



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1IRM  
Title : Crystal structure of apo heme oxygenase-1  
Authors : Sugishima, M.; Sakamoto, H.; Kakuta, Y.; Omata, Y.; Hayashi, S.; Noguchi, M.; Fukuyama, K.  
Deposited on : 2001-10-09  
Resolution : 2.55 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.

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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	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

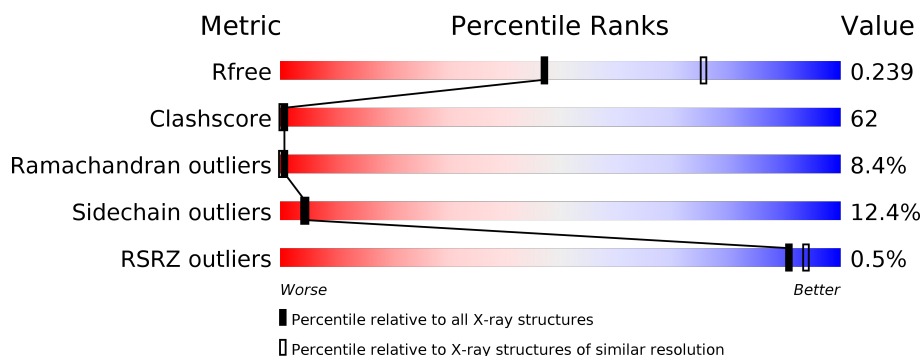
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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  $\geq 3$ , 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	267	<div> <div>24%</div> <div>39%</div> <div>8%</div> <div>•</div> <div>28%</div> </div>
1	B	267	<div> <div>16%</div> <div>42%</div> <div>12%</div> <div>•</div> <div>28%</div> </div>
1	C	267	<div> <div>22%</div> <div>42%</div> <div>9%</div> <div>27%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4836 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 apo heme oxygenase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	196	Total	C	N	O	S	0	0	0
			1604	1032	274	292	6			
1	A	192	Total	C	N	O	S	0	0	0
			1568	1012	267	283	6			
1	B	192	Total	C	N	O	S	0	0	0
			1577	1017	268	286	6			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	32	Total	O	0	0
			32	32		
2	A	34	Total	O	0	0
			34	34		
2	B	21	Total	O	0	0
			21	21		

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

- Chain C:  22%  42%  9%  27%

Sequence logo for Chain C. The y-axis lists amino acids, and the x-axis lists positions from 1 to 220. The height of each letter indicates its relative frequency at that position. The color bar at the top indicates the conservation score for each position: 22% (green), 42% (yellow), 9% (orange), and 27% (grey).

- Chain A: 24% 39% 8% 28%

Amino Acid	Percentage
MET	24%
GLU	39%
ARG	8%
PRO	28%
GLN	24%
LEU	39%
ASP	8%
SER	28%
MET	24%
SER	39%
GLN	8%
ASP	28%
LEU	24%
SER	39%
GLU	8%
ALA	28%
LYS	24%
GLU	39%
ALA	8%
THR	28%
LYS	24%
VAL	39%
HIS	8%
ILE	28%
ARG	24%
ALA	39%
ASN	8%
S31	28%
F33	24%
M34	39%
R35	8%
N36	28%
F37	24%
Q38	39%
K39	8%
Q40	28%
Y41	24%
V42	39%
S43	8%
F47	28%
K48	24%
I49	39%
V50	8%
H51	28%
A52	24%
I57	39%
Y58	8%
T59	28%
A60	24%
L61	39%
E62	8%
E63	28%
E64	24%
T65	39%

- Chain B:  16% 42% 12% 2% 28%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.21Å 70.21Å 140.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.62 – 2.55 46.82 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.0 (46.62-2.55) 97.1 (46.82-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.74 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.202 , 0.307 0.184 , 0.239	Depositor DCC
$R_{free}$ test set	1254 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 45.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.260 for -h,-k,l 0.486 for h,-h-k,-l 0.265 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4836	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.2346e-03.*

<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](#)

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	0.49	0/1611	0.70	1/2181 (0.0%)
1	B	0.45	0/1619	0.68	0/2191
1	C	0.44	0/1648	0.68	0/2231
All	All	0.46	0/4878	0.69	1/6603 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	ARG	N-CA-C	5.69	126.36	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	1568	0	1544	171	0
1	B	1577	0	1549	248	0
1	C	1604	0	1569	170	0
2	A	34	0	0	4	0
2	B	21	0	0	7	0
2	C	32	0	0	4	0
All	All	4836	0	4662	581	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 62.

All (581) 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:B:136:ARG:HA	1:B:136:ARG:HE	1.09	1.17
1:A:152:GLN:HE22	1:A:153:LYS:HG3	1.11	1.14
1:C:59:THR:HA	1:C:86:ARG:HD3	1.28	1.12
1:A:37:PHE:HA	1:A:42:VAL:HB	1.44	0.99
1:B:55:TYR:HB2	1:B:89:LEU:HD22	1.43	0.97
1:A:152:GLN:HA	1:A:157:LEU:HD23	1.49	0.94
1:A:158:PRO:HB2	1:A:162:GLU:HB2	1.47	0.94
1:C:38:GLN:HA	1:C:147:LEU:HD11	1.49	0.93
1:B:145:GLN:N	1:B:149:LYS:HG3	1.83	0.91
1:A:168:THR:HG22	1:A:170:PRO:HD3	1.49	0.91
1:B:204:LYS:O	1:B:207:PHE:HB3	1.70	0.91
1:A:136:ARG:HA	1:A:136:ARG:HE	1.33	0.90
1:A:176:THR:HG21	1:B:188:THR:O	1.71	0.90
1:B:222:THR:HG22	1:B:223:GLU:H	1.38	0.88
1:B:35:ARG:O	1:B:39:LYS:HB3	1.73	0.88
1:C:101:TRP:O	1:C:105:ILE:HG23	1.73	0.88
1:B:152:GLN:HE21	1:B:152:GLN:H	1.19	0.88
1:A:218:GLN:HG3	1:A:222:THR:HG23	1.53	0.88
1:B:117:ARG:NH2	1:B:121:VAL:HG23	1.88	0.87
1:B:117:ARG:HG2	1:B:209:LEU:HD11	1.53	0.87
1:B:136:ARG:HA	1:B:136:ARG:NE	1.89	0.87
1:A:152:GLN:NE2	1:A:153:LYS:HG3	1.90	0.86
1:A:117:ARG:O	1:A:121:VAL:HG23	1.74	0.86
1:B:39:LYS:HZ2	1:B:39:LYS:HB3	1.40	0.86
1:C:59:THR:CA	1:C:86:ARG:HD3	2.06	0.85
1:C:116:LYS:O	1:C:120:GLU:HG3	1.76	0.85
1:B:117:ARG:HA	1:B:117:ARG:HH21	1.42	0.85
1:B:152:GLN:NE2	1:B:152:GLN:H	1.74	0.84
1:A:149:LYS:HZ1	1:B:185:ARG:NE	1.75	0.84
1:B:210:ASN:O	1:B:213:LEU:HB3	1.77	0.83
1:A:152:GLN:HB3	1:A:164:LEU:CD1	2.09	0.83
1:A:35:ARG:HG3	1:A:35:ARG:HH11	1.44	0.83
1:B:197:HIS:O	1:B:201:GLU:HG2	1.78	0.83
1:C:149:LYS:O	1:C:150:ILE:HG13	1.77	0.83
1:C:177:LYS:O	1:C:180:GLN:HG3	1.80	0.82
1:A:82:GLU:HB3	1:A:172:ILE:HD11	1.61	0.82
1:A:216:GLU:O	1:A:220:LEU:HG	1.79	0.82
1:B:211:ILE:O	1:B:213:LEU:N	2.13	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:GLU:HA	1:B:48:LYS:HE3	1.60	0.81
1:C:197:HIS:O	1:C:201:GLU:HG2	1.80	0.81
1:B:217:LEU:HA	1:B:220:LEU:HD12	1.61	0.81
1:C:36:ASN:O	1:C:41:GLN:HB3	1.81	0.81
1:C:145:GLN:O	1:C:145:GLN:HG2	1.79	0.80
1:C:155:MET:HB3	1:C:157:LEU:HD13	1.64	0.80
1:C:33:PHE:HB2	1:C:218:GLN:CD	2.02	0.80
1:C:113:HIS:ND1	1:C:209:LEU:HD21	1.97	0.80
1:B:136:ARG:HE	1:B:136:ARG:CA	1.91	0.79
1:A:33:PHE:HA	1:A:36:ASN:HB3	1.62	0.79
1:A:141:LEU:HD23	1:A:142:SER:N	1.98	0.78
1:A:149:LYS:HZ1	1:B:185:ARG:HE	1.30	0.78
1:A:213:LEU:O	1:A:217:LEU:HG	1.84	0.78
1:B:102:GLN:HA	1:B:102:GLN:HE21	1.45	0.78
1:B:32:GLU:OE2	1:B:33:PHE:HB2	1.83	0.78
1:A:107:TYR:CE1	1:A:112:GLN:HG2	2.18	0.78
1:B:152:GLN:HG3	1:B:164:LEU:HD13	1.65	0.77
1:B:195:VAL:O	1:B:199:VAL:HG23	1.84	0.77
1:B:210:ASN:ND2	1:B:214:PHE:HE1	1.84	0.76
1:B:56:HIS:HD2	1:B:107:TYR:HD1	1.32	0.76
1:C:134:TYR:CE1	1:C:138:LEU:HD12	2.19	0.76
1:C:71:ASN:OD1	1:C:73:VAL:HG22	1.85	0.76
1:B:55:TYR:HA	1:B:89:LEU:HD13	1.67	0.76
1:A:136:ARG:NE	1:A:136:ARG:HA	2.02	0.75
1:B:136:ARG:HH12	1:B:210:ASN:ND2	1.83	0.74
1:A:145:GLN:HG2	1:A:146:VAL:N	2.00	0.74
1:A:194:GLU:OE1	1:A:198:ARG:HD3	1.87	0.74
1:C:204:LYS:HA	1:C:207:PHE:HD2	1.53	0.74
1:A:35:ARG:H	1:A:35:ARG:HD2	1.51	0.74
1:B:209:LEU:O	1:B:212:GLU:HG3	1.86	0.74
1:B:117:ARG:HH22	1:B:121:VAL:HG23	1.51	0.73
1:B:55:TYR:CB	1:B:89:LEU:HD22	2.17	0.73
1:B:152:GLN:N	1:B:152:GLN:HE21	1.85	0.73
1:C:152:GLN:HB3	1:C:164:LEU:HD12	1.71	0.73
1:C:64:GLU:OE1	1:C:67:ARG:HD2	1.88	0.73
1:B:71:ASN:OD1	1:B:73:VAL:HG13	1.88	0.72
1:A:35:ARG:N	1:A:35:ARG:HD2	2.04	0.72
1:A:105:ILE:O	1:A:105:ILE:HD12	1.89	0.72
1:B:117:ARG:CA	1:B:117:ARG:HH21	2.01	0.72
1:A:42:VAL:HG13	2:A:279:HOH:O	1.90	0.72
1:A:208:LEU:O	1:A:211:ILE:HB	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:GLY:O	1:A:42:VAL:HG12	1.88	0.71
1:A:84:HIS:O	1:A:85:ARG:HB2	1.90	0.71
1:A:145:GLN:HG2	1:A:146:VAL:H	1.56	0.71
1:A:138:LEU:HD22	1:A:179:LYS:HG3	1.73	0.71
1:A:152:GLN:O	1:A:156:ALA:HA	1.92	0.70
1:C:89:LEU:O	1:C:93:MET:HG2	1.90	0.70
1:C:46:GLY:O	1:C:50:VAL:HG23	1.91	0.70
1:A:152:GLN:HA	1:A:157:LEU:CD2	2.21	0.69
1:B:34:MET:SD	1:B:214:PHE:CG	2.85	0.69
1:A:107:TYR:CZ	1:A:112:GLN:HG2	2.26	0.69
1:B:137:TYR:O	1:B:141:LEU:HB3	1.92	0.69
1:C:174:ASN:HB3	1:C:177:LYS:HB2	1.74	0.69
1:C:35:ARG:C	1:C:37:PHE:H	1.95	0.69
1:B:198:ARG:NH1	1:B:198:ARG:HB2	2.08	0.68
1:A:218:GLN:HG3	1:A:222:THR:CG2	2.24	0.68
1:B:114:TYR:HA	1:B:209:LEU:HD22	1.74	0.68
1:B:222:THR:HG22	1:B:223:GLU:N	2.09	0.68
1:B:56:HIS:CD2	1:B:107:TYR:HD1	2.11	0.68
1:C:76:PRO:HB3	1:C:185:ARG:HD2	1.76	0.68
1:A:217:LEU:HA	1:A:220:LEU:HD12	1.76	0.68
1:B:121:VAL:HA	1:B:125:HIS:HB2	1.76	0.67
1:B:43:SER:O	1:B:155:MET:SD	2.52	0.67
1:A:152:GLN:HB3	1:A:164:LEU:HD11	1.76	0.67
1:B:107:TYR:CE2	1:B:112:GLN:HG2	2.30	0.67
1:B:32:GLU:HG3	1:B:33:PHE:H	1.59	0.67
1:B:92:ASP:O	1:B:95:PHE:HB3	1.95	0.67
1:C:155:MET:CB	1:C:157:LEU:HD13	2.25	0.67
1:B:207:PHE:CE1	1:B:211:ILE:HD11	2.30	0.66
1:C:134:TYR:CD1	1:C:138:LEU:HD12	2.30	0.66
1:C:220:LEU:O	1:C:220:LEU:HD23	1.95	0.66
1:B:117:ARG:NH2	1:B:120:GLU:HB2	2.11	0.65
1:B:152:GLN:HE21	1:B:153:LYS:H	1.42	0.65
1:C:33:PHE:HB2	1:C:218:GLN:NE2	2.10	0.65
1:C:152:GLN:HB3	1:C:164:LEU:CD1	2.26	0.65
1:A:35:ARG:HG3	1:A:35:ARG:NH1	2.07	0.65
2:C:287:HOH:O	1:A:102:GLN:HB3	1.96	0.64
1:A:149:LYS:HD2	1:B:185:ARG:HH21	1.62	0.64
1:A:152:GLN:HB3	1:A:164:LEU:HD12	1.80	0.64
1:C:154:ALA:O	1:C:155:MET:HG3	1.97	0.64
1:A:114:TYR:HE2	1:A:210:ASN:ND2	1.96	0.64
1:B:65:ILE:O	1:B:69:LYS:HB3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:GLN:O	1:C:116:LYS:HE3	1.98	0.63
1:A:127:GLU:OE1	1:A:198:ARG:NH2	2.31	0.63
1:B:60:ALA:CB	1:B:115:VAL:HG13	2.29	0.63
1:B:134:TYR:O	1:B:138:LEU:HB2	1.98	0.63
1:B:31:SER:HB3	1:B:34:MET:CG	2.29	0.63
1:B:39:LYS:HG2	1:B:40:GLY:N	2.13	0.63
1:A:117:ARG:C	1:A:121:VAL:HG23	2.18	0.63
1:B:33:PHE:CD1	1:B:218:GLN:HG3	2.33	0.63
1:C:51:MET:HB3	1:C:93:MET:CE	2.28	0.63
1:B:102:GLN:CA	1:B:102:GLN:HE21	2.11	0.63
1:C:91:GLN:HA	1:C:91:GLN:HE21	1.63	0.63
1:B:117:ARG:NH2	1:B:117:ARG:O	2.32	0.62
1:C:141:LEU:O	1:C:143:GLY:N	2.32	0.62
1:B:93:MET:HB3	1:B:101:TRP:CE3	2.33	0.62
1:C:140:ASP:OD1	1:C:166:PHE:HZ	1.82	0.62
1:A:80:PRO:HA	1:A:84:HIS:CG	2.35	0.62
1:C:43:SER:O	1:C:44:ARG:HB2	2.00	0.62
1:C:36:ASN:HB3	1:C:41:GLN:HG2	1.80	0.62
1:A:158:PRO:CB	1:A:162:GLU:HB2	2.25	0.62
1:B:125:HIS:HB3	1:B:128:LEU:HB2	1.82	0.61
1:C:34:MET:HB2	1:C:214:PHE:CB	2.29	0.61
1:B:205:THR:O	1:B:209:LEU:HG	2.00	0.61
1:A:37:PHE:CA	1:A:42:VAL:HB	2.26	0.61
1:A:209:LEU:O	1:A:212:GLU:HG3	2.01	0.61
1:B:152:GLN:HG3	1:B:164:LEU:CD1	2.30	0.61
1:C:38:GLN:HA	1:C:147:LEU:CD1	2.25	0.61
1:B:56:HIS:HD2	1:B:107:TYR:CD1	2.17	0.61
1:A:71:ASN:OD1	1:A:73:VAL:HG13	2.01	0.60
1:C:37:PHE:CE2	1:C:50:VAL:HG11	2.36	0.60
1:B:155:MET:O	1:B:157:LEU:HD13	2.01	0.60
1:A:76:PRO:O	1:A:185:ARG:HD3	2.00	0.60
1:C:83:LEU:HD11	1:C:178:PHE:HE2	1.66	0.60
1:A:90:GLU:HG2	1:A:101:TRP:CH2	2.37	0.60
1:A:42:VAL:O	1:A:42:VAL:HG13	2.01	0.60
1:B:206:ALA:HA	1:B:209:LEU:HD12	1.84	0.60
1:C:127:GLU:HG2	1:C:128:LEU:HD23	1.84	0.60
1:C:204:LYS:O	1:C:208:LEU:N	2.33	0.60
1:C:206:ALA:HA	1:C:209:LEU:HB2	1.83	0.60
1:A:149:LYS:NZ	1:B:185:ARG:NE	2.47	0.60
1:B:128:LEU:HD22	1:B:199:VAL:HA	1.82	0.60
1:C:202:GLU:HA	1:C:205:THR:OG1	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:PRO:O	1:C:185:ARG:NH1	2.30	0.60
1:B:35:ARG:C	1:B:36:ASN:HD22	2.05	0.60
1:C:51:MET:HB3	1:C:93:MET:HE3	1.83	0.59
1:B:151:ALA:O	1:B:157:LEU:HD22	2.02	0.59
1:B:152:GLN:N	1:B:152:GLN:NE2	2.47	0.59
1:B:48:LYS:O	1:B:52:ALA:HB2	2.01	0.59
1:C:112:GLN:NE2	2:C:269:HOH:O	2.35	0.59
1:C:204:LYS:HA	1:C:207:PHE:CD2	2.37	0.59
1:A:205:THR:O	1:A:208:LEU:HB3	2.03	0.59
1:A:37:PHE:CD2	1:A:42:VAL:HG21	2.37	0.59
1:C:58:TYR:OH	1:C:140:ASP:OD2	2.21	0.59
1:B:52:ALA:HB1	1:B:106:PRO:HD2	1.84	0.59
1:B:135:THR:O	1:B:139:GLY:N	2.36	0.59
1:A:191:MET:HB2	1:A:195:VAL:HG12	1.84	0.59
1:B:111:THR:C	1:B:113:HIS:H	2.04	0.58
1:B:39:LYS:NZ	1:B:40:GLY:H	2.00	0.58
1:B:39:LYS:HG2	1:B:40:GLY:H	1.68	0.58
1:C:145:GLN:O	1:C:149:LYS:HB3	2.02	0.58
1:A:126:PRO:C	1:A:128:LEU:H	2.06	0.58
1:A:160:SER:OG	1:A:162:GLU:HG2	2.03	0.58
1:A:37:PHE:HA	1:A:42:VAL:CB	2.27	0.58
1:B:114:TYR:HE2	1:B:210:ASN:HA	1.68	0.58
1:B:186:MET:O	1:B:189:LEU:HB2	2.03	0.58
1:C:48:LYS:HE2	1:C:97:TYR:CE1	2.39	0.58
1:A:191:MET:HB2	1:A:195:VAL:CG1	2.34	0.58
1:C:105:ILE:HG13	1:C:105:ILE:O	2.03	0.57
1:B:216:GLU:O	1:B:217:LEU:C	2.43	0.57
1:C:209:LEU:O	1:C:212:GLU:HG3	2.03	0.57
1:B:138:LEU:HD11	1:B:182:TYR:CD1	2.39	0.57
1:B:182:TYR:O	1:B:184:ALA:N	2.37	0.57
1:B:80:PRO:HA	1:B:84:HIS:CG	2.40	0.57
1:B:57:ILE:HG23	1:B:118:LEU:HD21	1.86	0.57
1:A:90:GLU:HG2	1:A:101:TRP:HH2	1.70	0.57
1:C:76:PRO:HD2	1:C:189:LEU:HD11	1.87	0.57
1:B:175:PRO:O	1:B:177:LYS:N	2.37	0.57
1:B:71:ASN:CG	1:B:73:VAL:HG22	2.25	0.57
1:C:60:ALA:O	1:C:63:GLU:HG2	2.04	0.57
1:C:148:LYS:O	1:C:152:GLN:HG2	2.05	0.57
1:C:204:LYS:CA	1:C:207:PHE:HD2	2.16	0.57
1:C:48:LYS:HB3	1:C:97:TYR:CZ	2.39	0.57
1:A:162:GLU:HA	1:A:162:GLU:OE1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:ARG:HB2	1:B:198:ARG:HH11	1.70	0.56
1:A:169:PHE:O	1:A:172:ILE:N	2.38	0.56
1:A:152:GLN:O	1:A:156:ALA:CA	2.53	0.56
1:B:152:GLN:NE2	1:B:153:LYS:H	2.03	0.56
1:B:175:PRO:C	1:B:177:LYS:H	2.08	0.56
1:A:149:LYS:HD2	1:B:185:ARG:NH2	2.21	0.56
1:B:117:ARG:HD3	2:B:274:HOH:O	2.05	0.56
1:B:211:ILE:O	1:B:214:PHE:N	2.38	0.56
1:C:134:TYR:HE1	1:C:138:LEU:HD12	1.66	0.56
1:C:77:LEU:HD23	1:C:185:ARG:HB3	1.87	0.56
1:B:64:GLU:HG3	1:B:118:LEU:O	2.05	0.56
1:C:121:VAL:HG13	1:C:125:HIS:O	2.06	0.56
1:C:34:MET:HA	1:C:214:PHE:HD2	1.69	0.56
1:B:111:THR:HG23	1:B:115:VAL:CG2	2.36	0.56
1:C:151:ALA:HB1	1:C:155:MET:HE2	1.88	0.56
1:B:209:LEU:O	1:B:210:ASN:C	2.44	0.55
1:A:60:ALA:HB3	1:A:118:LEU:HD23	1.88	0.55
1:B:117:ARG:NH2	1:B:121:VAL:CG2	2.67	0.55
1:C:108:THR:O	1:C:112:GLN:HG3	2.06	0.55
1:B:54:LEU:HD13	1:B:166:PHE:CZ	2.42	0.55
1:C:59:THR:HG23	1:C:86:ARG:CZ	2.35	0.55
1:B:31:SER:HB3	1:B:34:MET:HG3	1.88	0.55
1:C:115:VAL:HG12	1:C:119:HIS:CD2	2.41	0.55
1:C:127:GLU:HG2	1:C:128:LEU:CD2	2.37	0.55
1:C:203:ALA:O	1:C:207:PHE:N	2.39	0.55
1:A:36:ASN:OD1	1:A:36:ASN:O	2.24	0.55
1:B:97:TYR:CE2	1:B:105:ILE:HG22	2.42	0.55
1:B:147:LEU:HB3	2:B:275:HOH:O	2.06	0.55
1:C:127:GLU:O	1:C:199:VAL:HG22	2.07	0.55
1:A:132:HIS:HE1	1:A:202:GLU:HG3	1.72	0.55
1:C:219:ALA:HA	1:C:222:THR:HG23	1.89	0.55
1:A:110:ALA:O	1:A:212:GLU:OE1	2.25	0.55
1:B:42:VAL:CG2	1:B:47:PHE:HB2	2.36	0.55
1:A:105:ILE:CD1	1:A:105:ILE:O	2.54	0.54
1:B:61:LEU:HD22	1:B:136:ARG:HG3	1.88	0.54
1:B:45:GLU:OE2	1:B:48:LYS:NZ	2.35	0.54
1:B:38:GLN:HA	1:B:147:LEU:HD21	1.89	0.54
1:C:177:LYS:HA	1:C:180:GLN:CG	2.37	0.54
1:A:76:PRO:HG2	1:A:189:LEU:HD13	1.88	0.54
1:B:111:THR:HG23	1:B:115:VAL:HG21	1.89	0.54
1:B:117:ARG:NE	1:B:202:GLU:OE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:VAL:HG22	1:A:47:PHE:CA	2.36	0.54
1:B:102:GLN:HA	1:B:102:GLN:NE2	2.19	0.54
1:B:180:GLN:O	1:B:184:ALA:HB2	2.08	0.54
1:B:37:PHE:HZ	1:B:140:ASP:OD2	1.90	0.54
1:B:39:LYS:CG	1:B:40:GLY:H	2.20	0.54
1:B:182:TYR:C	1:B:184:ALA:H	2.10	0.54
1:C:58:TYR:O	1:C:62:GLU:HG3	2.07	0.54
1:B:152:GLN:HE21	1:B:152:GLN:CA	2.21	0.54
1:B:35:ARG:O	1:B:39:LYS:NZ	2.37	0.54
1:B:61:LEU:HD21	1:B:137:TYR:CE2	2.43	0.53
1:C:61:LEU:CD2	1:C:136:ARG:HG3	2.38	0.53
1:C:48:LYS:HB3	1:C:97:TYR:OH	2.08	0.53
1:B:121:VAL:HG11	1:B:129:LEU:HA	1.90	0.53
1:B:55:TYR:CA	1:B:89:LEU:HD22	2.38	0.53
1:A:38:GLN:O	1:A:40:GLY:N	2.41	0.53
1:A:68:ASN:HD22	1:A:71:ASN:HD22	1.56	0.53
1:B:211:ILE:O	1:B:212:GLU:C	2.47	0.53
1:B:62:GLU:C	1:B:64:GLU:H	2.10	0.53
1:C:155:MET:HE3	1:C:157:LEU:HD22	1.91	0.53
1:B:134:TYR:CD1	1:B:138:LEU:HD12	2.43	0.53
1:A:138:LEU:O	1:A:142:SER:HB2	2.09	0.53
1:B:107:TYR:CZ	1:B:112:GLN:HG2	2.44	0.53
1:B:108:THR:HG23	2:B:276:HOH:O	2.07	0.53
1:B:210:ASN:O	1:B:214:PHE:HD1	1.91	0.53
1:A:65:ILE:HD11	1:A:137:TYR:OH	2.08	0.53
1:B:117:ARG:HG2	1:B:209:LEU:CD1	2.34	0.53
1:A:42:VAL:HG22	1:A:47:PHE:HA	1.90	0.53
1:B:42:VAL:HG21	1:B:47:PHE:HB2	1.90	0.53
1:B:185:ARG:HH11	1:B:185:ARG:HG3	1.72	0.53
1:A:75:ALA:C	1:A:77:LEU:H	2.12	0.53
1:B:209:LEU:HA	1:B:212:GLU:CG	2.39	0.53
1:C:205:THR:O	1:C:209:LEU:N	2.37	0.53
1:A:42:VAL:O	1:A:43:SER:O	2.26	0.52
1:B:31:SER:O	1:B:32:GLU:CB	2.57	0.52
1:A:128:LEU:O	1:A:129:LEU:C	2.47	0.52
1:A:136:ARG:CA	1:A:136:ARG:HE	2.15	0.52
1:A:61:LEU:O	1:A:65:ILE:HG13	2.10	0.52
1:C:41:GLN:O	1:C:42:VAL:O	2.27	0.52
1:A:76:PRO:O	1:A:185:ARG:HB3	2.10	0.52
1:A:83:LEU:HD12	1:A:83:LEU:O	2.08	0.52
1:B:175:PRO:HG2	1:B:176:THR:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:LEU:HD13	1:C:217:LEU:HD22	1.90	0.52
1:C:133:ALA:O	1:C:137:TYR:HD2	1.93	0.52
1:A:144:GLY:HA2	1:A:147:LEU:HB2	1.91	0.52
1:A:213:LEU:HG	1:A:214:PHE:N	2.24	0.52
1:B:73:VAL:O	1:B:74:TYR:HB2	2.10	0.52
1:A:118:LEU:HD13	1:A:118:LEU:H	1.75	0.52
1:B:82:GLU:O	1:B:169:PHE:CD2	2.63	0.52
1:B:60:ALA:HB2	1:B:115:VAL:HG13	1.91	0.52
1:C:157:LEU:HD23	1:C:164:LEU:CD1	2.40	0.52
1:B:34:MET:SD	1:B:214:PHE:CD2	3.03	0.52
1:A:138:LEU:O	1:A:142:SER:N	2.42	0.51
1:C:216:GLU:O	1:C:220:LEU:HB2	2.10	0.51
1:A:114:TYR:O	1:A:118:LEU:HD22	2.09	0.51
1:A:61:LEU:O	1:A:61:LEU:HG	2.10	0.51
1:A:62:GLU:OE1	1:A:86:ARG:HB2	2.09	0.51
1:C:60:ALA:HB3	1:C:118:LEU:HD23	1.92	0.51
1:B:204:LYS:C	1:B:207:PHE:HB3	2.30	0.51
1:C:63:GLU:O	1:C:66:GLU:HB2	2.08	0.51
1:A:114:TYR:CD2	1:A:209:LEU:HB3	2.45	0.51
1:B:185:ARG:NH1	1:B:185:ARG:HG3	2.23	0.51
1:B:36:ASN:ND2	1:B:39:LYS:HZ1	2.08	0.51
1:C:35:ARG:C	1:C:37:PHE:N	2.62	0.51
1:A:34:MET:HG2	1:A:35:ARG:CZ	2.40	0.51
1:B:37:PHE:HZ	1:B:140:ASP:CG	2.13	0.51
1:C:85:ARG:NH1	1:C:166:PHE:O	2.44	0.51
1:C:179:LYS:HE2	1:C:183:ARG:HH21	1.75	0.51
1:B:79:PHE:O	1:B:83:LEU:HB2	2.11	0.51
1:B:82:GLU:N	1:B:82:GLU:OE1	2.44	0.51
1:A:58:TYR:OH	1:A:140:ASP:OD2	2.29	0.51
1:A:152:GLN:O	1:A:156:ALA:N	2.44	0.51
1:B:117:ARG:CZ	1:B:202:GLU:OE1	2.59	0.50
1:C:42:VAL:CG2	1:C:46:GLY:HA3	2.41	0.50
1:B:136:ARG:HH12	1:B:210:ASN:HD22	1.60	0.50
1:B:52:ALA:O	1:B:56:HIS:CE1	2.65	0.50
1:C:100:HIS:O	1:C:104:ALA:CB	2.60	0.50
1:C:202:GLU:O	1:C:205:THR:CB	2.59	0.50
1:A:140:ASP:OD2	1:A:166:PHE:HZ	1.95	0.50
1:B:152:GLN:HE21	1:B:153:LYS:N	2.07	0.50
1:B:147:LEU:HD12	1:B:167:PHE:CE1	2.46	0.50
1:C:34:MET:HB2	1:C:214:PHE:HB2	1.92	0.50
1:A:101:TRP:O	1:A:105:ILE:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ALA:HA	1:A:93:MET:SD	2.52	0.50
1:A:89:LEU:O	1:A:93:MET:HG2	2.12	0.50
1:C:141:LEU:O	1:C:142:SER:C	2.49	0.50
1:A:133:ALA:HA	1:A:137:TYR:CE2	2.46	0.50
1:A:146:VAL:HG12	1:B:185:ARG:NH2	2.27	0.50
1:A:185:ARG:HA	1:A:188:THR:HG23	1.94	0.50
1:B:200:THR:O	1:B:204:LYS:HG3	2.12	0.50
1:B:210:ASN:HD21	1:B:214:PHE:HE1	1.60	0.50
1:A:133:ALA:O	1:A:134:TYR:C	2.50	0.49
1:B:121:VAL:CG1	1:B:129:LEU:HA	2.42	0.49
1:A:185:ARG:O	1:A:188:THR:N	2.39	0.49
1:A:190:GLU:HB3	2:A:275:HOH:O	2.10	0.49
1:A:209:LEU:O	1:A:212:GLU:OE2	2.30	0.49
1:B:117:ARG:HH22	1:B:120:GLU:HB2	1.78	0.49
1:C:47:PHE:O	1:C:48:LYS:C	2.50	0.49
1:A:146:VAL:O	1:A:150:ILE:HG13	2.12	0.49
1:B:76:PRO:HB3	1:B:185:ARG:HB3	1.95	0.49
1:B:151:ALA:HB3	1:B:164:LEU:HD22	1.95	0.49
1:B:211:ILE:HG22	1:B:212:GLU:N	2.26	0.49
1:A:42:VAL:O	1:A:47:PHE:HB2	2.13	0.49
1:C:114:TYR:O	1:C:118:LEU:HB2	2.11	0.49
1:A:84:HIS:O	1:A:85:ARG:CB	2.57	0.49
1:B:124:THR:HG22	1:B:124:THR:O	2.13	0.49
1:C:83:LEU:HD11	1:C:178:PHE:CE2	2.47	0.49
1:A:61:LEU:HD22	1:A:136:ARG:HG3	1.95	0.49
1:C:33:PHE:CB	1:C:218:GLN:NE2	2.74	0.49
1:B:82:GLU:O	1:B:169:PHE:HD2	1.96	0.48
1:B:181:LEU:HD12	1:B:181:LEU:O	2.13	0.48
1:B:151:ALA:CB	1:B:164:LEU:HD22	2.43	0.48
1:C:175:PRO:O	1:C:179:LYS:HG3	2.13	0.48
1:C:34:MET:HA	1:C:214:PHE:CD2	2.47	0.48
1:B:39:LYS:HZ3	1:B:40:GLY:H	1.60	0.48
1:B:58:TYR:CD1	1:B:85:ARG:HB2	2.48	0.48
1:B:32:GLU:CG	1:B:33:PHE:N	2.77	0.48
1:A:169:PHE:O	1:A:170:PRO:C	2.52	0.48
1:A:66:GLU:O	1:A:69:LYS:HG2	2.14	0.48
1:B:149:LYS:HA	1:B:152:GLN:OE1	2.14	0.48
1:B:33:PHE:CE1	1:B:218:GLN:HG3	2.48	0.48
1:B:32:GLU:CG	1:B:33:PHE:H	2.25	0.48
1:C:100:HIS:O	1:C:104:ALA:HB2	2.14	0.48
1:B:147:LEU:HA	2:B:275:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ARG:HG2	1:B:166:PHE:CE1	2.48	0.48
1:B:182:TYR:C	1:B:184:ALA:N	2.66	0.48
1:C:177:LYS:C	1:C:180:GLN:HG3	2.33	0.48
1:A:126:PRO:C	1:A:128:LEU:N	2.67	0.48
1:B:75:ALA:HB3	1:B:76:PRO:HD3	1.95	0.48
1:A:77:LEU:HD21	1:A:186:MET:HA	1.96	0.48
1:A:114:TYR:CE2	1:A:210:ASN:ND2	2.80	0.47
1:A:49:LEU:HG	1:A:106:PRO:HG3	1.96	0.47
1:B:64:GLU:OE1	1:B:122:GLY:HA3	2.14	0.47
1:B:141:LEU:O	1:B:142:SER:C	2.53	0.47
1:A:31:SER:O	1:A:34:MET:HB3	2.13	0.47
1:B:31:SER:O	1:B:32:GLU:CG	2.62	0.47
1:A:152:GLN:CD	1:A:153:LYS:N	2.68	0.47
1:A:178:PHE:O	1:A:182:TYR:N	2.33	0.47
1:C:149:LYS:HG2	1:C:149:LYS:O	2.14	0.47
1:C:211:ILE:O	1:C:215:GLU:HG3	2.14	0.47
1:C:42:VAL:HG22	1:C:46:GLY:HA3	1.97	0.47
1:A:118:LEU:O	1:A:122:GLY:N	2.47	0.47
1:A:209:LEU:HA	1:A:212:GLU:HG3	1.96	0.47
1:B:73:VAL:HB	1:B:127:GLU:HA	1.96	0.47
1:C:83:LEU:O	1:C:84:HIS:C	2.52	0.47
1:A:168:THR:HG22	1:A:170:PRO:CD	2.34	0.47
1:C:184:ALA:O	1:C:187:ASN:HB2	2.14	0.47
1:C:61:LEU:HB2	1:C:118:LEU:HD21	1.97	0.47
1:A:128:LEU:O	1:A:131:ALA:N	2.46	0.47
1:A:135:THR:O	1:A:137:TYR:N	2.48	0.47
1:A:58:TYR:OH	1:A:136:ARG:O	2.21	0.47
1:B:83:LEU:HD21	1:B:178:PHE:CE2	2.50	0.47
1:B:39:LYS:CG	1:B:40:GLY:N	2.76	0.47
1:C:83:LEU:O	1:C:85:ARG:NE	2.47	0.47
1:A:152:GLN:HE22	1:A:153:LYS:CG	2.02	0.46
1:B:117:ARG:HG3	1:B:202:GLU:OE1	2.15	0.46
1:B:209:LEU:HA	1:B:212:GLU:HG2	1.96	0.46
1:B:36:ASN:N	1:B:36:ASN:HD22	2.14	0.46
1:B:79:PHE:HB2	1:B:83:LEU:HD12	1.98	0.46
1:B:148:LYS:O	1:B:150:ILE:N	2.49	0.46
1:C:137:TYR:O	1:C:141:LEU:HB2	2.15	0.46
1:C:224:GLU:OE1	1:C:224:GLU:HA	2.16	0.46
1:C:34:MET:O	1:C:38:GLN:OE1	2.34	0.46
1:A:145:GLN:CG	1:A:146:VAL:N	2.74	0.46
1:A:41:GLN:O	1:A:42:VAL:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:SER:N	2:A:271:HOH:O	2.41	0.46
1:A:62:GLU:O	1:A:66:GLU:HG2	2.16	0.46
1:C:48:LYS:C	1:C:97:TYR:OH	2.54	0.46
1:B:149:LYS:O	1:B:152:GLN:NE2	2.46	0.46
1:B:211:ILE:C	1:B:213:LEU:N	2.69	0.46
1:C:76:PRO:CB	1:C:185:ARG:HD2	2.43	0.46
1:C:202:GLU:O	1:C:205:THR:HB	2.15	0.46
1:C:217:LEU:O	1:C:221:LEU:HG	2.16	0.46
1:A:33:PHE:CG	1:A:218:GLN:HB2	2.52	0.45
1:B:114:TYR:CE2	1:B:210:ASN:HA	2.50	0.45
1:C:145:GLN:HG3	1:C:149:LYS:NZ	2.30	0.45
1:B:117:ARG:C	1:B:117:ARG:HH21	2.18	0.45
1:C:47:PHE:HZ	1:C:164:LEU:HD23	1.80	0.45
1:A:192:THR:OG1	1:A:194:GLU:HB3	2.17	0.45
1:B:111:THR:O	1:B:113:HIS:N	2.49	0.45
1:B:31:SER:O	1:B:32:GLU:HB3	2.17	0.45
1:A:145:GLN:O	1:A:149:LYS:HG3	2.17	0.45
1:A:76:PRO:O	1:A:77:LEU:HD23	2.16	0.45
1:A:115:VAL:O	1:A:119:HIS:CD2	2.69	0.45
1:B:197:HIS:O	1:B:197:HIS:ND1	2.50	0.45
1:A:117:ARG:HG3	1:A:121:VAL:CG2	2.47	0.45
1:A:149:LYS:NZ	1:B:185:ARG:CZ	2.80	0.45
1:A:37:PHE:CD2	1:A:50:VAL:HG11	2.52	0.45
1:B:101:TRP:O	1:B:102:GLN:C	2.55	0.45
1:C:34:MET:O	1:C:37:PHE:HB3	2.17	0.45
1:A:184:ALA:O	1:A:188:THR:HG23	2.17	0.45
1:A:80:PRO:O	1:A:84:HIS:HB2	2.17	0.45
1:B:145:GLN:HA	1:B:149:LYS:HE3	1.99	0.45
1:B:34:MET:C	1:B:36:ASN:H	2.19	0.45
1:A:217:LEU:O	1:A:221:LEU:HG	2.17	0.44
1:B:125:HIS:NE2	2:B:280:HOH:O	2.36	0.44
1:B:208:LEU:N	1:B:208:LEU:HD12	2.32	0.44
1:C:204:LYS:O	1:C:208:LEU:HB2	2.16	0.44
1:B:41:GLN:O	1:B:41:GLN:NE2	2.50	0.44
1:C:35:ARG:O	1:C:37:PHE:N	2.49	0.44
1:C:45:GLU:O	1:C:49:LEU:HB2	2.16	0.44
1:A:124:THR:O	1:A:125:HIS:ND1	2.50	0.44
1:A:74:TYR:HE1	1:A:130:VAL:HA	1.81	0.44
1:A:42:VAL:CG2	1:A:47:PHE:HA	2.47	0.44
1:C:207:PHE:O	1:C:211:ILE:HG13	2.17	0.44
1:C:49:LEU:HD12	1:C:221:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:SER:O	1:C:44:ARG:CB	2.65	0.44
1:B:56:HIS:ND1	1:B:56:HIS:N	2.65	0.44
1:B:85:ARG:O	1:B:89:LEU:HB2	2.16	0.44
1:B:77:LEU:HD21	1:B:186:MET:HA	1.99	0.44
1:C:195:VAL:O	1:C:198:ARG:N	2.50	0.44
1:A:101:TRP:O	1:A:105:ILE:HG13	2.18	0.44
1:A:117:ARG:O	1:A:118:LEU:C	2.56	0.44
1:A:82:GLU:HB3	1:A:172:ILE:CD1	2.41	0.44
1:B:80:PRO:HA	1:B:84:HIS:ND1	2.33	0.44
1:A:89:LEU:HD21	1:A:166:PHE:CD1	2.53	0.44
1:C:69:LYS:O	1:C:70:GLN:CG	2.66	0.44
1:B:60:ALA:HB1	1:B:115:VAL:HG13	1.99	0.44
1:B:72:PRO:HD2	2:B:278:HOH:O	2.17	0.44
1:C:155:MET:HB3	1:C:157:LEU:CD1	2.40	0.44
1:C:208:LEU:O	1:C:212:GLU:HG2	2.18	0.44
1:B:111:THR:C	1:B:113:HIS:N	2.68	0.43
1:B:48:LYS:HB3	1:B:96:TRP:CE3	2.52	0.43
1:C:58:TYR:CE2	1:C:166:PHE:HE1	2.36	0.43
1:A:194:GLU:OE1	1:A:198:ARG:CD	2.61	0.43
1:B:61:LEU:N	1:B:118:LEU:HD23	2.33	0.43
1:B:44:ARG:O	1:B:48:LYS:HG2	2.18	0.43
1:B:66:GLU:HA	1:B:66:GLU:OE1	2.18	0.43
1:C:145:GLN:O	1:C:145:GLN:CG	2.56	0.43
1:C:179:LYS:HE2	1:C:183:ARG:NH2	2.33	0.43
1:C:64:GLU:OE1	1:C:122:GLY:O	2.35	0.43
1:C:195:VAL:C	1:C:197:HIS:H	2.21	0.43
1:C:113:HIS:CE1	1:C:209:LEU:HD21	2.52	0.43
1:B:134:TYR:HD1	1:B:138:LEU:HD12	1.80	0.43
1:B:135:THR:O	1:B:139:GLY:HA3	2.18	0.43
1:C:47:PHE:HZ	1:C:164:LEU:CD2	2.32	0.43
1:B:148:LYS:NZ	1:B:168:THR:OG1	2.51	0.43
1:C:80:PRO:HG2	2:C:268:HOH:O	2.18	0.43
1:B:116:LYS:O	1:B:120:GLU:HG3	2.17	0.43
1:B:210:ASN:ND2	1:B:214:PHE:CE1	2.75	0.43
1:C:50:VAL:HG22	1:C:217:LEU:HD13	2.00	0.43
1:C:77:LEU:HD23	1:C:185:ARG:CB	2.48	0.43
1:B:117:ARG:NH2	1:B:117:ARG:HA	2.22	0.43
1:B:138:LEU:HA	1:B:141:LEU:HD22	1.99	0.43
1:B:149:LYS:C	1:B:152:GLN:OE1	2.57	0.43
1:B:170:PRO:C	1:B:172:ILE:H	2.22	0.43
1:B:34:MET:SD	1:B:214:PHE:CD1	3.11	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:ILE:HD13	1:C:74:TYR:OH	2.19	0.43
1:A:126:PRO:O	1:A:128:LEU:N	2.52	0.43
1:A:79:PHE:CZ	1:A:185:ARG:HD2	2.54	0.43
1:C:195:VAL:C	1:C:197:HIS:N	2.71	0.43
1:C:51:MET:HB3	1:C:93:MET:HE1	1.98	0.43
1:A:116:LYS:O	1:A:117:ARG:C	2.57	0.43
1:A:62:GLU:C	1:A:64:GLU:N	2.71	0.43
1:C:88:ALA:HB1	1:C:165:ALA:HB1	2.00	0.43
1:A:115:VAL:O	1:A:119:HIS:HD2	2.01	0.42
1:B:56:HIS:CE1	1:B:105:ILE:HD12	2.54	0.42
1:C:110:ALA:HB3	1:C:216:GLU:OE1	2.19	0.42
1:A:37:PHE:CD1	1:A:37:PHE:C	2.93	0.42
1:B:135:THR:O	1:B:139:GLY:CA	2.67	0.42
1:B:218:GLN:O	1:B:219:ALA:HB2	2.19	0.42
1:B:45:GLU:OE2	1:B:45:GLU:O	2.36	0.42
1:C:157:LEU:HD23	1:C:164:LEU:HD11	2.01	0.42
1:B:174:ASN:HB3	1:B:177:LYS:HB2	2.00	0.42
1:B:52:ALA:HA	1:B:93:MET:SD	2.59	0.42
1:C:147:LEU:O	1:C:151:ALA:CB	2.67	0.42
1:C:58:TYR:O	1:C:62:GLU:N	2.43	0.42
1:B:63:GLU:O	1:B:64:GLU:OE2	2.38	0.42
1:B:60:ALA:O	1:B:64:GLU:HG2	2.19	0.42
1:A:89:LEU:O	1:A:93:MET:CG	2.68	0.42
1:B:169:PHE:HB3	2:B:269:HOH:O	2.19	0.42
1:C:204:LYS:HA	1:C:207:PHE:HB3	2.01	0.42
1:C:222:THR:HG21	2:C:279:HOH:O	2.20	0.42
1:C:48:LYS:O	1:C:51:MET:HB2	2.19	0.42
1:C:75:ALA:HB3	1:C:76:PRO:HD3	2.02	0.42
1:B:121:VAL:O	1:B:121:VAL:HG12	2.19	0.42
1:B:146:VAL:O	1:B:147:LEU:C	2.58	0.42
1:B:217:LEU:CA	1:B:220:LEU:HD12	2.40	0.42
1:B:53:SER:C	1:B:55:TYR:N	2.73	0.42
1:B:79:PHE:O	1:B:83:LEU:N	2.49	0.42
1:A:209:LEU:HA	1:A:212:GLU:CG	2.50	0.42
1:B:118:LEU:HD12	1:B:132:HIS:CD2	2.55	0.42
1:B:205:THR:O	1:B:209:LEU:CG	2.68	0.42
1:C:183:ARG:O	1:C:186:MET:HB2	2.20	0.42
1:C:179:LYS:O	1:C:183:ARG:HG3	2.20	0.41
1:A:33:PHE:HA	1:A:36:ASN:CB	2.39	0.41
1:A:38:GLN:O	1:A:39:LYS:C	2.58	0.41
1:B:79:PHE:HD1	1:B:82:GLU:OE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:HIS:HB3	1:A:128:LEU:HG	2.01	0.41
1:A:178:PHE:O	1:A:181:LEU:N	2.53	0.41
1:B:127:GLU:H	1:B:127:GLU:CD	2.22	0.41
1:B:140:ASP:OD1	1:B:166:PHE:HZ	2.03	0.41
1:C:109:PRO:O	1:C:112:GLN:HB2	2.20	0.41
1:C:113:HIS:O	1:C:113:HIS:ND1	2.53	0.41
1:C:196:LYS:O	1:C:196:LYS:HG2	2.20	0.41
1:C:128:LEU:HB3	1:C:202:GLU:HG2	2.01	0.41
1:A:57:ILE:HD12	1:A:57:ILE:H	1.86	0.41
1:B:32:GLU:HG3	1:B:33:PHE:N	2.30	0.41
1:C:127:GLU:O	1:C:199:VAL:CG2	2.68	0.41
1:C:44:ARG:C	1:C:46:GLY:H	2.23	0.41
1:B:115:VAL:HG12	1:B:119:HIS:HD2	1.86	0.41
1:B:32:GLU:O	1:B:35:ARG:HB3	2.20	0.41
1:B:79:PHE:HB2	1:B:83:LEU:CG	2.50	0.41
1:C:209:LEU:HA	1:C:212:GLU:HG2	2.03	0.41
1:C:37:PHE:O	1:C:147:LEU:HD21	2.20	0.41
1:A:135:THR:HG22	2:A:276:HOH:O	2.20	0.41
1:B:114:TYR:CD1	1:B:209:LEU:HB3	2.55	0.41
1:B:154:ALA:O	1:B:155:MET:HG3	2.21	0.41
1:C:213:LEU:C	1:C:215:GLU:H	2.24	0.41
1:A:60:ALA:O	1:A:64:GLU:HG2	2.20	0.41
1:A:74:TYR:C	1:A:76:PRO:HD2	2.41	0.41
1:C:222:THR:OG1	1:C:223:GLU:OE1	2.38	0.41
1:C:37:PHE:CZ	1:C:50:VAL:HG11	2.56	0.41
1:B:58:TYR:OH	1:B:140:ASP:HB3	2.21	0.41
1:B:79:PHE:HB2	1:B:83:LEU:HG	2.01	0.41
1:C:136:ARG:O	1:C:140:ASP:N	2.49	0.41
1:C:62:GLU:OE2	1:C:84:HIS:HA	2.21	0.41
1:A:75:ALA:C	1:A:77:LEU:N	2.73	0.41
1:B:178:PHE:C	1:B:180:GLN:N	2.71	0.41
1:B:76:PRO:CB	1:B:185:ARG:HB3	2.51	0.41
1:A:145:GLN:HG2	1:A:146:VAL:HG13	2.03	0.40
1:A:62:GLU:OE2	1:A:84:HIS:O	2.40	0.40
1:B:49:LEU:HD22	1:B:217:LEU:HD22	2.02	0.40
1:C:147:LEU:O	1:C:151:ALA:HB2	2.21	0.40
1:C:133:ALA:HB1	1:C:182:TYR:OH	2.21	0.40
1:C:78:TYR:CD2	1:C:80:PRO:HD3	2.56	0.40
1:B:150:ILE:C	1:B:152:GLN:H	2.24	0.40
1:B:83:LEU:O	1:B:137:TYR:CE1	2.74	0.40
1:A:58:TYR:OH	1:A:140:ASP:CG	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:GLN:CA	1:B:149:LYS:HG3	2.49	0.40
1:B:222:THR:CG2	1:B:223:GLU:H	2.11	0.40
1:B:53:SER:O	1:B:54:LEU:C	2.60	0.40
1:B:93:MET:SD	1:B:105:ILE:HG21	2.60	0.40
1:A:207:PHE:O	1:A:211:ILE:HG12	2.22	0.40
1:B:146:VAL:HG12	1:B:147:LEU:N	2.36	0.40
1:C:151:ALA:HB1	1:C:155:MET:CE	2.50	0.40
1:C:76:PRO:HD2	1:C:189:LEU:CD1	2.51	0.40
1:C:82:GLU:O	1:C:172:ILE:HD11	2.21	0.40
1:C:114:TYR:HA	1:C:209:LEU:HD22	2.03	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	190/267 (71%)	143 (75%)	33 (17%)	14 (7%)	1	0
1	B	188/267 (70%)	129 (69%)	39 (21%)	20 (11%)	0	0
1	C	194/267 (73%)	138 (71%)	42 (22%)	14 (7%)	1	0
All	All	572/801 (71%)	410 (72%)	114 (20%)	48 (8%)	1	0

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	41	GLN
1	C	42	VAL
1	C	142	SER
1	A	38	GLN
1	A	39	LYS
1	A	41	GLN
1	A	43	SER

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Mol	Chain	Res	Type
1	B	32	GLU
1	B	74	TYR
1	B	175	PRO
1	B	176	THR
1	B	211	ILE
1	B	212	GLU
1	B	219	ALA
1	C	44	ARG
1	C	144	GLY
1	C	150	ILE
1	C	155	MET
1	A	134	TYR
1	A	135	THR
1	A	136	ARG
1	A	143	GLY
1	B	112	GLN
1	B	171	SER
1	B	183	ARG
1	B	222	THR
1	C	36	ASN
1	C	40	GLY
1	A	127	GLU
1	A	166	PHE
1	B	39	LYS
1	B	141	LEU
1	B	146	VAL
1	B	149	LYS
1	C	84	HIS
1	A	85	ARG
1	A	144	GLY
1	B	41	GLN
1	B	43	SER
1	B	73	VAL
1	C	74	TYR
1	C	136	ARG
1	A	75	ALA
1	B	38	GLN
1	B	135	THR
1	C	192	THR
1	C	214	PHE
1	A	76	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	164/233 (70%)	147 (90%)	17 (10%)	7	7
1	B	166/233 (71%)	141 (85%)	25 (15%)	3	2
1	C	168/233 (72%)	148 (88%)	20 (12%)	5	5
All	All	498/699 (71%)	436 (88%)	62 (12%)	4	4

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	30	ASN
1	C	34	MET
1	C	49	LEU
1	C	51	MET
1	C	84	HIS
1	C	85	ARG
1	C	89	LEU
1	C	91	GLN
1	C	114	TYR
1	C	116	LYS
1	C	147	LEU
1	C	168	THR
1	C	174	ASN
1	C	176	THR
1	C	180	GLN
1	C	205	THR
1	C	207	PHE
1	C	210	ASN
1	C	212	GLU
1	C	224	GLU
1	A	35	ARG
1	A	41	GLN
1	A	49	LEU
1	A	84	HIS
1	A	85	ARG
1	A	86	ARG

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Mol	Chain	Res	Type
1	A	103	GLU
1	A	107	TYR
1	A	113	HIS
1	A	118	LEU
1	A	136	ARG
1	A	141	LEU
1	A	145	GLN
1	A	182	TYR
1	A	194	GLU
1	A	212	GLU
1	A	222	THR
1	B	32	GLU
1	B	38	GLN
1	B	41	GLN
1	B	44	ARG
1	B	49	LEU
1	B	56	HIS
1	B	82	GLU
1	B	84	HIS
1	B	85	ARG
1	B	86	ARG
1	B	89	LEU
1	B	102	GLN
1	B	103	GLU
1	B	114	TYR
1	B	117	ARG
1	B	130	VAL
1	B	136	ARG
1	B	141	LEU
1	B	145	GLN
1	B	152	GLN
1	B	166	PHE
1	B	181	LEU
1	B	189	LEU
1	B	218	GLN
1	B	221	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	30	ASN
1	C	38	GLN

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Mol	Chain	Res	Type
1	C	41	GLN
1	C	56	HIS
1	C	91	GLN
1	C	112	GLN
1	C	119	HIS
1	C	210	ASN
1	C	218	GLN
1	A	68	ASN
1	A	102	GLN
1	A	112	GLN
1	A	132	HIS
1	A	145	GLN
1	A	152	GLN
1	A	187	ASN
1	A	210	ASN
1	B	36	ASN
1	B	41	GLN
1	B	56	HIS
1	B	102	GLN
1	B	112	GLN
1	B	113	HIS
1	B	119	HIS
1	B	132	HIS
1	B	152	GLN
1	B	210	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [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	192/267 (71%)	-0.05	1 (0%) 91 94	17, 35, 48, 59	0
1	B	192/267 (71%)	0.21	1 (0%) 91 94	24, 45, 60, 65	0
1	C	196/267 (73%)	-0.07	1 (0%) 91 94	16, 37, 59, 69	0
All	All	580/801 (72%)	0.03	3 (0%) 91 94	16, 39, 58, 69	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	156	ALA	4.3
1	A	33	PHE	3.0
1	C	31	SER	2.3

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.