.2 (20.00-3.20) 89.3 (46.57-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.245 , 0.314 0.240 , 0.312	Depositor DCC
R_{free} test set	1357 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	61.1	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 23.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	0 of 29109 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	9582	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.48	0/9456	0.69	3/12787 (0.0%)
2	G	0.99	1/134 (0.7%)	0.80	0/206
3	T	0.50	0/147	0.66	0/229
All	All	0.49	1/9737 (0.0%)	0.70	3/13222 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2002	C	O3'-P	-9.87	1.49	1.61

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	GLU	N-CA-CB	-11.03	90.75	110.60
1	A	934	LEU	CA-CB-CG	5.92	128.91	115.30
1	A	266	GLU	N-CA-C	5.65	126.24	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9287	0	9273	396	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	122	0	64	5	0
3	T	131	0	67	3	0
4	A	32	0	12	11	0
5	A	2	0	0	0	0
6	A	8	0	0	0	0
All	All	9582	0	9416	402	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 21.

All (402) 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:A:265:ILE:CG2	1:A:265:ILE:O	2.05	1.01
1:A:1094:HIS:H	1:A:1102:THR:HG22	1.27	0.97
1:A:1018:GLY:H	4:A:2501:GTP:HN21	1.02	0.91
1:A:265:ILE:O	1:A:265:ILE:HG22	1.69	0.90
1:A:710:ARG:O	1:A:714:ASN:ND2	2.05	0.88
1:A:1018:GLY:N	4:A:2501:GTP:HN21	1.71	0.88
1:A:491:ILE:HG23	1:A:520:ILE:HD11	1.59	0.85
1:A:264:GLY:C	1:A:266:GLU:H	1.80	0.84
1:A:1018:GLY:H	4:A:2501:GTP:N2	1.75	0.84
1:A:356:THR:HG22	1:A:359:ARG:H	1.42	0.84
1:A:558:ASN:HB3	1:A:1210:ARG:HD3	1.61	0.81
1:A:593:VAL:HG12	1:A:671:GLY:HA3	1.64	0.80
1:A:226:GLU:O	1:A:232:GLN:NE2	2.14	0.79
1:A:768:GLU:O	1:A:771:SER:OG	2.00	0.79
1:A:1050:VAL:HG13	1:A:1055:ILE:HG22	1.67	0.76
1:A:949:THR:HG22	1:A:953:ARG:HD3	1.67	0.76
1:A:523:VAL:HG12	1:A:542:GLY:HA2	1.66	0.76
1:A:961:THR:HG22	1:A:963:ASN:H	1.50	0.75
1:A:178:PRO:HG3	1:A:229:LEU:HD13	1.66	0.75
1:A:387:ILE:HD11	1:A:476:LEU:HD11	1.68	0.75
1:A:839:VAL:HA	1:A:842:MET:HB3	1.69	0.74
1:A:65:LYS:HB2	1:A:97:LEU:HD11	1.69	0.73
1:A:265:ILE:O	1:A:265:ILE:HG23	1.87	0.73
1:A:1206:ASP:OD1	1:A:1210:ARG:NH1	2.22	0.73
1:A:401:ARG:HB3	1:A:441:LEU:HD21	1.71	0.73
1:A:467:ALA:HA	1:A:470:GLU:HB2	1.71	0.72
1:A:505:ILE:HB	1:A:508:ARG:HB2	1.70	0.72
1:A:797:CYS:O	1:A:801:ASN:ND2	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1092:GLY:HA3	2:G:2007:C:H4'	1.71	0.71
1:A:372:TYR:CE1	1:A:410:VAL:HG21	2.26	0.71
1:A:530:VAL:HG22	1:A:652:ALA:HB2	1.72	0.70
1:A:377:ILE:HG23	1:A:671:GLY:HA2	1.74	0.70
1:A:301:THR:HA	1:A:387:ILE:HG22	1.73	0.70
1:A:550:LEU:HD13	1:A:550:LEU:H	1.55	0.70
1:A:158:ALA:HA	1:A:253:VAL:HA	1.74	0.69
1:A:951:ASN:HD22	1:A:1049:THR:HG22	1.58	0.69
1:A:867:PHE:HB3	1:A:1204:LEU:HD13	1.75	0.69
1:A:946:ASN:HA	3:T:2103:G:H4'	1.74	0.68
1:A:543:VAL:HG13	1:A:561:VAL:HG22	1.73	0.68
1:A:1015:SER:HB3	1:A:1022:THR:OG1	1.94	0.67
1:A:792:ALA:HA	1:A:795:ALA:HB3	1.77	0.67
1:A:21:MET:HG3	1:A:424:MET:O	1.95	0.67
1:A:264:GLY:C	1:A:266:GLU:N	2.48	0.67
1:A:836:VAL:HG22	1:A:837:PRO:HD2	1.76	0.66
1:A:510:THR:OG1	1:A:566:ILE:O	2.07	0.66
2:G:2007:C:O2	3:T:2102:G:N2	2.19	0.66
1:A:970:SER:HB2	1:A:1075:THR:HG23	1.78	0.66
1:A:854:THR:HG22	1:A:920:PRO:HA	1.78	0.65
1:A:1094:HIS:N	1:A:1102:THR:HG22	2.08	0.65
1:A:592:GLU:HG2	1:A:642:LYS:HG2	1.79	0.65
1:A:442:LEU:HD12	1:A:452:THR:HG21	1.78	0.65
1:A:56:VAL:HG11	1:A:267:LYS:HD3	1.79	0.64
1:A:264:GLY:O	1:A:266:GLU:N	2.28	0.64
1:A:953:ARG:O	1:A:956:HIS:HB3	1.97	0.64
1:A:968:ASP:H	1:A:1081:THR:HG22	1.63	0.63
1:A:62:ILE:HD11	1:A:260:GLU:O	1.99	0.63
1:A:1077:ASN:O	1:A:1081:THR:HG23	1.98	0.63
1:A:846:CYS:SG	1:A:929:GLY:HA3	2.39	0.62
1:A:502:VAL:O	1:A:1197:ARG:NH1	2.31	0.62
1:A:304:HIS:HD2	1:A:306:ASP:H	1.46	0.62
1:A:301:THR:HB	1:A:363:HIS:NE2	2.15	0.62
1:A:594:TYR:OH	1:A:600:GLU:OE1	2.10	0.62
1:A:167:LYS:HG2	1:A:171:MET:HE3	1.81	0.62
1:A:740:PHE:CE2	1:A:746:CYS:HA	2.34	0.62
1:A:165:LEU:O	1:A:168:HIS:N	2.32	0.62
1:A:76:VAL:HG11	1:A:93:ALA:HB1	1.82	0.61
1:A:611:TYR:HB3	1:A:626:ILE:HD11	1.82	0.61
1:A:860:TYR:HA	1:A:865:PHE:HD1	1.64	0.61
1:A:1083:SER:O	1:A:1088:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:499:ILE:HD12	1:A:512:VAL:HG11	1.81	0.61
1:A:590:GLU:HG3	1:A:644:VAL:HG22	1.83	0.61
1:A:717:ILE:HD12	1:A:718:GLU:H	1.64	0.61
1:A:663:GLU:HG3	1:A:1182:ILE:HD12	1.83	0.61
1:A:835:ASP:N	1:A:835:ASP:OD2	2.22	0.60
1:A:312:LEU:O	1:A:316:ILE:HG13	2.00	0.60
1:A:614:GLN:HA	1:A:623:THR:HA	1.82	0.60
1:A:1164:GLY:HA3	1:A:1187:VAL:HB	1.84	0.60
1:A:322:LYS:NZ	1:A:470:GLU:OE2	2.27	0.60
1:A:615:PHE:N	1:A:622:VAL:O	2.33	0.60
1:A:93:ALA:HA	1:A:96:VAL:HG12	1.83	0.59
1:A:20:MET:H	1:A:394:ASP:HA	1.68	0.59
1:A:923:ASN:HB3	1:A:927:GLN:HE21	1.67	0.59
1:A:304:HIS:CD2	1:A:306:ASP:H	2.20	0.59
1:A:935:ARG:NH2	1:A:1024:GLU:OE1	2.36	0.58
1:A:530:VAL:HG13	1:A:576:VAL:HG22	1.85	0.58
1:A:369:HIS:NE2	1:A:406:LEU:HD23	2.19	0.58
1:A:62:ILE:HG23	1:A:74:LEU:O	2.03	0.58
1:A:851:GLY:HA2	1:A:861:GLY:HA3	1.85	0.58
1:A:752:ARG:NH1	1:A:754:ASP:OD1	2.37	0.57
1:A:951:ASN:ND2	1:A:1049:THR:HG22	2.20	0.57
1:A:949:THR:CG2	1:A:953:ARG:HD3	2.33	0.57
1:A:534:GLU:O	1:A:536:GLN:N	2.37	0.57
1:A:155:LEU:O	1:A:257:ILE:N	2.26	0.57
1:A:70:TYR:OH	1:A:100:ALA:O	2.22	0.57
1:A:769:ILE:HG12	1:A:1106:ILE:HG12	1.84	0.57
1:A:1026:GLU:OE2	4:A:2501:GTP:O2'	2.19	0.57
1:A:885:ARG:NH1	1:A:892:ILE:H	2.03	0.57
1:A:1100:ASP:OD1	1:A:1102:THR:HG23	2.04	0.57
1:A:1069:PHE:HA	1:A:1072:VAL:HG22	1.87	0.57
1:A:404:ILE:HD12	1:A:441:LEU:HD22	1.87	0.57
1:A:372:TYR:HE1	1:A:410:VAL:HG11	1.69	0.56
4:A:2501:GTP:O4'	2:G:2008:C:H2'	2.05	0.56
1:A:609:LYS:HA	1:A:628:LEU:HD23	1.87	0.56
1:A:417:VAL:HB	1:A:454:ILE:HD13	1.87	0.56
1:A:773:TYR:HA	1:A:1107:ARG:O	2.05	0.56
1:A:61:VAL:HG13	1:A:84:ALA:HB1	1.88	0.56
1:A:369:HIS:CD2	1:A:406:LEU:HD23	2.41	0.56
1:A:732:LEU:HD13	1:A:766:LYS:HE2	1.88	0.56
1:A:61:VAL:HG22	1:A:89:PHE:HE1	1.71	0.56
1:A:1141:TYR:O	1:A:1145:ARG:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:LYS:HG3	1:A:268:VAL:H	1.70	0.55
1:A:59:ASP:O	1:A:77:ASN:HB2	2.06	0.55
1:A:78:CYS:HB3	1:A:89:PHE:CE2	2.41	0.55
1:A:899:PRO:HB2	1:A:999:PRO:HG2	1.87	0.55
1:A:734:ALA:O	1:A:1136:ARG:HB2	2.07	0.55
1:A:107:ASP:HB3	1:A:110:VAL:HG23	1.87	0.55
1:A:760:PHE:O	1:A:763:ASN:N	2.40	0.55
1:A:878:LEU:HD13	1:A:897:ILE:HD11	1.88	0.55
1:A:12:LEU:HD22	1:A:27:LEU:HD13	1.88	0.55
1:A:901:ASN:H	1:A:901:ASN:HD22	1.53	0.55
1:A:236:MET:HG2	1:A:608:PHE:CZ	2.42	0.54
1:A:1087:PHE:O	1:A:1088:ARG:NH2	2.39	0.54
1:A:404:ILE:HD13	1:A:442:LEU:HD23	1.89	0.54
1:A:723:LEU:HD23	1:A:1110:ILE:HG12	1.89	0.54
1:A:134:ARG:NH1	1:A:263:GLU:OE2	2.41	0.54
1:A:782:THR:OG1	1:A:783:GLU:N	2.40	0.54
1:A:1185:VAL:HG12	1:A:1186:PRO:HD2	1.90	0.54
1:A:208:PRO:HD2	1:A:211:ILE:HG13	1.90	0.54
1:A:8:LEU:HG	1:A:11:GLU:HB2	1.90	0.53
1:A:396:PRO:HG3	1:A:437:GLU:O	2.08	0.53
1:A:192:GLU:HA	1:A:195:TYR:HB3	1.89	0.53
1:A:902:LYS:NZ	1:A:1002:ARG:HH12	2.06	0.53
1:A:74:LEU:HD21	1:A:96:VAL:HG13	1.91	0.53
1:A:272:PHE:CZ	1:A:313:THR:HG21	2.43	0.53
1:A:309:LYS:O	1:A:313:THR:HG22	2.08	0.53
1:A:836:VAL:HG23	1:A:988:GLY:HA3	1.90	0.53
1:A:290:PHE:N	1:A:292:ARG:HH21	2.06	0.53
1:A:1074:PHE:CD2	1:A:1074:PHE:N	2.76	0.52
1:A:919:GLU:OE2	1:A:998:SER:HB2	2.08	0.52
1:A:927:GLN:OE1	1:A:1020:GLY:N	2.33	0.52
1:A:271:ASP:OD1	1:A:272:PHE:N	2.42	0.52
1:A:757:PRO:HB3	1:A:1099:VAL:HG11	1.92	0.52
1:A:496:LEU:HD11	1:A:576:VAL:HB	1.90	0.52
1:A:373:VAL:C	1:A:375:ASN:H	2.13	0.52
1:A:152:ILE:HG12	1:A:260:GLU:HG3	1.90	0.52
1:A:60:GLY:HA3	1:A:77:ASN:HB2	1.91	0.51
1:A:400:THR:HA	1:A:403:HIS:ND1	2.24	0.51
1:A:426:ASP:OD1	1:A:426:ASP:N	2.44	0.51
1:A:793:ALA:HB1	1:A:974:ASP:HB3	1.93	0.51
1:A:1136:ARG:HD3	1:A:1136:ARG:H	1.74	0.51
1:A:946:ASN:N	1:A:946:ASN:OD1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:931:GLY:O	1:A:1024:GLU:HG2	2.10	0.51
1:A:38:ILE:HA	1:A:41:MET:HG3	1.92	0.51
1:A:128:GLU:O	1:A:130:ILE:N	2.43	0.51
1:A:809:TYR:HE1	1:A:812:ASP:HA	1.76	0.51
1:A:1156:THR:O	1:A:1173:ASN:ND2	2.43	0.51
1:A:919:GLU:HB2	1:A:924:MET:HG2	1.93	0.51
1:A:724:ALA:O	1:A:727:ILE:N	2.44	0.51
1:A:40:ASN:O	1:A:44:SER:OG	2.27	0.51
1:A:497:LEU:HD12	1:A:516:VAL:HB	1.93	0.50
1:A:870:PRO:HB2	1:A:895:SER:HB3	1.93	0.50
1:A:73:ILE:HG12	1:A:74:LEU:H	1.76	0.50
1:A:267:LYS:NZ	1:A:268:VAL:O	2.45	0.50
1:A:1116:LEU:HB3	1:A:1148:LEU:HD21	1.92	0.50
1:A:749:PHE:CD1	1:A:767:ALA:HB2	2.47	0.50
1:A:1150:LYS:HD2	1:A:1150:LYS:H	1.75	0.50
1:A:267:LYS:CG	1:A:268:VAL:H	2.24	0.50
1:A:1077:ASN:ND2	1:A:1080:LYS:HD3	2.27	0.50
1:A:581:GLY:HA2	1:A:584:LYS:HE2	1.92	0.50
1:A:285:MET:O	1:A:286:SER:OG	2.28	0.50
1:A:951:ASN:HD22	1:A:1049:THR:CG2	2.25	0.50
1:A:857:ASN:O	1:A:860:TYR:N	2.42	0.50
1:A:1192:THR:HB	1:A:1248:SER:HB3	1.94	0.50
1:A:784:ALA:HA	1:A:787:TRP:HD1	1.77	0.50
1:A:712:ALA:O	1:A:715:THR:HB	2.12	0.50
1:A:495:PHE:HA	1:A:519:GLY:HA3	1.94	0.50
1:A:388:LEU:HB3	1:A:417:VAL:HG22	1.93	0.49
1:A:824:MET:HE1	1:A:1040:ILE:HD13	1.92	0.49
1:A:1104:PHE:HZ	1:A:1123:LEU:HD12	1.75	0.49
1:A:531:GLY:HA3	1:A:575:GLN:HG2	1.93	0.49
1:A:856:ASN:ND2	1:A:865:PHE:O	2.42	0.49
1:A:499:ILE:HD11	1:A:577:LEU:HB2	1.93	0.49
1:A:512:VAL:HG21	1:A:577:LEU:HD22	1.94	0.49
1:A:606:PRO:HB3	1:A:636:MET:HG2	1.94	0.49
1:A:20:MET:HA	1:A:20:MET:HE3	1.94	0.49
1:A:82:PHE:HE1	1:A:406:LEU:HB2	1.78	0.49
1:A:435:GLU:HA	1:A:438:VAL:HG12	1.94	0.49
1:A:447:PHE:O	1:A:449:GLY:N	2.39	0.49
1:A:591:SER:OG	1:A:592:GLU:N	2.46	0.49
1:A:1191:HIS:CD2	1:A:1192:THR:H	2.31	0.49
1:A:48:LYS:O	1:A:51:LYS:HB3	2.13	0.49
1:A:1017:MET:HG2	4:A:2501:GTP:C2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ILE:O	1:A:147:GLN:NE2	2.45	0.49
1:A:567:LYS:HG3	1:A:570:GLU:OE1	2.13	0.49
1:A:930:ILE:HG13	1:A:931:GLY:N	2.28	0.48
1:A:980:LEU:CD1	1:A:1072:VAL:HB	2.43	0.48
4:A:2501:GTP:C8	2:G:2008:C:C4	3.00	0.48
1:A:558:ASN:HB3	1:A:1210:ARG:HB3	1.95	0.48
1:A:930:ILE:HA	1:A:933:ILE:HG22	1.95	0.48
1:A:534:GLU:O	1:A:536:GLN:HG3	2.13	0.48
1:A:521:ILE:O	1:A:553:GLY:N	2.36	0.48
1:A:356:THR:CG2	1:A:359:ARG:H	2.20	0.48
1:A:1066:ARG:HH22	1:A:1078:THR:HG22	1.79	0.48
1:A:500:GLU:OE1	1:A:1210:ARG:NH2	2.46	0.48
1:A:1191:HIS:HB3	1:A:1251:THR:OG1	2.14	0.48
1:A:1050:VAL:HA	1:A:1055:ILE:HA	1.95	0.48
1:A:1037:VAL:O	1:A:1040:ILE:HG22	2.13	0.48
1:A:821:CYS:O	1:A:825:ALA:N	2.38	0.48
1:A:142:VAL:HG11	1:A:161:ALA:O	2.14	0.48
1:A:723:LEU:O	1:A:727:ILE:HG13	2.14	0.48
1:A:405:LEU:HB2	1:A:445:TYR:HE2	1.78	0.48
1:A:923:ASN:HB3	1:A:927:GLN:NE2	2.27	0.47
1:A:460:LEU:HA	1:A:463:LEU:HD12	1.96	0.47
1:A:319:VAL:O	1:A:323:THR:OG1	2.31	0.47
1:A:72:ILE:HD12	1:A:136:ALA:O	2.15	0.47
1:A:977:SER:HB2	1:A:980:LEU:H	1.80	0.47
1:A:46:ALA:HA	1:A:49:ALA:HB3	1.96	0.47
1:A:356:THR:HG22	1:A:359:ARG:N	2.22	0.47
1:A:126:ILE:HG23	1:A:399:GLN:NE2	2.30	0.47
1:A:1173:ASN:HB3	1:A:1176:ALA:HB2	1.97	0.47
1:A:272:PHE:HZ	1:A:313:THR:HG21	1.79	0.47
1:A:477:ALA:HA	1:A:480:LEU:HD23	1.97	0.46
1:A:103:GLY:O	1:A:105:ILE:N	2.48	0.46
1:A:377:ILE:CG2	1:A:671:GLY:HA2	2.44	0.46
1:A:585:PRO:HA	1:A:652:ALA:HA	1.97	0.46
1:A:361:TYR:CE1	1:A:480:LEU:HB3	2.50	0.46
1:A:459:ALA:O	1:A:463:LEU:HG	2.16	0.46
1:A:172:HIS:CE1	1:A:232:GLN:HG2	2.51	0.46
1:A:919:GLU:HG3	1:A:1019:ASN:HA	1.98	0.46
1:A:716:ARG:HB2	1:A:716:ARG:HE	1.63	0.46
1:A:179:GLU:H	1:A:227:VAL:HG23	1.80	0.46
1:A:301:THR:HG22	1:A:364:VAL:O	2.16	0.46
1:A:1018:GLY:N	4:A:2501:GTP:N2	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:933:ILE:O	1:A:937:ARG:HB2	2.16	0.46
1:A:1000:LYS:HE3	1:A:1010:THR:HG22	1.96	0.46
1:A:832:LEU:HG	1:A:941:TRP:NE1	2.30	0.46
1:A:219:ARG:HH22	1:A:223:PHE:HB2	1.80	0.46
1:A:324:TYR:CE1	1:A:357:PRO:HD3	2.51	0.46
1:A:980:LEU:HD13	1:A:1072:VAL:HB	1.97	0.46
1:A:39:GLU:OE1	1:A:42:ARG:NH2	2.49	0.46
1:A:493:LYS:HD3	1:A:518:ARG:HD3	1.98	0.46
1:A:664:GLY:HA3	1:A:1260:ALA:HB3	1.97	0.46
1:A:377:ILE:HD12	1:A:592:GLU:O	2.16	0.46
1:A:719:VAL:HG21	1:A:723:LEU:HD13	1.98	0.46
1:A:202:ALA:HB1	1:A:207:LYS:HD2	1.98	0.46
1:A:1143:LYS:HA	1:A:1146:LYS:HE2	1.97	0.46
1:A:440:GLU:O	1:A:444:GLN:HG3	2.16	0.46
1:A:15:ARG:NH1	1:A:38:ILE:HD13	2.31	0.46
1:A:103:GLY:O	1:A:105:ILE:HG13	2.16	0.46
1:A:503:PHE:CD1	1:A:1203:TYR:HD2	2.34	0.46
1:A:808:ASP:O	1:A:810:SER:N	2.49	0.46
1:A:947:ASP:OD1	1:A:949:THR:HB	2.16	0.45
1:A:34:ILE:O	1:A:38:ILE:HG23	2.17	0.45
1:A:993:LEU:O	1:A:997:ARG:HB3	2.17	0.45
1:A:58:ALA:HA	1:A:265:ILE:HG21	1.98	0.45
1:A:219:ARG:NH2	1:A:223:PHE:HB2	2.32	0.45
1:A:416:ILE:HG23	1:A:453:PRO:HG2	1.97	0.45
1:A:647:LEU:HG	1:A:647:LEU:H	1.52	0.45
1:A:1122:ASN:OD1	1:A:1125:ARG:NH2	2.48	0.45
1:A:861:GLY:O	1:A:866:LYS:NZ	2.34	0.45
1:A:949:THR:C	1:A:951:ASN:H	2.20	0.45
1:A:1033:LEU:O	1:A:1037:VAL:HG23	2.15	0.45
1:A:187:SER:C	1:A:189:GLU:H	2.19	0.45
1:A:948:GLN:HB2	1:A:1091:CYS:SG	2.57	0.45
1:A:800:THR:O	1:A:804:LEU:HB2	2.17	0.45
1:A:228:SER:O	1:A:232:GLN:HB2	2.17	0.45
1:A:143:LEU:HA	1:A:157:ALA:HA	1.97	0.45
1:A:848:PHE:HD2	1:A:867:PHE:CZ	2.34	0.45
1:A:723:LEU:HD23	1:A:1110:ILE:CG1	2.46	0.45
1:A:522:LYS:HA	1:A:552:GLU:HA	1.98	0.45
4:A:2501:GTP:C4'	2:G:2008:C:H2'	2.47	0.45
1:A:476:LEU:O	1:A:480:LEU:HD22	2.17	0.45
1:A:372:TYR:HE1	1:A:410:VAL:HG21	1.77	0.45
1:A:3:GLU:HG2	1:A:426:ASP:OD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1057:LEU:HD13	1:A:1065:LEU:HD22	1.99	0.45
1:A:715:THR:HG22	1:A:715:THR:O	2.17	0.45
1:A:487:PRO:O	1:A:489:ARG:N	2.50	0.45
1:A:626:ILE:HD12	1:A:626:ILE:O	2.17	0.44
1:A:866:LYS:HA	1:A:871:GLN:HE21	1.82	0.44
1:A:573:ARG:NH2	1:A:619:THR:O	2.50	0.44
1:A:1082:PHE:CD1	1:A:1087:PHE:HD1	2.36	0.44
1:A:1157:ILE:O	1:A:1167:VAL:HA	2.18	0.44
1:A:514:GLY:HA2	1:A:1210:ARG:NH2	2.32	0.44
1:A:927:GLN:HA	1:A:996:LEU:HD23	1.99	0.44
1:A:937:ARG:HD2	1:A:937:ARG:HA	1.86	0.44
1:A:734:ALA:HB1	1:A:1136:ARG:O	2.18	0.44
1:A:182:LYS:HB2	1:A:185:ASP:OD2	2.17	0.44
1:A:184:GLU:N	1:A:184:GLU:OE1	2.50	0.44
1:A:727:ILE:HG12	1:A:1144:TYR:CE2	2.53	0.44
1:A:583:ILE:HD11	1:A:652:ALA:C	2.38	0.44
1:A:1082:PHE:CE1	1:A:1087:PHE:CD1	3.06	0.44
1:A:612:ARG:HB3	1:A:1180:GLY:HA3	2.00	0.44
1:A:1017:MET:HG2	4:A:2501:GTP:N3	2.33	0.44
1:A:952:GLN:HB3	1:A:1091:CYS:HB2	1.99	0.44
1:A:949:THR:O	1:A:951:ASN:N	2.51	0.44
1:A:579:LYS:HG3	1:A:580:PRO:HD2	1.99	0.44
1:A:1178:ASN:OD1	1:A:1178:ASN:N	2.50	0.44
1:A:796:GLU:O	1:A:799:LEU:N	2.50	0.44
1:A:511:VAL:HB	1:A:562:LEU:HD23	1.99	0.44
1:A:120:VAL:HA	1:A:123:VAL:HG12	2.00	0.44
1:A:956:HIS:O	1:A:959:SER:OG	2.27	0.43
1:A:1179:ARG:HB2	1:A:1184:TYR:CD2	2.53	0.43
1:A:873:CYS:SG	1:A:874:THR:N	2.91	0.43
1:A:997:ARG:HD2	1:A:1014:ILE:O	2.19	0.43
1:A:369:HIS:CE1	1:A:406:LEU:HD23	2.53	0.43
1:A:1002:ARG:HG3	1:A:1008:VAL:HG12	2.00	0.43
1:A:355:ASP:OD1	1:A:360:HIS:ND1	2.40	0.43
4:A:2501:GTP:O2B	4:A:2501:GTP:H5''	2.18	0.43
1:A:304:HIS:CD2	1:A:305:VAL:N	2.87	0.43
1:A:1025:LEU:O	1:A:1029:ILE:HG12	2.18	0.43
1:A:442:LEU:HA	1:A:442:LEU:HD23	1.85	0.43
1:A:968:ASP:N	1:A:1081:THR:HG22	2.32	0.43
1:A:726:SER:HG	1:A:1144:TYR:HH	1.58	0.43
1:A:833:ILE:HD13	1:A:833:ILE:HA	1.85	0.43
1:A:64:THR:HG22	1:A:73:ILE:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:SER:HB2	1:A:207:LYS:HG2	2.00	0.43
1:A:574:GLY:HA3	1:A:620:THR:HG22	2.00	0.43
1:A:1082:PHE:CE1	1:A:1087:PHE:HD1	2.37	0.43
1:A:13:ARG:HH22	1:A:396:PRO:HD2	1.83	0.43
1:A:413:PRO:HB2	1:A:414:TYR:CD1	2.53	0.43
1:A:229:LEU:HA	1:A:229:LEU:HD12	1.80	0.43
1:A:1048:VAL:HG22	1:A:1057:LEU:HB2	2.00	0.43
1:A:413:PRO:HB2	1:A:414:TYR:HD1	1.84	0.43
1:A:1125:ARG:H	1:A:1125:ARG:HG3	1.66	0.42
1:A:233:PRO:HA	1:A:241:THR:HA	2.01	0.42
1:A:568:ARG:HH11	1:A:1199:GLU:CD	2.23	0.42
1:A:302:ILE:HG23	1:A:388:LEU:HD23	2.01	0.42
1:A:35:GLU:O	1:A:39:GLU:HG2	2.18	0.42
1:A:869:LEU:HA	1:A:870:PRO:HD2	1.76	0.42
1:A:906:VAL:HG23	1:A:907:PRO:HD2	2.00	0.42
1:A:126:ILE:HG22	1:A:127:GLY:N	2.33	0.42
1:A:368:GLY:O	1:A:372:TYR:N	2.52	0.42
1:A:728:ALA:O	1:A:732:LEU:HG	2.20	0.42
1:A:260:GLU:HG2	1:A:261:VAL:H	1.84	0.42
1:A:1156:THR:HA	1:A:1166:LEU:O	2.19	0.42
1:A:297:VAL:HG12	1:A:299:VAL:HG13	2.02	0.42
1:A:200:ASP:O	1:A:204:GLN:HB2	2.20	0.42
1:A:108:VAL:O	1:A:111:LEU:HD23	2.20	0.42
1:A:1019:ASN:HB3	1:A:1022:THR:OG1	2.20	0.42
1:A:1197:ARG:HD2	1:A:1202:SER:OG	2.20	0.42
1:A:12:LEU:HD12	1:A:12:LEU:HA	1.89	0.42
1:A:642:LYS:HE2	1:A:642:LYS:HB3	1.60	0.42
1:A:495:PHE:CZ	1:A:521:ILE:HB	2.55	0.42
1:A:737:GLN:HG3	1:A:762:ILE:CG2	2.50	0.42
1:A:978:LEU:HD23	1:A:978:LEU:HA	1.80	0.42
1:A:1177:LYS:HA	1:A:1177:LYS:HD3	1.81	0.42
1:A:876:ARG:NH2	1:A:995:ASP:OD2	2.53	0.42
1:A:27:LEU:HA	1:A:30:ALA:HB3	2.02	0.42
1:A:1110:ILE:HD12	1:A:1115:ASP:HB2	2.02	0.42
1:A:902:LYS:HZ2	1:A:1002:ARG:HH12	1.67	0.42
1:A:503:PHE:CG	1:A:1203:TYR:HB2	2.55	0.42
1:A:568:ARG:HH12	1:A:1197:ARG:HH11	1.68	0.41
1:A:316:ILE:HG22	1:A:316:ILE:O	2.20	0.41
1:A:568:ARG:NH1	1:A:1197:ARG:HH11	2.18	0.41
1:A:870:PRO:HB3	1:A:893:ARG:HB3	2.02	0.41
1:A:405:LEU:O	1:A:409:GLN:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ILE:HG23	1:A:185:ASP:OD1	2.20	0.41
1:A:171:MET:HE2	1:A:633:GLU:HG3	2.02	0.41
1:A:399:GLN:NE2	1:A:399:GLN:H	2.19	0.41
1:A:603:ARG:HG3	1:A:603:ARG:H	1.42	0.41
1:A:169:ILE:O	1:A:173:VAL:HG23	2.19	0.41
1:A:374:LYS:HG3	1:A:594:TYR:CE1	2.55	0.41
1:A:1028:LEU:O	1:A:1032:SER:HB2	2.20	0.41
1:A:73:ILE:HB	1:A:155:LEU:HD23	2.01	0.41
1:A:35:GLU:O	1:A:38:ILE:HG12	2.20	0.41
1:A:111:LEU:HA	1:A:114:GLN:HB3	2.02	0.41
1:A:166:VAL:HA	1:A:169:ILE:HG13	2.02	0.41
1:A:266:GLU:HB3	1:A:267:LYS:H	1.53	0.41
3:T:2103:G:H2'	3:T:2104:U:O4'	2.20	0.41
1:A:82:PHE:O	1:A:402:GLU:HG3	2.20	0.41
1:A:10:LYS:HG3	1:A:11:GLU:N	2.36	0.41
1:A:737:GLN:HG3	1:A:762:ILE:HG21	2.03	0.41
1:A:855:THR:OG1	1:A:871:GLN:OE1	2.30	0.41
1:A:730:ASP:OD2	1:A:1143:LYS:NZ	2.52	0.41
1:A:710:ARG:NH1	1:A:1253:LYS:HD3	2.36	0.41
1:A:74:LEU:HB2	1:A:97:LEU:HD23	2.02	0.41
1:A:550:LEU:CD1	1:A:550:LEU:H	2.30	0.41
1:A:731:LEU:O	1:A:734:ALA:HB3	2.21	0.41
1:A:870:PRO:HA	1:A:893:ARG:HB2	2.02	0.41
1:A:749:PHE:HD1	1:A:767:ALA:HB2	1.85	0.41
1:A:237:GLU:C	1:A:239:SER:H	2.23	0.41
1:A:245:LEU:HD22	1:A:245:LEU:O	2.20	0.41
1:A:731:LEU:HD13	1:A:1140:VAL:HG21	2.03	0.41
1:A:903:ALA:O	1:A:1004:PRO:HD3	2.21	0.41
1:A:75:GLU:HG3	1:A:133:ARG:HE	1.86	0.41
1:A:719:VAL:HG12	1:A:721:GLY:H	1.86	0.40
1:A:1000:LYS:HE2	1:A:1000:LYS:HB3	1.89	0.40
1:A:356:THR:HG23	1:A:357:PRO:HD2	2.04	0.40
1:A:874:THR:OG1	1:A:899:PRO:HA	2.21	0.40
1:A:13:ARG:O	1:A:17:GLY:N	2.54	0.40
1:A:1060:CYS:O	1:A:1063:PRO:HD2	2.21	0.40
1:A:991:GLU:O	1:A:994:MET:N	2.55	0.40
1:A:449:GLY:O	1:A:452:THR:HG22	2.21	0.40
1:A:496:LEU:HD13	1:A:578:ALA:HB2	2.04	0.40
1:A:453:PRO:HB2	1:A:479:PHE:CD2	2.56	0.40
1:A:245:LEU:O	1:A:249:HIS:HB2	2.21	0.40
1:A:591:SER:HB2	1:A:673:VAL:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:LEU:HD12	1:A:600:GLU:HB3	2.02	0.40
1:A:587:THR:HA	1:A:647:LEU:HD11	2.03	0.40
1:A:1079:LYS:HA	1:A:1079:LYS:HD3	1.79	0.40
1:A:1013:LYS:HE2	1:A:1013:LYS:HB3	1.81	0.40
1:A:154:VAL:HG12	1:A:258:ARG:CB	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
1	A	1193/1289 (93%)	995 (83%)	152 (13%)	46 (4%)	4 28

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	129	ASN
1	A	209	LYS
1	A	324	TYR
1	A	464	GLU
1	A	488	GLU
1	A	535	THR
1	A	777	SER
1	A	809	TYR
1	A	53	ALA
1	A	104	LYS
1	A	141	ASP
1	A	265	ILE
1	A	266	GLU
1	A	374	LYS
1	A	641	ILE

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Mol	Chain	Res	Type
1	A	801	ASN
1	A	895	SER
1	A	921	GLY
1	A	950	ILE
1	A	1107	ARG
1	A	1263	SER
1	A	68	GLY
1	A	208	PRO
1	A	323	THR
1	A	413	PRO
1	A	771	SER
1	A	779	GLY
1	A	863	PRO
1	A	465	GLY
1	A	724	ALA
1	A	780	ILE
1	A	793	ALA
1	A	813	PHE
1	A	150	ALA
1	A	188	ALA
1	A	448	PRO
1	A	879	LYS
1	A	1111	VAL
1	A	531	GLY
1	A	875	PRO
1	A	367	PRO
1	A	650	PRO
1	A	566	ILE
1	A	916	ILE
1	A	920	PRO

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	995/1060 (94%)	845 (85%)	150 (15%)	3 17

All (150) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	33	ASP
1	A	38	ILE
1	A	41	MET
1	A	52	LYS
1	A	56	VAL
1	A	59	ASP
1	A	75	GLU
1	A	76	VAL
1	A	79	GLN
1	A	86	ASP
1	A	117	GLU
1	A	133	ARG
1	A	141	ASP
1	A	143	LEU
1	A	148	HIS
1	A	165	LEU
1	A	166	VAL
1	A	181	ILE
1	A	197	VAL
1	A	203	MET
1	A	207	LYS
1	A	210	GLU
1	A	221	LYS
1	A	235	VAL
1	A	237	GLU
1	A	239	SER
1	A	241	THR
1	A	245	LEU
1	A	249	HIS
1	A	256	PHE
1	A	258	ARG
1	A	265	ILE
1	A	266	GLU
1	A	279	MET
1	A	292	ARG
1	A	302	ILE
1	A	305	VAL
1	A	306	ASP
1	A	313	THR
1	A	323	THR
1	A	349	THR

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Mol	Chain	Res	Type
1	A	353	GLU
1	A	356	THR
1	A	384	ASP
1	A	387	ILE
1	A	388	LEU
1	A	390	VAL
1	A	397	MET
1	A	399	GLN
1	A	401	ARG
1	A	419	LEU
1	A	429	GLU
1	A	433	LEU
1	A	441	LEU
1	A	454	ILE
1	A	460	LEU
1	A	492	ASP
1	A	502	VAL
1	A	516	VAL
1	A	530	VAL
1	A	535	THR
1	A	537	LYS
1	A	539	THR
1	A	541	THR
1	A	547	ARG
1	A	550	LEU
1	A	567	LYS
1	A	568	ARG
1	A	569	GLU
1	A	576	VAL
1	A	587	THR
1	A	599	ASP
1	A	603	ARG
1	A	614	GLN
1	A	622	VAL
1	A	627	GLU
1	A	637	PRO
1	A	642	LYS
1	A	646	THR
1	A	647	LEU
1	A	654	ASP
1	A	663	GLU
1	A	666	ARG

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Mol	Chain	Res	Type
1	A	667	THR
1	A	672	VAL
1	A	673	VAL
1	A	706	SER
1	A	710	ARG
1	A	715	THR
1	A	718	GLU
1	A	756	THR
1	A	762	ILE
1	A	771	SER
1	A	774	ASP
1	A	776	PHE
1	A	800	THR
1	A	809	TYR
1	A	831	LYS
1	A	832	LEU
1	A	835	ASP
1	A	836	VAL
1	A	843	LEU
1	A	848	PHE
1	A	855	THR
1	A	858	ARG
1	A	874	THR
1	A	891	ASP
1	A	894	ILE
1	A	901	ASN
1	A	906	VAL
1	A	913	ASP
1	A	930	ILE
1	A	934	LEU
1	A	936	ASP
1	A	937	ARG
1	A	939	ARG
1	A	946	ASN
1	A	962	ASN
1	A	970	SER
1	A	973	SER
1	A	980	LEU
1	A	995	ASP
1	A	1012	GLU
1	A	1028	LEU
1	A	1041	LEU

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Mol	Chain	Res	Type
1	A	1043	LEU
1	A	1044	ASP
1	A	1053	ASP
1	A	1055	ILE
1	A	1074	PHE
1	A	1076	THR
1	A	1089	GLU
1	A	1099	VAL
1	A	1108	HIS
1	A	1110	ILE
1	A	1116	LEU
1	A	1123	LEU
1	A	1128	THR
1	A	1136	ARG
1	A	1138	HIS
1	A	1145	ARG
1	A	1150	LYS
1	A	1178	ASN
1	A	1182	ILE
1	A	1185	VAL
1	A	1193	ARG
1	A	1204	LEU
1	A	1212	LEU
1	A	1235	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	369	HIS
1	A	951	ASN
1	A	1191	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	G	4/8 (50%)	1 (25%)	0
3	T	5/8 (62%)	2 (40%)	0
All	All	9/16 (56%)	3 (33%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	G	2004	U
3	T	2103	G
3	T	2105	A

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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GTP	A	2501	5	25,34,34	1.13	3 (12%)	34,54,54	2.12	9 (26%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GTP	A	2501	5	-	0/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2501	GTP	C6-C5	2.14	1.45	1.41
4	A	2501	GTP	C6-N1	2.34	1.37	1.33
4	A	2501	GTP	O4'-C1'	2.95	1.44	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2501	GTP	C2'-C1'-N9	-6.17	104.86	114.29
4	A	2501	GTP	C5-C6-N1	-4.44	117.51	123.59
4	A	2501	GTP	N3-C2-N1	-4.11	121.18	127.44
4	A	2501	GTP	C4'-O4'-C1'	-3.15	106.25	109.72
4	A	2501	GTP	C4-C5-N7	-3.04	106.68	109.48
4	A	2501	GTP	C6-C5-C4	-2.07	118.43	120.90
4	A	2501	GTP	O2B-PB-O3B	2.23	115.22	105.09
4	A	2501	GTP	N2-C2-N1	2.90	122.00	117.20
4	A	2501	GTP	C6-N1-C2	4.51	122.20	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2501	GTP	11	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1203/1289 (93%)	-0.04	32 (2%) 58 44	46, 94, 142, 200	0
2	G	7/8 (87%)	1.24	0 100 100	139, 187, 216, 222	0
3	T	6/8 (75%)	0.23	0 100 100	126, 164, 171, 181	0
All	All	1216/1305 (93%)	-0.03	32 (2%) 59 45	46, 94, 145, 222	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	ALA	6.5
1	A	268	VAL	6.2
1	A	162	ASP	3.9
1	A	520	ILE	3.9
1	A	743	GLU	3.8
1	A	6	ALA	3.3
1	A	163	GLU	3.3
1	A	350	SER	3.1
1	A	320	LEU	3.1
1	A	267	LYS	3.1
1	A	513	THR	3.0
1	A	191	VAL	2.8
1	A	166	VAL	2.8
1	A	16	THR	2.7
1	A	701	SER	2.7
1	A	559	VAL	2.7
1	A	643	MET	2.5
1	A	648	ILE	2.5
1	A	5	THR	2.4
1	A	317	THR	2.4
1	A	326	GLY	2.4
1	A	169	ILE	2.3
1	A	36	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	164	GLU	2.3
1	A	316	ILE	2.2
1	A	322	LYS	2.2
1	A	200	ASP	2.2
1	A	180	PHE	2.0
1	A	473	ILE	2.0
1	A	8	LEU	2.0
1	A	430	LEU	2.0
1	A	1175	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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
5	CA	A	2503	1/1	0.96	0.28	2.07	67,67,67,67	0
4	GTP	A	2501	32/32	0.90	0.23	0.21	96,111,122,126	0
5	CA	A	2502	1/1	0.96	0.21	0.08	86,86,86,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.