



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2024 – 10:20 AM EST

PDB ID : 3LMU  
Title : Crystal structure of DTD from Plasmodium falciparum  
Authors : Manickam, Y.; Bhatt, T.K.; Khan, S.; Sharma, A.  
Deposited on : 2010-02-01  
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<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>.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

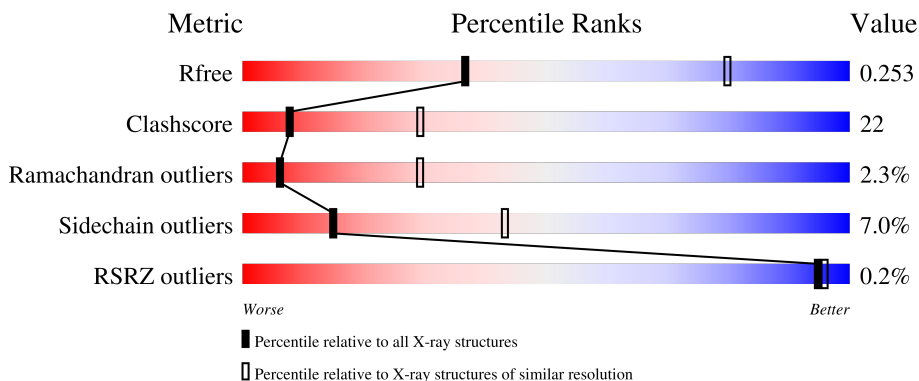
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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  $\geq 3$ , 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	164	
1	B	164	
1	C	164	
1	D	164	
1	E	164	

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Mol	Chain	Length	Quality of chain
1	F	164	<p>%</p> <p>52% 34% 12%</p>
1	G	164	<p>38% 45% 7% 10%</p>
1	H	164	<p>48% 37% 5% 10%</p>

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
2	IOD	D	167	-	-	X	-
2	IOD	G	165	-	-	X	-

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9279 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 D-tyrosyl-tRNA(Tyr) deacylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	155	1204	778	201	222	3	0	0	0
1	B	148	1174	756	198	217	3	2	0	0
1	C	148	1176	760	196	217	3	0	0	0
1	D	148	1172	757	194	218	3	2	0	0
1	E	145	1134	735	185	211	3	0	0	0
1	F	144	1126	730	184	209	3	0	0	0
1	G	148	1120	720	186	211	3	0	0	0
1	H	148	1147	743	190	211	3	0	0	0

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	I	0	0
			1	1		
2	B	5	Total	I	0	0
			5	5		
2	C	4	Total	I	0	0
			4	4		
2	D	6	Total	I	0	0
			6	6		
2	E	1	Total	I	0	0
			1	1		
2	F	4	Total	I	0	0
			4	4		

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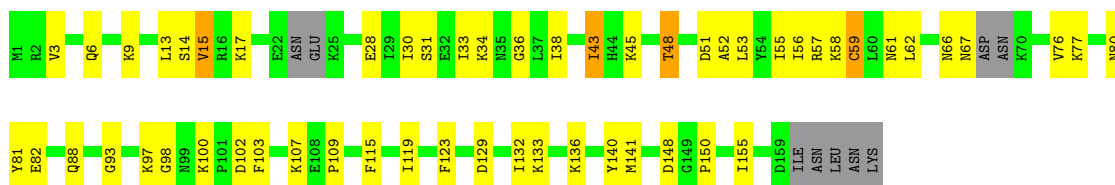
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
2	G	3	Total I 3 3	0	0
2	H	2	Total I 2 2	0	0

### 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.

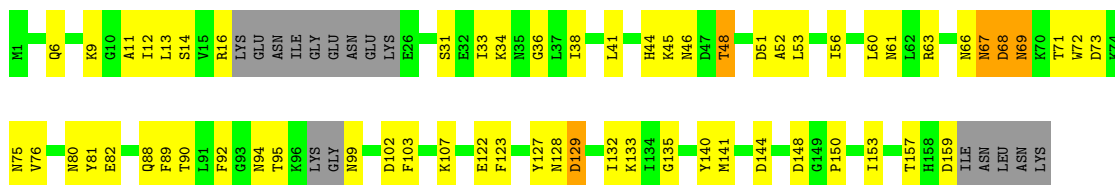
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain A: 



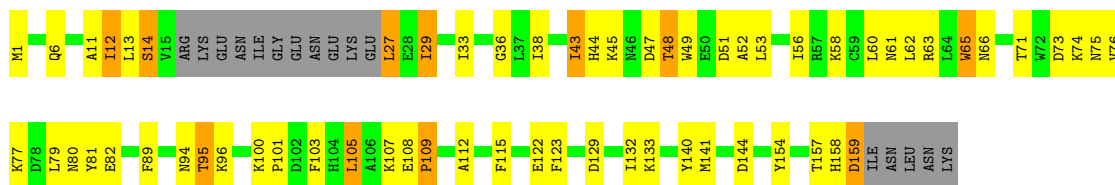
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain B: 



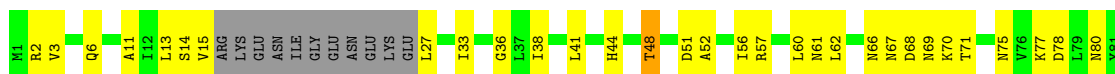
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain C: 



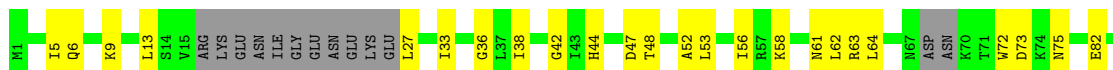
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain D: 





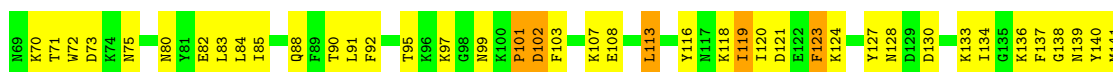
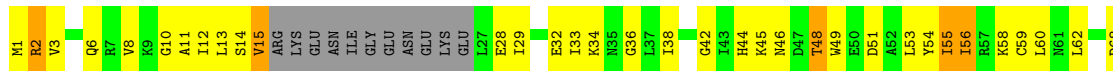
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase



- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase



- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase



- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase



ASN  
LYS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.18Å 77.18Å 214.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.96 – 3.30 48.64 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (33.96-3.30) 99.9 (48.64-3.30)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.63 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.5_2	Depositor
R, $R_{free}$	0.185 , 0.256 0.182 , 0.253	Depositor DCC
$R_{free}$ test set	971 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.9	Xtrriage
Anisotropy	0.295	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 42.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	9279	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: IOD

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	0.57	0/1225	0.62	0/1661
1	B	0.65	0/1195	0.63	0/1621
1	C	0.57	0/1199	0.60	0/1628
1	D	0.59	0/1195	0.62	0/1623
1	E	0.61	0/1154	0.62	0/1567
1	F	0.55	0/1148	0.61	0/1560
1	G	0.58	0/1141	0.65	0/1560
1	H	0.60	0/1169	0.64	0/1591
All	All	0.59	0/9426	0.62	0/12811

There are no bond length outliers.

There are no bond angle outliers.

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	1204	0	1147	34	0
1	B	1174	0	1126	40	0
1	C	1176	0	1143	55	0
1	D	1172	0	1127	47	0
1	E	1134	0	1080	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1126	0	1065	51	0
1	G	1120	0	1029	79	0
1	H	1147	0	1093	69	0
2	A	1	0	0	0	0
2	B	5	0	0	0	0
2	C	4	0	0	1	0
2	D	6	0	0	4	0
2	E	1	0	0	0	0
2	F	4	0	0	0	0
2	G	3	0	0	4	0
2	H	2	0	0	2	0
All	All	9279	0	8810	395	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 22.

All (395) 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:D:99:ASN:OD1	2:D:167:IOD:I	2.19	1.30
1:D:99:ASN:ND2	2:D:167:IOD:I	2.49	1.15
1:D:99:ASN:CG	2:D:167:IOD:I	2.54	1.14
1:E:61:ASN:HA	1:E:75:ASN:HD22	1.22	1.03
1:H:9:LYS:HG2	1:H:148:ASP:HB2	1.39	1.03
1:G:6:GLN:HB2	1:G:38:ILE:HG22	1.48	0.95
1:G:33:ILE:HG22	1:G:133:LYS:HG3	1.49	0.94
1:G:56:ILE:HD11	1:G:119:ILE:HG22	1.51	0.93
1:H:90:THR:HA	1:H:103:PHE:HE1	1.33	0.91
1:C:105:LEU:HD12	1:C:105:LEU:H	1.35	0.91
1:B:94:ASN:HB3	1:B:102:ASP:HB3	1.53	0.90
1:D:68:ASP:O	1:D:70:LYS:N	2.07	0.87
1:H:90:THR:HA	1:H:103:PHE:CE1	2.13	0.83
1:E:105:LEU:HD12	1:E:105:LEU:H	1.47	0.79
1:F:107:LYS:HG2	1:F:112:ALA:HB2	1.65	0.79
1:G:99:ASN:OD1	1:H:58:LYS:NZ	2.18	0.77
1:E:61:ASN:HA	1:E:75:ASN:ND2	2.01	0.75
1:G:6:GLN:HB2	1:G:38:ILE:CG2	2.16	0.74
1:C:94:ASN:HD21	1:C:96:LYS:HE3	1.54	0.73
1:F:76:VAL:HG23	1:F:81:TYR:HB2	1.69	0.72
1:A:43:ILE:HD12	1:A:43:ILE:H	1.53	0.71
1:H:5:ILE:HB	1:H:153:ILE:HB	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:82:GLU:C	1:G:83:LEU:HD12	2.11	0.71
1:C:12:ILE:HG22	1:C:29:ILE:HG12	1.72	0.70
1:D:68:ASP:C	1:D:70:LYS:H	1.95	0.70
1:G:56:ILE:HD11	1:G:119:ILE:CG2	2.21	0.70
1:C:43:ILE:H	1:C:43:ILE:HD12	1.55	0.70
1:D:93:GLY:HA2	1:D:102:ASP:O	1.92	0.70
1:H:56:ILE:HD11	1:H:119:ILE:HG23	1.74	0.69
1:C:105:LEU:HD12	1:C:105:LEU:N	2.08	0.69
1:G:116:TYR:O	1:G:120:ILE:HG12	1.93	0.69
1:A:76:VAL:HG23	1:A:81:TYR:HB2	1.75	0.68
1:C:14:SER:HB3	1:C:27:LEU:HD22	1.73	0.68
1:A:15:VAL:HG22	1:A:30:ILE:HD13	1.74	0.68
1:F:44:HIS:HE2	1:F:105:LEU:HD23	1.59	0.68
1:G:2:ARG:HG3	1:G:92:PHE:CZ	2.30	0.67
1:H:9:LYS:CG	1:H:148:ASP:HB2	2.22	0.67
1:C:49:TRP:HB2	2:C:168:IOD:I	2.65	0.67
1:G:2:ARG:HG3	1:G:92:PHE:CE2	2.29	0.67
1:G:137:PHE:CD2	1:G:138:GLY:N	2.62	0.67
1:G:137:PHE:HD2	1:G:138:GLY:N	1.94	0.66
1:A:15:VAL:HG11	1:A:136:LYS:HB3	1.77	0.66
1:A:52:ALA:O	1:A:56:ILE:HG13	1.96	0.66
1:H:44:HIS:HE1	1:H:46:ASN:HB2	1.62	0.65
1:G:44:HIS:HD2	1:G:46:ASN:H	1.44	0.65
1:H:7:ARG:HB2	1:H:151:VAL:HB	1.79	0.65
1:G:84:LEU:HD12	1:G:133:LYS:HB2	1.79	0.64
1:E:99:ASN:O	1:F:62:LEU:HD23	1.96	0.64
1:G:136:LYS:O	1:G:139:ASN:HB2	1.98	0.64
1:G:157:THR:C	1:G:159:ASP:H	2.02	0.63
1:C:105:LEU:H	1:C:105:LEU:CD1	2.09	0.62
1:B:61:ASN:HA	1:B:75:ASN:HD22	1.64	0.62
1:H:69:ASN:OD1	2:H:166:IOD:I	2.87	0.62
1:G:33:ILE:CG2	1:G:133:LYS:HG3	2.27	0.62
1:F:90:THR:HA	1:F:103:PHE:CE1	2.34	0.62
1:H:76:VAL:HG23	1:H:81:TYR:HB2	1.82	0.62
1:A:45:LYS:HA	1:A:107:LYS:HB2	1.82	0.61
1:E:58:LYS:HD2	1:E:62:LEU:HD21	1.82	0.61
1:E:150:PRO:HB2	1:F:88:GLN:OE1	1.99	0.61
1:H:44:HIS:CE1	1:H:46:ASN:H	2.18	0.61
1:H:123:PHE:HB3	1:H:132:ILE:HD12	1.82	0.61
1:B:52:ALA:O	1:B:56:ILE:HG13	2.00	0.61
1:H:15:VAL:HG12	1:H:140:TYR:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:44:HIS:CE1	1:H:46:ASN:HB2	2.35	0.61
1:F:45:LYS:HA	1:F:107:LYS:HE3	1.81	0.61
1:H:136:LYS:HG2	1:H:139:ASN:HB2	1.83	0.61
1:A:6:GLN:HB2	1:A:38:ILE:HG22	1.83	0.60
1:E:95:THR:HG21	1:F:62:LEU:HD11	1.83	0.60
1:F:45:LYS:HG3	1:F:46:ASN:OD1	2.02	0.60
1:E:108:GLU:HG2	1:E:109:PRO:HD2	1.83	0.60
1:F:54:TYR:O	1:F:58:LYS:HG2	2.00	0.60
1:H:11:ALA:HA	1:H:144:ASP:O	2.01	0.60
1:F:74:LYS:HB2	1:F:79:LEU:HD11	1.83	0.60
1:D:94:ASN:HB3	1:D:102:ASP:HB3	1.84	0.60
1:C:6:GLN:HB2	1:C:38:ILE:HG22	1.83	0.59
1:H:41:LEU:HD12	1:H:42:GLY:N	2.17	0.59
1:H:6:GLN:HB2	1:H:38:ILE:HG22	1.83	0.59
1:F:6:GLN:HB2	1:F:38:ILE:HG22	1.84	0.59
1:C:76:VAL:HG23	1:C:81:TYR:HB2	1.85	0.59
1:E:99:ASN:HD22	1:F:61:ASN:HB3	1.68	0.59
1:C:43:ILE:H	1:C:43:ILE:CD1	2.13	0.59
1:A:15:VAL:CG2	1:A:30:ILE:HG21	2.34	0.58
1:G:44:HIS:CD2	1:G:46:ASN:H	2.20	0.58
1:G:116:TYR:CZ	2:G:165:IOD:I	3.26	0.58
1:G:120:ILE:O	1:G:124:LYS:HG3	2.03	0.58
1:H:107:LYS:HG2	1:H:112:ALA:HB2	1.85	0.58
1:C:94:ASN:ND2	1:C:96:LYS:HE3	2.18	0.58
1:G:116:TYR:OH	2:G:165:IOD:I	2.90	0.58
1:A:93:GLY:HA2	1:A:103:PHE:CD1	2.38	0.58
1:C:52:ALA:O	1:C:56:ILE:HG13	2.04	0.58
1:D:108:GLU:OE1	1:D:110:ASN:HB2	2.04	0.57
1:G:154:TYR:O	1:G:155:ILE:HG12	2.04	0.57
1:F:61:ASN:HA	1:F:75:ASN:ND2	2.20	0.57
1:C:103:PHE:CD2	1:C:103:PHE:N	2.73	0.57
1:H:54:TYR:CD2	1:H:157:THR:HG22	2.39	0.57
1:C:6:GLN:HB2	1:C:38:ILE:CG2	2.33	0.57
1:H:6:GLN:HB2	1:H:38:ILE:CG2	2.34	0.57
1:E:94:ASN:OD1	1:E:94:ASN:C	2.43	0.57
1:D:6:GLN:HB2	1:D:38:ILE:HG22	1.87	0.56
1:G:3:VAL:HG12	1:G:155:ILE:HB	1.88	0.56
1:D:13:LEU:C	1:D:13:LEU:HD23	2.27	0.56
1:A:15:VAL:HG13	1:A:141:MET:HG2	1.87	0.56
1:B:13:LEU:HD22	1:B:135:GLY:HA2	1.88	0.56
1:D:14:SER:HB3	1:D:27:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:6:GLN:HB2	1:F:38:ILE:CG2	2.35	0.55
1:F:108:GLU:HG2	1:F:109:PRO:HD2	1.87	0.55
1:G:154:TYR:CZ	1:H:154:TYR:CE2	2.95	0.55
1:A:6:GLN:HB2	1:A:38:ILE:CG2	2.36	0.55
1:B:6:GLN:HB2	1:B:38:ILE:HG22	1.87	0.55
1:E:123:PHE:HB3	1:E:132:ILE:HG13	1.89	0.55
1:G:157:THR:O	1:G:159:ASP:N	2.34	0.55
1:C:14:SER:HB3	1:C:27:LEU:CD2	2.37	0.55
1:G:88:GLN:HA	1:G:88:GLN:OE1	2.06	0.55
1:A:15:VAL:CG2	1:A:30:ILE:HD13	2.36	0.55
1:E:158:HIS:O	1:E:159:ASP:OD1	2.25	0.55
1:G:13:LEU:HD11	1:G:141:MET:SD	2.47	0.55
1:D:56:ILE:HG22	1:D:60:LEU:HD12	1.89	0.54
1:E:6:GLN:HB2	1:E:38:ILE:HG22	1.89	0.54
1:E:105:LEU:HD12	1:E:105:LEU:N	2.20	0.54
1:D:57:ARG:O	1:D:61:ASN:HB2	2.08	0.54
1:D:6:GLN:HB2	1:D:38:ILE:CG2	2.37	0.54
1:G:44:HIS:HD1	1:G:92:PHE:HE1	1.52	0.54
1:H:100:LYS:HG3	1:H:101:PRO:CD	2.38	0.54
1:G:113:LEU:O	1:G:113:LEU:HD12	2.07	0.53
1:H:87:SER:HB3	2:H:165:IOD:I	2.78	0.53
1:G:85:ILE:N	1:G:85:ILE:HD13	2.23	0.53
1:E:88:GLN:NE2	1:F:150:PRO:HB2	2.23	0.53
1:A:123:PHE:HB3	1:A:132:ILE:HG13	1.91	0.53
1:F:105:LEU:N	1:F:105:LEU:HD12	2.24	0.53
1:E:89:PHE:CD1	1:H:69:ASN:ND2	2.76	0.53
1:E:62:LEU:HD11	1:F:95:THR:HG21	1.91	0.53
1:B:6:GLN:HB2	1:B:38:ILE:CG2	2.39	0.53
1:F:90:THR:HA	1:F:103:PHE:HE1	1.73	0.53
1:G:12:ILE:HG21	1:G:29:ILE:HD13	1.89	0.53
1:B:123:PHE:HB3	1:B:132:ILE:HG13	1.90	0.53
1:G:13:LEU:HD23	1:G:14:SER:N	2.23	0.53
1:B:44:HIS:HB2	1:B:92:PHE:CZ	2.44	0.52
1:D:105:LEU:HD13	2:D:170:IOD:I	2.79	0.52
1:F:76:VAL:HG23	1:F:81:TYR:CB	2.36	0.52
1:G:71:THR:HG1	1:G:72:TRP:HD1	1.55	0.52
1:A:13:LEU:HD21	1:A:141:MET:SD	2.49	0.52
1:E:6:GLN:HB2	1:E:38:ILE:CG2	2.39	0.52
1:E:42:GLY:C	1:E:92:PHE:HE2	2.13	0.52
1:F:44:HIS:HB2	1:F:92:PHE:CZ	2.44	0.52
1:F:108:GLU:OE2	1:F:110:ASN:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:LEU:HD23	1:E:72:TRP:HZ3	1.74	0.52
1:G:11:ALA:HA	1:G:144:ASP:O	2.10	0.52
1:A:88:GLN:OE1	1:B:150:PRO:HB2	2.10	0.52
1:F:123:PHE:HB3	1:F:132:ILE:HG13	1.92	0.52
1:H:100:LYS:HG3	1:H:101:PRO:HD2	1.91	0.52
1:C:63:ARG:HH21	1:C:73:ASP:HA	1.75	0.51
1:D:60:LEU:O	1:D:77:LYS:HE2	2.10	0.51
1:B:63:ARG:HG2	1:B:73:ASP:O	2.11	0.51
1:E:44:HIS:HB2	1:E:92:PHE:CZ	2.46	0.51
1:H:7:ARG:CB	1:H:151:VAL:HB	2.40	0.51
1:A:55:ILE:O	1:A:59:CYS:HB2	2.10	0.51
1:E:156:ASP:O	1:E:158:HIS:N	2.44	0.51
1:A:53:LEU:HA	1:A:56:ILE:HD12	1.93	0.51
1:A:66:ASN:O	1:A:67:ASN:OD1	2.29	0.51
1:B:11:ALA:HA	1:B:144:ASP:O	2.11	0.51
1:B:44:HIS:HE1	1:B:46:ASN:OD1	1.94	0.51
1:B:67:ASN:O	1:B:68:ASP:O	2.28	0.50
1:G:140:TYR:C	1:G:140:TYR:CD2	2.84	0.50
1:E:52:ALA:O	1:E:56:ILE:HG13	2.12	0.50
1:H:42:GLY:C	1:H:92:PHE:HE2	2.15	0.50
1:D:68:ASP:C	1:D:70:LYS:N	2.62	0.50
1:G:48:THR:O	1:G:51:ASP:HB2	2.11	0.50
1:H:44:HIS:HB2	1:H:92:PHE:CZ	2.47	0.50
1:G:116:TYR:CE2	2:G:165:IOD:I	3.35	0.50
1:H:49:TRP:NE1	1:H:53:LEU:HD11	2.27	0.50
1:E:63:ARG:HG3	1:F:99:ASN:O	2.12	0.49
1:F:58:LYS:O	1:F:62:LEU:HB2	2.11	0.49
1:F:107:LYS:HG2	1:F:112:ALA:CB	2.40	0.49
1:G:136:LYS:HG2	1:G:139:ASN:OD1	2.12	0.49
1:C:61:ASN:HB3	1:D:99:ASN:HD22	1.76	0.49
1:C:140:TYR:C	1:C:140:TYR:CD2	2.84	0.49
1:B:13:LEU:HB3	1:B:31:SER:HB3	1.94	0.49
1:F:13:LEU:HB3	1:F:31:SER:HB3	1.94	0.49
1:F:56:ILE:CD1	1:F:122:GLU:HB3	2.43	0.49
1:B:33:ILE:CG2	1:B:133:LYS:HG3	2.42	0.49
1:G:13:LEU:HD23	1:G:13:LEU:C	2.33	0.49
1:D:123:PHE:HB3	1:D:132:ILE:HG13	1.93	0.49
1:B:13:LEU:HD21	1:B:141:MET:SD	2.52	0.48
1:G:2:ARG:HA	1:G:155:ILE:O	2.13	0.48
1:H:149:GLY:HA3	1:H:150:PRO:C	2.33	0.48
1:D:75:ASN:C	1:D:75:ASN:OD1	2.52	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:LYS:HA	1:C:107:LYS:HE3	1.96	0.48
1:C:61:ASN:HB3	1:D:99:ASN:ND2	2.28	0.48
1:E:36:GLY:HA3	1:E:82:GLU:O	2.13	0.48
1:F:140:TYR:C	1:F:140:TYR:CD2	2.86	0.48
1:B:103:PHE:N	1:B:103:PHE:CD2	2.81	0.48
1:F:29:ILE:HG22	1:F:30:ILE:N	2.29	0.48
1:G:12:ILE:CG2	1:G:29:ILE:HD13	2.44	0.48
1:B:60:LEU:HD11	1:B:127:TYR:HB2	1.94	0.48
1:H:38:ILE:HG23	1:H:38:ILE:O	2.12	0.48
1:H:75:ASN:O	1:H:78:ASP:HB2	2.12	0.48
1:H:127:TYR:CZ	1:H:131:LYS:HG3	2.49	0.48
1:C:61:ASN:CB	1:D:99:ASN:ND2	2.77	0.48
1:E:42:GLY:O	1:E:92:PHE:HE2	1.97	0.48
1:F:107:LYS:HE3	1:F:107:LYS:HB2	1.56	0.48
1:H:127:TYR:CD1	1:H:127:TYR:C	2.87	0.48
1:B:89:PHE:CE1	1:B:103:PHE:CD1	3.01	0.47
1:H:94:ASN:OD1	1:H:96:LYS:HE3	2.14	0.47
1:A:58:LYS:O	1:A:62:LEU:HG	2.14	0.47
1:E:94:ASN:OD1	1:E:95:THR:N	2.47	0.47
1:G:10:GLY:HA2	1:G:34:LYS:O	2.15	0.47
1:A:76:VAL:HG23	1:A:81:TYR:CB	2.43	0.47
1:G:84:LEU:CD1	1:G:133:LYS:HB2	2.43	0.47
1:A:13:LEU:HB3	1:A:31:SER:HB3	1.96	0.47
1:C:36:GLY:HA3	1:C:82:GLU:O	2.14	0.47
1:G:150:PRO:O	1:G:151:VAL:HG23	2.15	0.47
1:G:150:PRO:O	1:G:151:VAL:CG2	2.63	0.47
1:H:113:LEU:O	1:H:117:ASN:HB2	2.15	0.47
1:H:157:THR:C	1:H:159:ASP:H	2.17	0.47
1:D:56:ILE:CD1	1:D:122:GLU:HB3	2.45	0.47
1:B:71:THR:O	1:B:72:TRP:HB2	2.15	0.47
1:C:56:ILE:HG22	1:C:60:LEU:HD12	1.96	0.47
1:C:123:PHE:HB3	1:C:132:ILE:HG13	1.96	0.47
1:F:33:ILE:CG2	1:F:133:LYS:HG3	2.45	0.47
1:F:56:ILE:HD13	1:F:122:GLU:HB3	1.96	0.47
1:A:36:GLY:HA3	1:A:82:GLU:O	2.15	0.47
1:C:154:TYR:CE2	1:D:154:TYR:CZ	3.03	0.47
1:D:11:ALA:HA	1:D:144:ASP:O	2.15	0.47
1:D:2:ARG:NH1	1:D:92:PHE:CD1	2.82	0.46
1:G:33:ILE:HB	1:G:82:GLU:HB2	1.97	0.46
1:C:33:ILE:CG2	1:C:133:LYS:HG3	2.45	0.46
1:G:15:VAL:HG22	1:G:28:GLU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:123:PHE:HB3	1:H:132:ILE:CD1	2.46	0.46
1:F:107:LYS:O	1:F:108:GLU:C	2.54	0.46
1:F:122:GLU:OE1	1:F:122:GLU:HA	2.16	0.46
1:B:76:VAL:HG23	1:B:81:TYR:HB2	1.98	0.46
1:E:140:TYR:CD2	1:E:140:TYR:C	2.88	0.46
1:C:154:TYR:CZ	1:D:154:TYR:CE2	3.03	0.46
1:G:62:LEU:HD23	1:G:62:LEU:HA	1.75	0.46
1:H:94:ASN:HD21	1:H:96:LYS:HB2	1.81	0.46
1:B:90:THR:HG22	1:B:103:PHE:HE1	1.81	0.46
1:C:1:MET:H3	1:C:157:THR:HG1	1.59	0.46
1:E:13:LEU:HD21	1:E:141:MET:SD	2.56	0.45
1:G:157:THR:C	1:G:159:ASP:N	2.69	0.45
1:H:148:ASP:OD1	1:H:148:ASP:C	2.55	0.45
1:D:52:ALA:O	1:D:56:ILE:HG13	2.15	0.45
1:G:12:ILE:HG13	1:G:32:GLU:HG3	1.98	0.45
1:G:116:TYR:CE1	1:G:120:ILE:HD11	2.51	0.45
1:G:128:ASN:HD21	1:G:130:ASP:HB2	1.81	0.45
1:C:107:LYS:HG2	1:C:112:ALA:HB2	1.97	0.45
1:D:94:ASN:O	1:D:101:PRO:HA	2.16	0.45
1:G:8:VAL:HG22	1:G:36:GLY:O	2.16	0.45
1:D:75:ASN:O	1:D:78:ASP:HB2	2.16	0.45
1:F:103:PHE:O	1:F:106:ALA:HB3	2.16	0.45
1:G:151:VAL:HG13	1:H:90:THR:HG21	1.97	0.45
1:D:36:GLY:HA3	1:D:82:GLU:O	2.16	0.45
1:A:150:PRO:HB2	1:B:88:GLN:OE1	2.17	0.45
1:C:58:LYS:NZ	1:D:98:GLY:O	2.50	0.45
1:E:44:HIS:O	1:E:47:ASP:HB2	2.17	0.45
1:E:128:ASN:OD1	1:E:129:ASP:N	2.50	0.45
1:G:158:HIS:N	1:G:158:HIS:CD2	2.83	0.45
1:H:52:ALA:HB1	1:H:119:ILE:HG12	1.97	0.45
1:H:58:LYS:HA	1:H:58:LYS:HD3	1.63	0.45
1:B:53:LEU:HA	1:B:56:ILE:HD12	1.99	0.45
1:F:75:ASN:O	1:F:78:ASP:HB2	2.17	0.44
1:F:128:ASN:OD1	1:F:129:ASP:N	2.50	0.44
1:G:88:GLN:HE21	1:H:152:THR:CB	2.30	0.44
1:H:79:LEU:HD13	1:H:81:TYR:CE2	2.52	0.44
1:C:43:ILE:HG21	1:C:115:PHE:HD1	1.82	0.44
1:B:140:TYR:CD2	1:B:140:TYR:C	2.91	0.44
1:G:83:LEU:HD12	1:G:83:LEU:N	2.32	0.44
1:C:13:LEU:HD23	1:C:13:LEU:C	2.38	0.44
1:D:14:SER:CB	1:D:27:LEU:HD22	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:36:GLY:HA3	1:F:82:GLU:O	2.18	0.44
1:G:49:TRP:NE1	1:G:53:LEU:HD21	2.32	0.44
1:D:13:LEU:HD23	1:D:14:SER:N	2.33	0.44
1:H:49:TRP:HE1	1:H:53:LEU:HD11	1.82	0.44
1:A:57:ARG:O	1:A:61:ASN:HB2	2.17	0.44
1:C:157:THR:C	1:C:159:ASP:H	2.21	0.44
1:D:93:GLY:HA2	1:D:103:PHE:CD1	2.52	0.44
1:C:66:ASN:OD1	1:C:71:THR:HA	2.18	0.44
1:D:27:LEU:HD23	1:D:27:LEU:HA	1.71	0.44
1:G:99:ASN:HD22	1:H:61:ASN:CB	2.30	0.44
1:E:109:PRO:HG2	1:H:70:LYS:HA	2.00	0.44
1:G:13:LEU:HD23	1:G:14:SER:O	2.17	0.44
1:G:99:ASN:HD22	1:H:61:ASN:HB2	1.83	0.44
1:H:88:GLN:HG3	1:H:91:LEU:HG	1.99	0.44
1:D:44:HIS:HB2	1:D:92:PHE:CZ	2.53	0.43
1:E:64:LEU:HD22	1:E:151:VAL:HG11	2.00	0.43
1:F:94:ASN:HB3	1:F:102:ASP:HB3	2.00	0.43
1:H:136:LYS:HG2	1:H:139:ASN:CB	2.48	0.43
1:C:89:PHE:CE1	1:C:103:PHE:CD1	3.06	0.43
1:D:33:ILE:CG2	1:D:133:LYS:HG3	2.48	0.43
1:E:62:LEU:CD1	1:F:95:THR:HG21	2.49	0.43
1:G:154:TYR:CZ	1:H:154:TYR:CD2	3.06	0.43
1:H:56:ILE:HG23	1:H:123:PHE:CE1	2.53	0.43
1:E:105:LEU:H	1:E:105:LEU:CD1	2.25	0.43
1:C:53:LEU:HD23	1:C:53:LEU:HA	1.85	0.43
1:E:100:LYS:HA	1:E:101:PRO:HD3	1.80	0.43
1:B:128:ASN:OD1	1:B:129:ASP:N	2.51	0.43
1:C:75:ASN:OD1	1:C:75:ASN:C	2.56	0.43
1:H:156:ASP:O	1:H:158:HIS:N	2.52	0.43
1:A:33:ILE:CG2	1:A:133:LYS:HG3	2.49	0.43
1:E:156:ASP:O	1:E:157:THR:C	2.57	0.43
1:F:100:LYS:HA	1:F:101:PRO:HD3	1.83	0.43
1:C:108:GLU:HA	1:C:109:PRO:HD2	1.76	0.43
1:D:140:TYR:CD2	1:D:140:TYR:C	2.91	0.43
1:E:64:LEU:HD23	1:E:72:TRP:CZ3	2.53	0.43
1:A:43:ILE:HG21	1:A:115:PHE:HD1	1.84	0.43
1:C:48:THR:HG23	1:C:51:ASP:OD2	2.19	0.43
1:E:9:LYS:HG2	1:E:148:ASP:HB2	2.00	0.43
1:B:9:LYS:HG2	1:B:148:ASP:HB2	2.00	0.42
1:B:61:ASN:HA	1:B:75:ASN:ND2	2.32	0.42
1:D:66:ASN:OD1	1:D:71:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:GLU:HA	1:C:122:GLU:OE1	2.20	0.42
1:E:53:LEU:HD23	1:E:53:LEU:HA	1.85	0.42
1:F:11:ALA:HA	1:F:144:ASP:O	2.19	0.42
1:G:1:MET:HA	1:G:42:GLY:O	2.19	0.42
1:G:149:GLY:HA3	1:G:150:PRO:C	2.39	0.42
1:G:101:PRO:O	1:G:102:ASP:HB2	2.19	0.42
1:H:94:ASN:ND2	1:H:96:LYS:H	2.17	0.42
1:H:153:ILE:HA	1:H:153:ILE:HD13	1.79	0.42
1:B:45:LYS:HA	1:B:107:LYS:HB2	2.02	0.42
1:D:118:LYS:HE3	1:D:118:LYS:HB2	1.87	0.42
1:B:33:ILE:HG22	1:B:133:LYS:HG3	2.01	0.42
1:C:62:LEU:HA	1:C:62:LEU:HD23	1.82	0.42
1:G:56:ILE:HG23	1:G:123:PHE:CD1	2.54	0.42
1:G:70:LYS:O	1:G:73:ASP:HB2	2.19	0.42
1:B:53:LEU:HA	1:B:53:LEU:HD23	1.81	0.42
1:C:158:HIS:C	1:C:159:ASP:OD1	2.58	0.42
1:F:53:LEU:HD23	1:F:53:LEU:HA	1.86	0.42
1:H:14:SER:HB2	1:H:27:LEU:CD2	2.49	0.42
1:D:66:ASN:OD1	1:D:71:THR:HB	2.19	0.42
1:E:56:ILE:HD11	1:E:119:ILE:HG23	2.01	0.42
1:A:14:SER:HA	1:A:28:GLU:O	2.20	0.42
1:A:140:TYR:CD2	1:A:140:TYR:C	2.92	0.42
1:B:157:THR:C	1:B:159:ASP:H	2.23	0.42
1:C:11:ALA:HA	1:C:144:ASP:O	2.20	0.42
1:E:33:ILE:CG2	1:E:133:LYS:HG3	2.49	0.42
1:G:90:THR:HG22	1:G:103:PHE:CE1	2.55	0.42
1:G:92:PHE:O	1:G:103:PHE:HA	2.20	0.42
1:H:88:GLN:OE1	1:H:88:GLN:HA	2.19	0.42
1:D:48:THR:HG23	1:D:51:ASP:OD2	2.20	0.42
1:C:100:LYS:HA	1:C:101:PRO:HD3	1.82	0.41
1:E:63:ARG:HB3	1:E:73:ASP:O	2.19	0.41
1:G:75:ASN:C	1:G:75:ASN:OD1	2.58	0.41
1:H:54:TYR:HD2	1:H:157:THR:HG22	1.82	0.41
1:H:56:ILE:CD1	1:H:119:ILE:HG23	2.48	0.41
1:B:48:THR:HG23	1:B:51:ASP:OD2	2.20	0.41
1:E:58:LYS:O	1:E:62:LEU:HG	2.19	0.41
1:F:44:HIS:O	1:F:47:ASP:HB2	2.19	0.41
1:B:71:THR:O	1:B:72:TRP:CB	2.67	0.41
1:C:65:TRP:CG	1:C:79:LEU:HD11	2.55	0.41
1:G:49:TRP:O	1:G:53:LEU:HG	2.20	0.41
1:H:128:ASN:HB3	1:H:131:LYS:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:LEU:HD12	1:B:41:LEU:HA	1.78	0.41
1:C:107:LYS:HE3	1:C:107:LYS:HB2	1.86	0.41
1:G:45:LYS:HA	1:G:107:LYS:HA	2.03	0.41
1:H:13:LEU:HD21	1:H:141:MET:SD	2.61	0.41
1:H:42:GLY:C	1:H:92:PHE:CE2	2.94	0.41
1:B:153:ILE:HD13	1:B:153:ILE:HA	1.91	0.41
1:D:41:LEU:HD12	1:D:41:LEU:HA	1.77	0.41
1:G:148:ASP:OD1	1:G:148:ASP:C	2.58	0.41
1:E:5:ILE:HB	1:E:153:ILE:HB	2.01	0.41
1:F:76:VAL:CG2	1:F:81:TYR:HB2	2.44	0.41
1:F:91:LEU:HD23	1:F:91:LEU:HA	1.73	0.41
1:G:55:ILE:O	1:G:58:LYS:N	2.54	0.41
1:A:3:VAL:HG12	1:A:155:ILE:HB	2.03	0.41
1:E:63:ARG:HD3	1:F:100:LYS:CB	2.50	0.41
1:B:36:GLY:HA3	1:B:82:GLU:O	2.21	0.41
1:B:66:ASN:OD1	1:B:71:THR:HA	2.21	0.41
1:B:67:ASN:O	1:B:68:ASP:C	2.58	0.41
1:C:44:HIS:O	1:C:47:ASP:HB2	2.20	0.41
1:E:107:LYS:HG2	1:E:108:GLU:N	2.36	0.41
1:F:61:ASN:HA	1:F:75:ASN:HD22	1.84	0.41
1:G:118:LYS:O	1:G:121:ASP:HB2	2.21	0.41
1:A:9:LYS:HG2	1:A:148:ASP:HB2	2.02	0.41
1:A:48:THR:HG23	1:A:51:ASP:OD2	2.21	0.41
1:A:52:ALA:HB1	1:A:119:ILE:HG12	2.03	0.41
1:A:98:GLY:C	1:A:100:LYS:H	2.24	0.41
1:B:122:GLU:HA	1:B:122:GLU:OE1	2.21	0.41
1:C:43:ILE:CG2	1:C:115:PHE:HD1	2.33	0.41
1:D:3:VAL:HG12	1:D:155:ILE:HB	2.03	0.41
1:F:5:ILE:HB	1:F:153:ILE:HB	2.03	0.41
1:G:107:LYS:O	1:G:108:GLU:C	2.59	0.41
1:C:13:LEU:HD11	1:C:141:MET:SD	2.61	0.41
1:H:116:TYR:CE1	1:H:120:ILE:HD11	2.56	0.41
1:C:43:ILE:CG2	1:C:115:PHE:CD1	3.05	0.40
1:C:60:LEU:O	1:C:77:LYS:HE2	2.21	0.40
1:C:79:LEU:HD13	1:C:81:TYR:CE2	2.56	0.40
1:G:54:TYR:O	1:G:55:ILE:C	2.59	0.40
1:G:141:MET:HE1	2:G:165:IOD:I	2.91	0.40
1:H:56:ILE:HG23	1:H:123:PHE:CD1	2.56	0.40
1:H:127:TYR:O	1:H:128:ASN:HB2	2.20	0.40
1:A:43:ILE:CG2	1:A:115:PHE:HD1	2.34	0.40
1:H:13:LEU:HD21	1:H:141:MET:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:60:LEU:HD11	1:G:123:PHE:HD1	1.86	0.40
1:C:107:LYS:HG2	1:C:112:ALA:N	2.36	0.40
1:C:95:THR:HG21	1:D:62:LEU:CD2	2.51	0.40
1:D:153:ILE:HD13	1:D:153:ILE:HA	1.94	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	149/164 (91%)	128 (86%)	18 (12%)	3 (2%)	<b>7</b> 32
1	B	142/164 (87%)	126 (89%)	14 (10%)	2 (1%)	<b>11</b> 38
1	C	144/164 (88%)	128 (89%)	15 (10%)	1 (1%)	<b>22</b> 54
1	D	144/164 (88%)	124 (86%)	16 (11%)	4 (3%)	<b>5</b> 25
1	E	137/164 (84%)	120 (88%)	14 (10%)	3 (2%)	<b>6</b> 30
1	F	138/164 (84%)	114 (83%)	23 (17%)	1 (1%)	<b>22</b> 54
1	G	144/164 (88%)	118 (82%)	18 (12%)	8 (6%)	<b>2</b> <b>11</b>
1	H	144/164 (88%)	120 (83%)	20 (14%)	4 (3%)	<b>5</b> 25
All	All	1142/1312 (87%)	978 (86%)	138 (12%)	26 (2%)	<b>6</b> 29

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	97	LYS
1	B	68	ASP
1	D	69	ASN
1	G	97	LYS
1	G	101	PRO
1	G	102	ASP

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Mol	Chain	Res	Type
1	B	69	ASN
1	E	157	THR
1	G	55	ILE
1	G	158	HIS
1	E	158	HIS
1	G	68	ASP
1	H	158	HIS
1	D	67	ASN
1	D	97	LYS
1	D	101	PRO
1	G	56	ILE
1	G	59	CYS
1	H	157	THR
1	A	109	PRO
1	H	124	LYS
1	A	102	ASP
1	C	109	PRO
1	F	30	ILE
1	E	101	PRO
1	H	149	GLY

### 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	121/151 (80%)	112 (93%)	9 (7%)	13	40
1	B	122/151 (81%)	111 (91%)	11 (9%)	9	32
1	C	125/151 (83%)	112 (90%)	13 (10%)	7	25
1	D	123/151 (82%)	119 (97%)	4 (3%)	38	66
1	E	117/151 (78%)	112 (96%)	5 (4%)	29	59
1	F	115/151 (76%)	110 (96%)	5 (4%)	29	59
1	G	111/151 (74%)	98 (88%)	13 (12%)	5	21
1	H	117/151 (78%)	110 (94%)	7 (6%)	19	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	951/1208 (79%)	884 (93%)	67 (7%)	15 43

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	17	LYS
1	A	34	LYS
1	A	43	ILE
1	A	48	THR
1	A	59	CYS
1	A	77	LYS
1	A	80	ASN
1	A	129	ASP
1	B	12	ILE
1	B	14	SER
1	B	16	ARG
1	B	34	LYS
1	B	48	THR
1	B	67	ASN
1	B	69	ASN
1	B	80	ASN
1	B	95	THR
1	B	99	ASN
1	B	129	ASP
1	C	12	ILE
1	C	14	SER
1	C	27	LEU
1	C	29	ILE
1	C	43	ILE
1	C	48	THR
1	C	65	TRP
1	C	74	LYS
1	C	80	ASN
1	C	95	THR
1	C	105	LEU
1	C	129	ASP
1	C	159	ASP
1	D	15	VAL
1	D	48	THR
1	D	80	ASN
1	D	129	ASP

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Mol	Chain	Res	Type
1	E	27	LEU
1	E	48	THR
1	E	103	PHE
1	E	105	LEU
1	E	129	ASP
1	F	48	THR
1	F	80	ASN
1	F	95	THR
1	F	104	HIS
1	F	107	LYS
1	G	2	ARG
1	G	15	VAL
1	G	48	THR
1	G	80	ASN
1	G	91	LEU
1	G	95	THR
1	G	113	LEU
1	G	119	ILE
1	G	123	PHE
1	G	127	TYR
1	G	134	ILE
1	G	142	ASN
1	G	148	ASP
1	H	14	SER
1	H	27	LEU
1	H	31	SER
1	H	41	LEU
1	H	48	THR
1	H	69	ASN
1	H	127	TYR

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

Mol	Chain	Res	Type
1	A	67	ASN
1	E	88	GLN
1	H	69	ASN

### 5.3.3 RNA

There are no RNA molecules in this entry.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 26 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	155/164 (94%)	-0.37	0 100 100	27, 42, 57, 68	0
1	B	148/164 (90%)	-0.26	0 100 100	31, 43, 66, 83	1 (0%)
1	C	148/164 (90%)	-0.34	0 100 100	29, 43, 61, 73	0
1	D	148/164 (90%)	-0.49	0 100 100	32, 41, 60, 66	2 (1%)
1	E	145/164 (88%)	-0.41	0 100 100	31, 44, 64, 73	0
1	F	144/164 (87%)	-0.15	2 (1%) 75 75	33, 47, 65, 83	0
1	G	148/164 (90%)	-0.15	0 100 100	34, 63, 87, 100	0
1	H	148/164 (90%)	-0.33	0 100 100	37, 55, 74, 88	0
All	All	1184/1312 (90%)	-0.31	2 (0%) 95 96	27, 46, 72, 100	3 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	1	MET	3.4
1	F	155	ILE	2.2

### 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 monosaccharides 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	IOD	B	167	1/1	0.60	0.29	85,85,85,85	1
2	IOD	B	169	1/1	0.81	0.13	76,76,76,76	1
2	IOD	C	167	1/1	0.83	0.13	74,74,74,74	1
2	IOD	D	168	1/1	0.94	0.14	54,54,54,54	1
2	IOD	C	168	1/1	0.95	0.12	55,55,55,55	1
2	IOD	B	168	1/1	0.95	0.07	74,74,74,74	1
2	IOD	D	170	1/1	0.95	0.06	63,63,63,63	1
2	IOD	F	168	1/1	0.95	0.23	44,44,44,44	1
2	IOD	G	167	1/1	0.95	0.18	97,97,97,97	1
2	IOD	H	166	1/1	0.95	0.08	61,61,61,61	1
2	IOD	D	169	1/1	0.97	0.09	56,56,56,56	1
2	IOD	F	166	1/1	0.97	0.12	79,79,79,79	1
2	IOD	F	167	1/1	0.97	0.07	77,77,77,77	0
2	IOD	B	165	1/1	0.98	0.07	73,73,73,73	0
2	IOD	C	166	1/1	0.98	0.07	62,62,62,62	1
2	IOD	D	166	1/1	0.98	0.06	72,72,72,72	0
2	IOD	H	165	1/1	0.98	0.07	63,63,63,63	1
2	IOD	D	167	1/1	0.98	0.06	46,46,46,46	1
2	IOD	B	166	1/1	0.99	0.06	80,80,80,80	0
2	IOD	A	165	1/1	0.99	0.12	48,48,48,48	0
2	IOD	G	165	1/1	0.99	0.07	75,75,75,75	0
2	IOD	G	166	1/1	0.99	0.06	72,72,72,72	0
2	IOD	E	165	1/1	0.99	0.11	54,54,54,54	0
2	IOD	F	165	1/1	0.99	0.06	90,90,90,90	0
2	IOD	C	165	1/1	0.99	0.07	65,65,65,65	0
2	IOD	D	165	1/1	1.00	0.11	54,54,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.