



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 30, 2021 – 05:45 PM EDT

PDB ID : 3MP5  
Title : Crystal Structure of Human Lyase R41M in complex with HMG-CoA  
Authors : Fu, Z.; Runquist, J.A.; Montgomery, C.; Mizioroko, H.M.; Kim, J.-J.P.  
Deposited on : 2010-04-24  
Resolution : 2.25 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
buster-report : 1.1.7 (2018)  
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) : 2.23.2

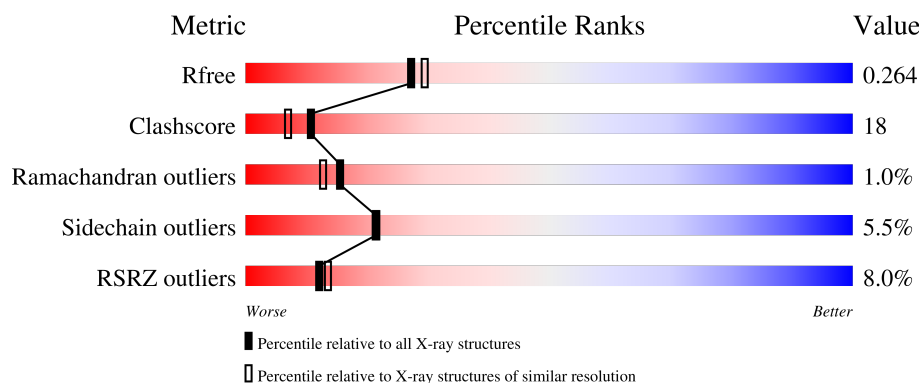
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	298	<div> <div>4%</div> <div>75%</div> <div>21%</div> <div>..</div> </div>
1	B	298	<div> <div>7%</div> <div>65%</div> <div>31%</div> <div>..</div> </div>
1	C	298	<div> <div>11%</div> <div>59%</div> <div>35%</div> <div>..</div> </div>
1	D	298	<div> <div>5%</div> <div>68%</div> <div>26%</div> <div>..</div> </div>
1	E	298	<div> <div>4%</div> <div>67%</div> <div>28%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	298	<div><div></div><div>17%</div><div>59%</div><div>36%</div><div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13438 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.

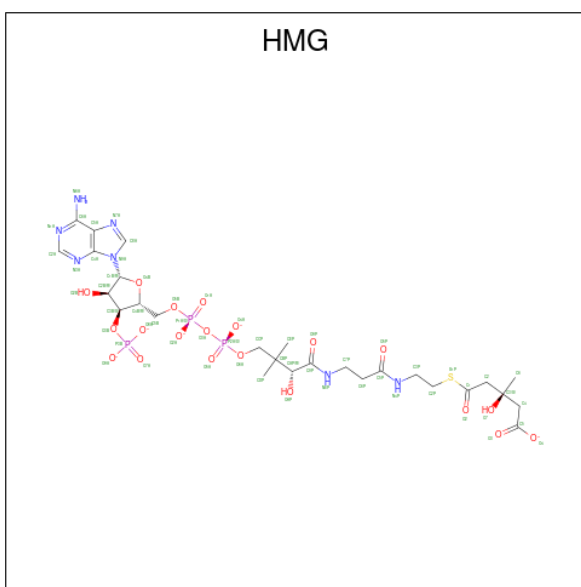
- Molecule 1 is a protein called Hydroxymethylglutaryl-CoA lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2186	1389	362	417	18			
1	B	296	Total	C	N	O	S	0	0	0
			2186	1389	362	417	18			
1	C	288	Total	C	N	O	S	0	0	0
			2134	1357	353	407	17			
1	D	294	Total	C	N	O	S	0	0	0
			2173	1382	359	414	18			
1	E	296	Total	C	N	O	S	0	0	0
			2186	1389	362	417	18			
1	F	294	Total	C	N	O	S	0	0	0
			2169	1377	360	414	18			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	MET	ARG	engineered mutation	UNP P35914
B	41	MET	ARG	engineered mutation	UNP P35914
C	41	MET	ARG	engineered mutation	UNP P35914
D	41	MET	ARG	engineered mutation	UNP P35914
E	41	MET	ARG	engineered mutation	UNP P35914
F	41	MET	ARG	engineered mutation	UNP P35914

- Molecule 2 is 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A (three-letter code: HMG) (formula: C<sub>27</sub>H<sub>39</sub>N<sub>7</sub>O<sub>20</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	S	
			58	27	7	20	3	1	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

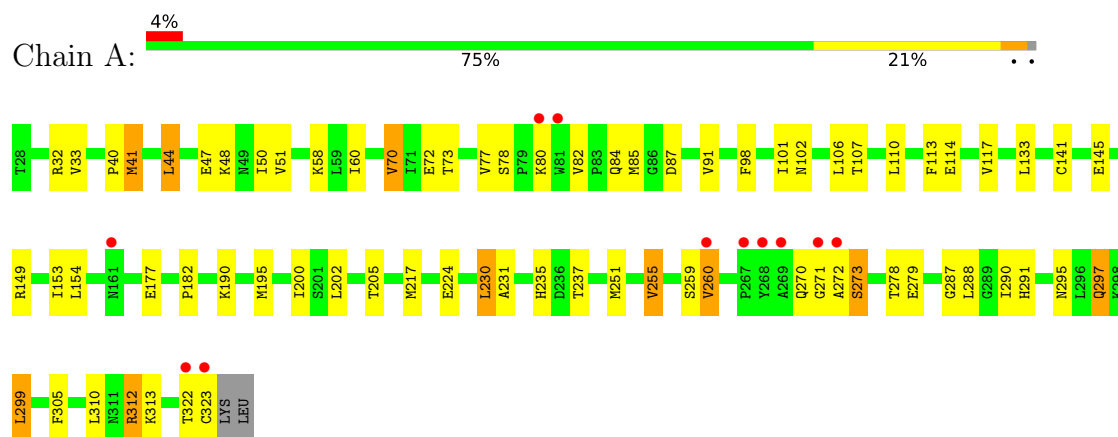
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		
4	B	62	Total	O	0	0
			62	62		
4	C	30	Total	O	0	0
			30	30		
4	D	66	Total	O	0	0
			66	66		
4	E	59	Total	O	0	0
			59	59		
4	F	22	Total	O	0	0
			22	22		

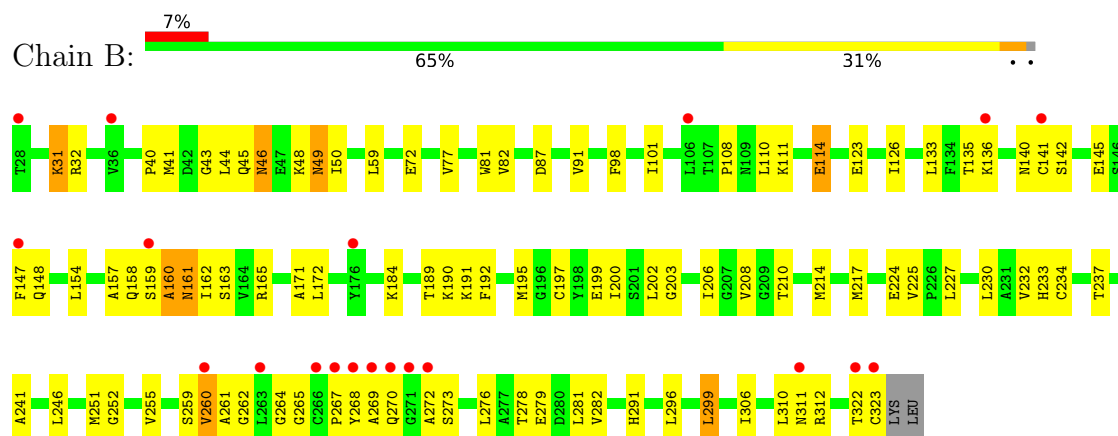
### 3 Residue-property plots [i](#)

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.

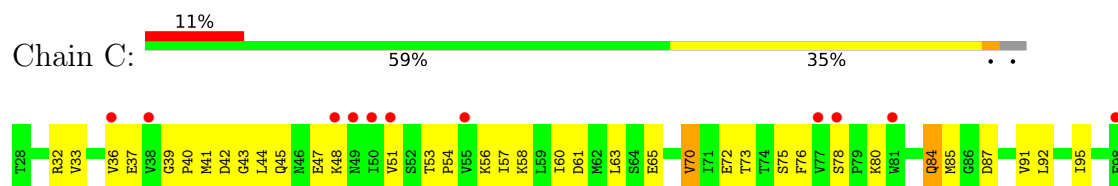
#### • Molecule 1: Hydroxymethylglutaryl-CoA lyase

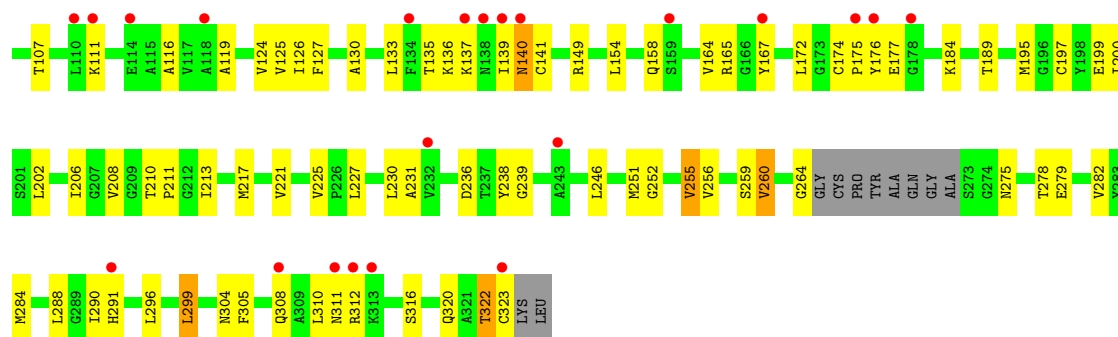


#### • Molecule 1: Hydroxymethylglutaryl-CoA lyase

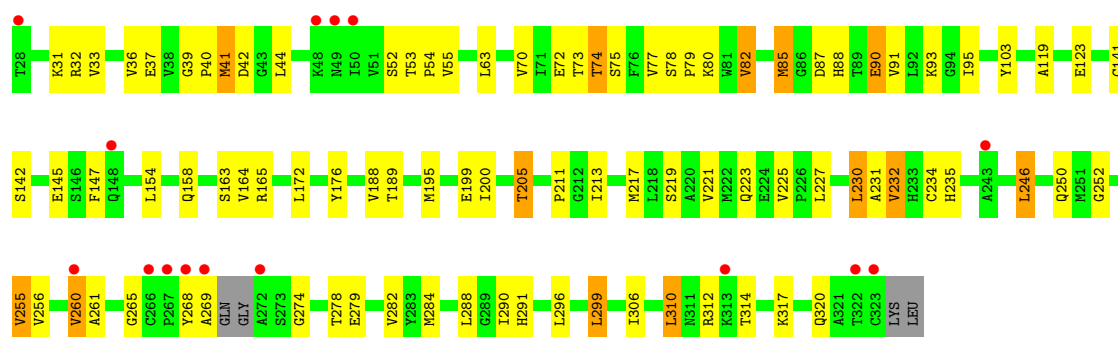


#### • Molecule 1: Hydroxymethylglutaryl-CoA lyase

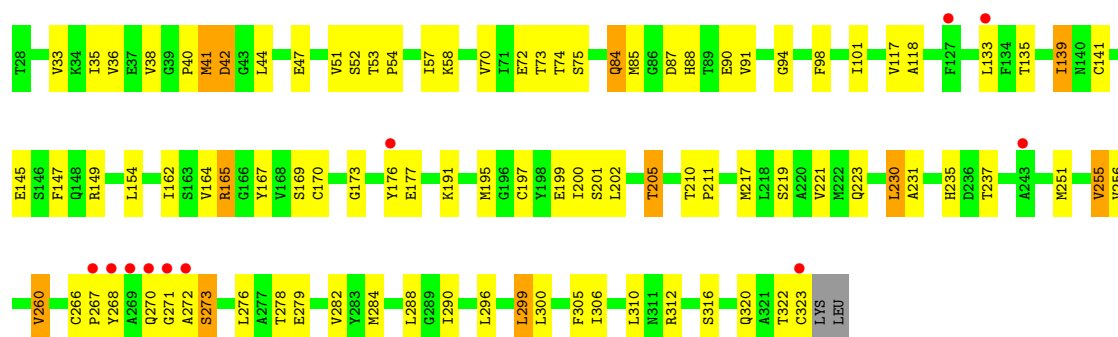




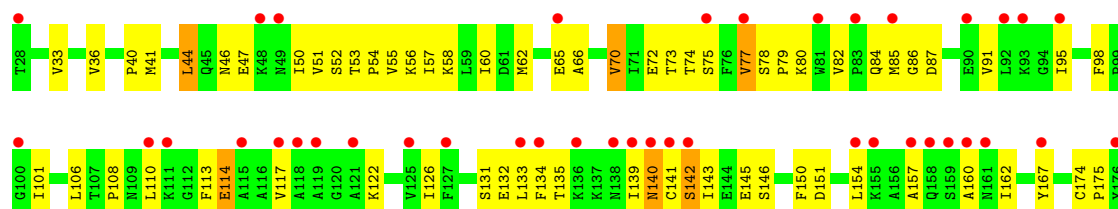
• Molecule 1: Hydroxymethylglutaryl-CoA lyase

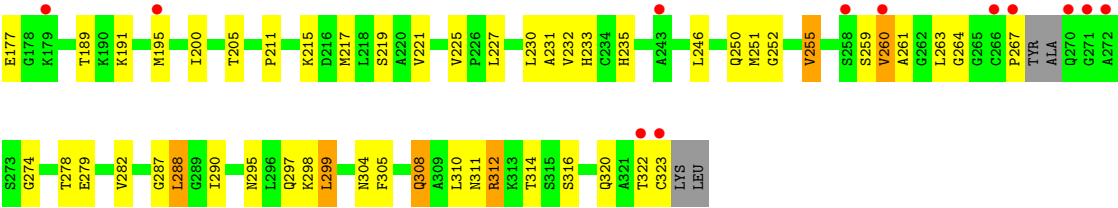


• Molecule 1: Hydroxymethylglutaryl-CoA lyase



• Molecule 1: Hydroxymethylglutaryl-CoA lyase







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	197.98Å 116.66Å 86.52Å 90.00° 112.16° 90.00°	Depositor
Resolution (Å)	28.35 – 2.25 28.35 – 2.25	Depositor EDS
% Data completeness (in resolution range)	94.8 (28.35-2.25) 94.9 (28.35-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 2.24Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.221 , 0.271 0.214 , 0.264	Depositor DCC
$R_{free}$ test set	8220 reflections (10.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 42.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13438	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: MG, HMG

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	0.40	0/2221	0.63	0/3007
1	B	0.38	0/2221	0.62	0/3007
1	C	0.35	0/2166	0.56	0/2930
1	D	0.37	0/2207	0.59	0/2987
1	E	0.37	0/2221	0.59	0/3007
1	F	0.33	0/2202	0.56	0/2979
All	All	0.37	0/13238	0.59	0/17917

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	2186	0	2240	59	0
1	B	2186	0	2240	81	0
1	C	2134	0	2194	92	0
1	D	2173	0	2228	76	0
1	E	2186	0	2240	80	0
1	F	2169	0	2225	107	0
2	B	58	0	38	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	105	0	0	4	0
4	B	62	0	0	2	0
4	C	30	0	0	1	0
4	D	66	0	0	0	0
4	E	59	0	0	1	0
4	F	22	0	0	1	0
All	All	13438	0	13405	484	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 18.

All (484) 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:73:THR:HG22	1:D:74:THR:HG22	1.32	1.11
1:E:139:ILE:HD13	1:E:139:ILE:H	1.30	0.95
1:D:36:VAL:HA	1:D:70:VAL:HG13	1.49	0.95
1:C:288:LEU:HD11	1:D:211:PRO:HD2	1.47	0.95
1:C:211:PRO:HG2	1:D:288:LEU:HD21	1.49	0.93
1:D:40:PRO:HA	1:D:44:LEU:HD23	1.50	0.92
1:F:77:VAL:HG22	1:F:78:SER:H	1.37	0.90
1:E:211:PRO:HG2	1:F:288:LEU:HD11	1.55	0.89
1:C:133:LEU:HD12	1:C:177:GLU:HG2	1.55	0.88
1:F:142:SER:HB3	1:F:145:GLU:HG3	1.56	0.85
1:A:295:ASN:OD1	1:A:297:GLN:HG2	1.78	0.83
1:D:36:VAL:HG22	1:D:70:VAL:HG11	1.60	0.83
1:A:48:LYS:H	1:A:48:LYS:HD2	1.44	0.82
1:D:265:GLY:HA2	1:D:274:GLY:HA3	1.61	0.81
1:B:190:LYS:HD3	1:B:224:GLU:HB3	1.60	0.81
1:A:48:LYS:HD2	1:A:48:LYS:N	1.95	0.80
1:C:279:GLU:HG3	1:C:299:LEU:HD13	1.62	0.79
1:B:136:LYS:O	1:B:140:ASN:HA	1.83	0.79
1:D:142:SER:HB3	1:D:145:GLU:HG3	1.65	0.79
1:E:36:VAL:HA	1:E:70:VAL:HG13	1.66	0.78
1:D:172:LEU:HD22	1:D:213:ILE:HG22	1.65	0.78
1:A:231:ALA:HB2	1:A:255:VAL:HG22	1.65	0.77
1:B:203:GLY:HA2	1:B:233:HIS:HB3	1.66	0.76
1:C:48:LYS:H	1:C:48:LYS:HD2	1.51	0.74
1:F:75:SER:HB3	1:F:85:MET:HG2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:113:PHE:O	1:F:117:VAL:HG23	1.87	0.74
1:C:36:VAL:HA	1:C:70:VAL:HG22	1.69	0.74
1:C:84:GLN:H	1:C:84:GLN:NE2	1.85	0.74
1:F:77:VAL:HG22	1:F:78:SER:N	2.02	0.74
1:A:260:VAL:O	1:A:279:GLU:OE2	2.05	0.73
1:A:154:LEU:HD13	1:A:195:MET:HB3	1.70	0.73
1:F:77:VAL:HG11	1:F:82:VAL:CG1	2.18	0.72
1:C:211:PRO:CG	1:D:288:LEU:HD21	2.20	0.72
1:F:278:THR:O	1:F:282:VAL:HG13	1.89	0.72
1:A:279:GLU:HG3	1:A:299:LEU:HD13	1.70	0.72
1:D:91:VAL:O	1:D:95:ILE:HG23	1.90	0.72
1:B:189:THR:HG22	1:B:225:VAL:HG21	1.72	0.71
1:C:135:THR:HG22	1:C:141:CYS:O	1.91	0.71
1:C:284:MET:O	1:C:288:LEU:HD13	1.91	0.70
1:C:47:GLU:HG2	1:C:310:LEU:HD21	1.73	0.70
1:A:149:ARG:HH21	1:A:149:ARG:HG3	1.56	0.70
1:D:154:LEU:CD1	1:D:195:MET:HB3	2.21	0.70
1:B:154:LEU:O	1:B:158:GLN:HG3	1.91	0.70
1:A:41:MET:SD	1:A:106:LEU:HD13	2.32	0.69
1:B:31:LYS:H	1:B:31:LYS:HD3	1.58	0.69
1:A:231:ALA:CB	1:A:255:VAL:HG22	2.22	0.69
1:B:45:GLN:HE22	2:B:401:HMG:H3P2	1.57	0.69
1:E:154:LEU:CD1	1:E:195:MET:HB3	2.23	0.69
1:E:288:LEU:HD12	4:F:630:HOH:O	1.92	0.69
1:F:46:ASN:HD22	1:F:267:PRO:HG3	1.57	0.69
1:E:191:LYS:HG3	1:E:195:MET:HE1	1.75	0.68
1:F:47:GLU:HG2	1:F:310:LEU:HD21	1.75	0.68
1:C:278:THR:HG22	1:C:299:LEU:HD11	1.75	0.68
1:F:139:ILE:HG13	1:F:141:CYS:H	1.59	0.68
1:B:48:LYS:H	1:B:48:LYS:HD2	1.58	0.68
1:C:36:VAL:HG22	1:C:70:VAL:HG21	1.75	0.68
1:C:291:HIS:HB2	4:C:748:HOH:O	1.94	0.67
1:C:125:VAL:HG22	1:C:165:ARG:HB3	1.75	0.67
1:E:84:GLN:H	1:E:84:GLN:NE2	1.91	0.67
1:F:154:LEU:HD13	1:F:195:MET:O	1.93	0.67
1:D:284:MET:O	1:D:288:LEU:HD23	1.95	0.66
1:F:98:PHE:HB2	1:F:101:ILE:HD12	1.75	0.66
1:E:322:THR:O	1:E:323:CYS:HB2	1.95	0.66
1:E:288:LEU:HD11	1:F:211:PRO:HD2	1.77	0.66
1:E:36:VAL:HG22	1:E:70:VAL:HG11	1.76	0.66
1:A:297:GLN:CD	1:A:297:GLN:H	1.98	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:PRO:HA	1:D:44:LEU:CD2	2.24	0.65
1:C:126:ILE:HD11	1:C:197:CYS:SG	2.36	0.65
1:E:58:LYS:HD3	1:E:305:PHE:CZ	2.32	0.65
1:D:260:VAL:O	1:D:279:GLU:OE1	2.13	0.65
1:C:58:LYS:HD3	1:C:305:PHE:CZ	2.32	0.65
1:A:58:LYS:HD3	1:A:305:PHE:CZ	2.32	0.64
1:F:304:ASN:O	1:F:308:GLN:HG2	1.98	0.64
1:F:139:ILE:O	1:F:140:ASN:HB2	1.98	0.64
1:D:306:ILE:HG13	1:D:310:LEU:HD22	1.80	0.63
1:F:46:ASN:ND2	1:F:267:PRO:HG3	2.13	0.63
1:B:135:THR:HG22	1:B:141:CYS:O	1.99	0.63
1:E:47:GLU:HG2	1:E:310:LEU:HD21	1.79	0.63
1:B:98:PHE:HB2	1:B:101:ILE:HD12	1.81	0.63
1:B:40:PRO:HG2	1:B:72:GLU:O	1.98	0.62
1:C:84:GLN:H	1:C:84:GLN:HE21	1.44	0.62
1:B:46:ASN:HB2	1:B:265:GLY:O	1.98	0.62
1:F:264:GLY:O	1:F:274:GLY:HA3	1.99	0.62
1:F:52:SER:OG	1:F:55:VAL:HG23	1.98	0.62
1:F:53:THR:N	1:F:54:PRO:HD2	2.15	0.62
1:A:202:LEU:HD13	1:A:217:MET:SD	2.39	0.62
1:B:322:THR:O	1:B:323:CYS:HB2	1.99	0.61
1:D:265:GLY:HA2	1:D:274:GLY:CA	2.30	0.61
1:F:200:ILE:HD12	1:F:200:ILE:N	2.14	0.61
1:C:61:ASP:O	1:C:65:GLU:HG3	2.00	0.61
1:F:87:ASP:O	1:F:91:VAL:HG23	1.99	0.61
1:B:278:THR:O	1:B:282:VAL:HG13	2.01	0.61
1:E:278:THR:O	1:E:282:VAL:HG13	2.01	0.61
1:F:50:ILE:HG22	1:F:84:GLN:HG3	1.83	0.61
1:B:81:TRP:CH2	1:B:140:ASN:HB2	2.36	0.61
1:C:42:ASP:O	1:C:264:GLY:HA2	2.01	0.60
1:D:154:LEU:HD13	1:D:195:MET:O	2.02	0.60
1:D:227:LEU:HD21	1:D:252:GLY:HA3	1.83	0.60
1:C:304:ASN:O	1:C:308:GLN:HG3	2.01	0.60
1:E:231:ALA:CB	1:E:255:VAL:HG22	2.32	0.59
1:D:93:LYS:HE3	1:D:119:ALA:HA	1.83	0.59
1:E:154:LEU:HD13	1:E:195:MET:HB3	1.84	0.59
1:C:92:LEU:HD23	1:C:119:ALA:HB3	1.85	0.58
1:A:154:LEU:CD1	1:A:195:MET:HB3	2.32	0.58
1:E:53:THR:N	1:E:54:PRO:HD2	2.18	0.58
1:B:200:ILE:N	1:B:200:ILE:HD12	2.18	0.58
1:C:206:ILE:HG13	1:C:208:VAL:HG13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:310:LEU:HD23	1:F:312:ARG:HG2	1.84	0.58
1:D:231:ALA:CB	1:D:255:VAL:HG22	2.33	0.58
1:B:49:ASN:N	1:B:49:ASN:HD22	2.01	0.58
1:B:147:PHE:HE2	1:B:192:PHE:HE1	1.51	0.58
1:E:211:PRO:HG2	1:F:288:LEU:CD1	2.31	0.58
1:E:139:ILE:HD13	1:E:139:ILE:N	2.10	0.58
1:C:87:ASP:O	1:C:91:VAL:HG23	2.03	0.57
1:D:82:VAL:HG22	1:D:82:VAL:O	2.04	0.57
1:A:291:HIS:HB2	4:A:548:HOH:O	2.03	0.57
1:D:123:GLU:HG3	1:D:163:SER:OG	2.04	0.57
1:F:40:PRO:HA	1:F:44:LEU:CD2	2.34	0.57
1:E:165:ARG:NH2	1:E:199:GLU:OE2	2.36	0.57
1:E:84:GLN:H	1:E:84:GLN:HE21	1.51	0.57
1:A:98:PHE:HB2	1:A:101:ILE:HD12	1.87	0.57
1:E:210:THR:HG21	1:F:287:GLY:HA3	1.85	0.57
1:C:282:VAL:HG21	1:C:296:LEU:HD13	1.87	0.56
1:D:77:VAL:HG11	1:D:82:VAL:CG1	2.36	0.56
1:A:40:PRO:HA	1:A:44:LEU:HD22	1.85	0.56
1:A:273:SER:HB2	4:A:742:HOH:O	2.06	0.56
1:C:51:VAL:HG23	1:C:56:LYS:NZ	2.20	0.56
1:F:77:VAL:HG11	1:F:82:VAL:HG13	1.87	0.56
1:F:133:LEU:HD23	1:F:177:GLU:HG2	1.86	0.56
1:E:51:VAL:HG13	1:E:310:LEU:HD13	1.88	0.56
1:E:260:VAL:O	1:E:279:GLU:OE1	2.24	0.56
1:B:282:VAL:HG21	1:B:296:LEU:HD13	1.88	0.56
1:C:40:PRO:HG2	1:C:72:GLU:O	2.06	0.56
1:D:141:CYS:HB2	1:D:145:GLU:OE2	2.06	0.56
1:E:133:LEU:HD23	1:E:176:TYR:HB3	1.88	0.56
1:D:40:PRO:HG2	1:D:72:GLU:O	2.06	0.55
1:E:237:THR:HG23	1:E:272:ALA:HB3	1.88	0.55
1:A:50:ILE:HG22	1:A:84:GLN:HG3	1.87	0.55
1:E:40:PRO:HG2	1:E:72:GLU:O	2.06	0.55
1:F:141:CYS:O	1:F:142:SER:O	2.25	0.55
1:F:58:LYS:HD3	1:F:305:PHE:CZ	2.41	0.55
1:B:282:VAL:CG2	1:B:296:LEU:HD13	2.35	0.55
1:C:200:ILE:N	1:C:200:ILE:HD12	2.21	0.55
1:C:210:THR:HB	1:C:211:PRO:HD2	1.89	0.55
1:D:87:ASP:O	1:D:91:VAL:HG23	2.06	0.55
1:E:279:GLU:HG2	1:E:300:LEU:HD23	1.87	0.55
1:D:77:VAL:HG11	1:D:82:VAL:HG11	1.89	0.55
1:B:202:LEU:HD13	1:B:217:MET:SD	2.46	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:ARG:NH1	1:C:291:HIS:HD2	2.05	0.55
1:C:40:PRO:HA	1:C:44:LEU:CD2	2.37	0.55
1:E:251:MET:HE2	1:E:251:MET:HA	1.89	0.55
1:F:77:VAL:HG13	1:F:78:SER:N	2.21	0.55
1:F:154:LEU:CD1	1:F:195:MET:HB3	2.37	0.55
1:F:230:LEU:O	1:F:255:VAL:HG13	2.07	0.55
1:C:53:THR:N	1:C:54:PRO:HD2	2.22	0.54
1:C:136:LYS:O	1:C:140:ASN:HA	2.07	0.54
1:A:322:THR:O	1:A:323:CYS:HB2	2.06	0.54
1:C:154:LEU:CD1	1:C:195:MET:HB3	2.37	0.54
1:C:189:THR:HG22	1:C:225:VAL:HG21	1.89	0.54
1:A:230:LEU:O	1:A:255:VAL:HG13	2.08	0.54
1:B:154:LEU:HD13	1:B:195:MET:HB3	1.90	0.54
1:F:174:CYS:SG	1:F:175:PRO:HD2	2.47	0.54
1:B:237:THR:HG23	1:B:273:SER:HB2	1.89	0.54
1:C:278:THR:O	1:C:282:VAL:HG13	2.08	0.54
1:D:74:THR:OG1	1:D:75:SER:N	2.41	0.54
1:F:260:VAL:O	1:F:279:GLU:OE1	2.25	0.54
1:B:159:SER:O	1:B:160:ALA:HB2	2.07	0.53
1:F:278:THR:HG22	1:F:299:LEU:HD11	1.90	0.53
1:E:33:VAL:HG23	1:E:290:ILE:HG21	1.90	0.53
1:B:306:ILE:HG13	1:B:310:LEU:CD2	2.38	0.53
1:E:38:VAL:HB	1:E:42:ASP:HB2	1.89	0.53
1:A:47:GLU:HG3	1:A:310:LEU:HD21	1.91	0.53
1:D:75:SER:H	1:D:85:MET:HG2	1.73	0.53
1:C:230:LEU:O	1:C:255:VAL:HG13	2.09	0.53
1:E:278:THR:HG22	1:E:299:LEU:HD11	1.90	0.53
1:A:278:THR:HG22	1:A:299:LEU:HD11	1.89	0.53
1:E:199:GLU:C	1:E:200:ILE:HD12	2.29	0.53
1:C:135:THR:O	1:C:139:ILE:HG12	2.09	0.53
1:C:202:LEU:HD13	1:C:217:MET:SD	2.49	0.52
1:A:200:ILE:HD12	1:A:200:ILE:N	2.23	0.52
1:E:135:THR:HG23	1:E:139:ILE:HD11	1.90	0.52
1:F:259:SER:OG	1:F:263:LEU:HB2	2.09	0.52
1:B:291:HIS:HB2	4:B:643:HOH:O	2.08	0.52
1:F:51:VAL:HG23	1:F:56:LYS:HG3	1.91	0.52
1:B:43:GLY:HA2	1:B:264:GLY:HA2	1.90	0.52
1:B:171:ALA:O	1:B:172:LEU:HD23	2.10	0.52
1:E:282:VAL:CG2	1:E:296:LEU:HD13	2.40	0.52
1:D:200:ILE:HD12	1:D:200:ILE:N	2.24	0.52
1:F:117:VAL:HG13	1:F:162:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:62:MET:O	1:F:65:GLU:HB3	2.10	0.52
1:D:80:LYS:HE2	1:E:118:ALA:O	2.10	0.52
1:B:227:LEU:HD21	1:B:252:GLY:HA3	1.93	0.51
1:C:33:VAL:HG23	1:C:290:ILE:HG21	1.91	0.51
1:C:130:ALA:HB1	1:C:184:LYS:HG3	1.92	0.51
1:D:231:ALA:HB2	1:D:255:VAL:HG22	1.92	0.51
1:F:261:ALA:HB1	1:F:314:THR:OG1	2.11	0.51
1:C:259:SER:HB2	1:C:275:ASN:HB2	1.93	0.51
1:F:191:LYS:HE3	1:F:195:MET:SD	2.50	0.51
1:A:141:CYS:HB2	1:A:145:GLU:OE2	2.10	0.51
1:F:279:GLU:O	1:F:282:VAL:HG22	2.10	0.51
1:B:147:PHE:CE1	1:B:191:LYS:HG2	2.46	0.51
1:B:199:GLU:C	1:B:200:ILE:HD12	2.31	0.51
1:C:60:ILE:HD13	1:C:73:THR:HG23	1.92	0.51
1:D:36:VAL:HA	1:D:70:VAL:CG1	2.32	0.51
1:F:110:LEU:HD12	1:F:110:LEU:O	2.11	0.51
1:C:41:MET:SD	1:C:41:MET:C	2.89	0.51
1:D:73:THR:CG2	1:D:74:THR:HG22	2.23	0.51
1:E:74:THR:OG1	1:E:75:SER:N	2.44	0.51
1:A:237:THR:HG23	1:A:272:ALA:HB3	1.92	0.50
1:E:141:CYS:HB2	1:E:145:GLU:OE2	2.11	0.50
1:E:202:LEU:HD13	1:E:217:MET:SD	2.51	0.50
1:E:230:LEU:O	1:E:255:VAL:HG13	2.10	0.50
1:F:131:SER:C	1:F:143:ILE:HD11	2.31	0.50
1:A:51:VAL:HG13	1:A:310:LEU:HD13	1.93	0.50
1:A:113:PHE:O	1:A:117:VAL:HG23	2.11	0.50
1:C:39:GLY:O	1:C:43:GLY:HA3	2.11	0.50
1:E:139:ILE:HB	1:E:149:ARG:HH12	1.77	0.50
1:E:147:PHE:CD2	1:E:195:MET:HE1	2.46	0.50
1:D:37:GLU:HG2	1:D:63:LEU:HD13	1.94	0.50
1:F:56:LYS:HD2	1:F:87:ASP:OD1	2.11	0.50
1:F:134:PHE:HB2	1:F:174:CYS:SG	2.51	0.50
1:C:63:LEU:HD21	1:C:260:VAL:HG22	1.93	0.50
1:C:107:THR:OG1	1:C:124:VAL:HB	2.12	0.50
1:C:278:THR:CG2	1:C:299:LEU:HD11	2.41	0.50
1:B:49:ASN:ND2	1:B:49:ASN:H	2.10	0.50
1:A:149:ARG:HG3	1:A:149:ARG:NH2	2.25	0.49
1:D:154:LEU:HD23	1:D:164:VAL:HG21	1.94	0.49
1:B:133:LEU:HA	1:B:136:LYS:HD2	1.94	0.49
1:B:279:GLU:HG3	1:B:299:LEU:HD13	1.94	0.49
1:F:160:ALA:O	1:F:162:ILE:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:57:ILE:HD13	1:E:94:GLY:HA3	1.94	0.49
1:F:126:ILE:HD12	1:F:150:PHE:CG	2.47	0.49
1:F:295:ASN:CG	1:F:298:LYS:HG2	2.33	0.49
1:E:170:CYS:HA	1:E:173:GLY:O	2.12	0.49
1:F:215:LYS:HG3	1:F:251:MET:SD	2.52	0.49
1:F:139:ILE:CD1	1:F:146:SER:HB3	2.43	0.49
1:A:190:LYS:HD3	1:A:224:GLU:HB3	1.94	0.49
1:D:278:THR:O	1:D:282:VAL:HG13	2.12	0.49
1:F:131:SER:HB3	1:F:134:PHE:HB3	1.94	0.49
1:C:236:ASP:OD1	1:C:239:GLY:HA2	2.13	0.49
1:E:139:ILE:HB	1:E:149:ARG:NH1	2.28	0.49
1:F:142:SER:O	1:F:145:GLU:N	2.45	0.49
1:A:58:LYS:HD3	1:A:305:PHE:CE1	2.47	0.49
1:A:251:MET:HA	1:A:251:MET:CE	2.43	0.49
1:C:282:VAL:CG2	1:C:296:LEU:HD13	2.43	0.49
1:C:322:THR:HG22	1:C:323:CYS:N	2.27	0.49
1:D:232:VAL:HG13	1:D:234:CYS:SG	2.53	0.49
1:F:230:LEU:O	1:F:255:VAL:CG1	2.60	0.49
1:A:205:THR:HA	1:A:235:HIS:CD2	2.48	0.48
1:E:35:ILE:CD1	1:E:282:VAL:HG12	2.43	0.48
1:A:48:LYS:H	1:A:48:LYS:CD	2.21	0.48
1:A:51:VAL:CG1	1:A:310:LEU:HD13	2.43	0.48
1:D:176:TYR:HH	1:D:268:TYR:HE2	1.61	0.48
1:B:267:PRO:HG2	1:B:268:TYR:HD1	1.78	0.48
1:E:191:LYS:O	1:E:195:MET:HE2	2.13	0.48
1:D:279:GLU:OE1	1:D:279:GLU:N	2.45	0.48
1:D:317:LYS:HD3	1:D:320:GLN:OE1	2.13	0.48
1:F:322:THR:O	1:F:323:CYS:HB2	2.12	0.48
1:D:77:VAL:HG22	1:D:78:SER:N	2.29	0.48
1:E:205:THR:HA	1:E:235:HIS:CD2	2.49	0.48
1:F:227:LEU:HD21	1:F:252:GLY:HA3	1.94	0.48
1:F:295:ASN:OD1	1:F:298:LYS:HG2	2.13	0.48
1:C:227:LEU:HD21	1:C:252:GLY:HA3	1.94	0.48
1:D:154:LEU:HD13	1:D:195:MET:HB3	1.93	0.48
1:C:141:CYS:SG	1:C:149:ARG:NH2	2.86	0.47
1:D:282:VAL:CG2	1:D:296:LEU:HD13	2.44	0.47
1:E:98:PHE:CB	1:E:101:ILE:HD12	2.44	0.47
1:D:261:ALA:HB1	1:D:314:THR:OG1	2.13	0.47
1:A:107:THR:HG21	1:A:113:PHE:HA	1.96	0.47
1:B:259:SER:O	1:B:260:VAL:O	2.32	0.47
1:D:230:LEU:O	1:D:255:VAL:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:47:GLU:CG	1:F:310:LEU:HD21	2.42	0.47
1:C:199:GLU:C	1:C:200:ILE:HD12	2.34	0.47
1:C:230:LEU:O	1:C:255:VAL:CG1	2.63	0.47
1:A:82:VAL:HG22	1:A:82:VAL:O	2.14	0.47
1:B:269:ALA:HB3	1:B:272:ALA:HB2	1.97	0.47
1:C:63:LEU:HD21	1:C:260:VAL:CG2	2.44	0.47
1:D:268:TYR:O	1:D:269:ALA:HB2	2.15	0.47
1:B:206:ILE:HG13	1:B:208:VAL:HG13	1.97	0.47
1:C:316:SER:O	1:C:320:GLN:HG3	2.15	0.47
1:E:231:ALA:HB2	1:E:255:VAL:HG22	1.95	0.47
1:B:31:LYS:C	1:B:32:ARG:HG2	2.36	0.46
1:C:76:PHE:CZ	1:C:116:ALA:HA	2.50	0.46
1:F:40:PRO:HG2	1:F:72:GLU:O	2.16	0.46
1:F:139:ILE:HD11	1:F:146:SER:HB3	1.97	0.46
1:B:306:ILE:HD11	1:B:310:LEU:HD21	1.97	0.46
1:C:40:PRO:O	1:C:44:LEU:HD23	2.15	0.46
1:A:270:GLN:O	1:A:272:ALA:N	2.48	0.46
1:B:81:TRP:HH2	1:B:140:ASN:HB2	1.78	0.46
1:C:48:LYS:H	1:C:48:LYS:CD	2.22	0.46
1:D:39:GLY:O	1:D:44:LEU:HD22	2.15	0.46
1:D:44:LEU:HD11	1:D:306:ILE:HD11	1.97	0.46
1:D:282:VAL:HG21	1:D:296:LEU:HD13	1.97	0.46
1:B:126:ILE:HD11	1:B:197:CYS:SG	2.55	0.46
1:B:203:GLY:CA	1:B:233:HIS:HB3	2.41	0.46
1:D:217:MET:O	1:D:221:VAL:HG23	2.16	0.46
1:A:80:LYS:HE2	4:A:728:HOH:O	2.15	0.46
1:E:167:TYR:HD1	1:E:201:SER:HB3	1.80	0.46
1:F:78:SER:OG	1:F:80:LYS:HG3	2.15	0.46
1:B:110:LEU:O	1:B:114:GLU:HB2	2.15	0.46
1:C:75:SER:HB3	1:C:85:MET:HG3	1.98	0.46
1:E:231:ALA:HB1	1:E:255:VAL:HG22	1.97	0.46
1:C:217:MET:O	1:C:221:VAL:HG23	2.15	0.46
1:C:36:VAL:HG13	1:C:70:VAL:CG2	2.46	0.46
1:C:53:THR:O	1:C:57:ILE:HG13	2.16	0.46
1:F:154:LEU:HD13	1:F:195:MET:HB3	1.98	0.46
1:A:182:PRO:HG3	4:A:513:HOH:O	2.16	0.45
1:D:246:LEU:HD22	1:D:250:GLN:HG3	1.97	0.45
1:F:33:VAL:HG23	1:F:290:ILE:HG21	1.98	0.45
1:B:278:THR:HG22	1:B:299:LEU:HD11	1.97	0.45
1:A:78:SER:OG	1:A:80:LYS:HG2	2.16	0.45
1:D:32:ARG:HB3	1:D:291:HIS:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:THR:HG22	1:D:225:VAL:HG21	1.99	0.45
1:F:316:SER:O	1:F:320:GLN:HG3	2.16	0.45
1:A:113:PHE:CD2	1:A:153:ILE:HG23	2.51	0.45
1:B:269:ALA:O	1:B:270:GLN:HB3	2.16	0.45
1:A:133:LEU:HB2	1:A:177:GLU:HG3	1.98	0.45
1:E:284:MET:O	1:E:288:LEU:HD13	2.16	0.45
1:F:217:MET:O	1:F:221:VAL:HG23	2.16	0.45
1:E:73:THR:HG22	1:E:74:THR:HG22	1.99	0.45
1:A:297:GLN:CD	1:A:297:GLN:N	2.69	0.45
1:C:135:THR:CG2	1:C:139:ILE:HD11	2.47	0.45
1:C:172:LEU:HD22	1:C:213:ILE:HG22	1.99	0.45
1:D:147:PHE:CZ	1:D:188:VAL:HG13	2.52	0.45
1:B:110:LEU:HD12	1:B:110:LEU:HA	1.85	0.45
1:B:157:ALA:HB1	1:B:162:ILE:O	2.16	0.45
1:F:77:VAL:CG2	1:F:78:SER:H	2.11	0.45
1:A:87:ASP:O	1:A:91:VAL:HG23	2.17	0.45
1:B:77:VAL:HG21	1:B:82:VAL:CG1	2.47	0.45
1:D:33:VAL:HG23	1:D:290:ILE:HG21	1.99	0.45
1:F:60:ILE:HD12	1:F:95:ILE:HG21	1.99	0.45
1:F:189:THR:HG22	1:F:225:VAL:HG21	1.99	0.45
1:B:59:LEU:HD13	1:B:306:ILE:HB	1.99	0.44
1:D:77:VAL:CG1	1:D:82:VAL:HG13	2.47	0.44
1:D:246:LEU:CD2	1:D:250:GLN:HG3	2.47	0.44
1:F:53:THR:N	1:F:54:PRO:CD	2.80	0.44
1:B:48:LYS:H	1:B:48:LYS:CD	2.29	0.44
1:E:219:SER:O	1:E:223:GLN:HG2	2.17	0.44
1:B:145:GLU:HA	1:B:148:GLN:HG3	1.98	0.44
1:C:231:ALA:HA	1:C:255:VAL:HG13	2.00	0.44
1:E:133:LEU:HB3	1:E:177:GLU:HG3	1.99	0.44
1:C:44:LEU:HD22	1:C:44:LEU:H	1.82	0.44
1:C:135:THR:HG23	1:C:139:ILE:HD11	2.00	0.44
1:E:58:LYS:HD3	1:E:305:PHE:CE1	2.52	0.44
1:E:272:ALA:O	1:E:273:SER:CB	2.66	0.44
1:C:154:LEU:HD21	1:C:164:VAL:HG11	2.00	0.44
1:C:251:MET:HA	1:C:251:MET:CE	2.47	0.44
1:C:260:VAL:O	1:C:279:GLU:OE1	2.36	0.44
1:D:41:MET:SD	1:D:41:MET:C	2.96	0.44
1:E:133:LEU:CD2	1:E:176:TYR:HB3	2.47	0.44
1:E:52:SER:HB2	1:E:54:PRO:HD2	2.00	0.44
1:E:306:ILE:O	1:E:310:LEU:HB2	2.18	0.44
1:B:32:ARG:CZ	1:B:291:HIS:CD2	3.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:GLU:HG2	1:C:63:LEU:HD13	1.99	0.44
1:C:133:LEU:HB2	1:C:177:GLU:HG3	2.00	0.44
1:E:41:MET:HE2	1:E:85:MET:SD	2.58	0.44
1:F:47:GLU:OE1	1:F:47:GLU:HA	2.17	0.44
1:A:40:PRO:HG2	1:A:72:GLU:O	2.18	0.44
1:B:31:LYS:HE2	1:B:31:LYS:HB2	1.87	0.44
1:B:267:PRO:HG2	1:B:268:TYR:CD1	2.53	0.44
1:E:164:VAL:O	1:E:197:CYS:HA	2.18	0.44
1:F:132:GLU:N	1:F:177:GLU:OE1	2.51	0.44
1:B:184:LYS:HD2	1:B:184:LYS:HA	1.73	0.43
1:D:199:GLU:C	1:D:200:ILE:HD12	2.38	0.43
1:F:305:PHE:O	1:F:308:GLN:HB2	2.18	0.43
1:A:41:MET:HE3	1:A:85:MET:SD	2.58	0.43
1:F:66:ALA:HA	1:F:298:LYS:CB	2.47	0.43
1:F:122:LYS:HE3	1:F:122:LYS:HB2	1.78	0.43
1:C:51:VAL:CG1	1:C:310:LEU:HD13	2.49	0.43
1:E:272:ALA:O	1:E:273:SER:HB3	2.19	0.43
1:B:214:MET:HE3	1:B:232:VAL:HG21	1.99	0.43
1:C:87:ASP:OD2	1:C:87:ASP:N	2.52	0.43
1:F:73:THR:HG22	1:F:74:THR:HG22	2.00	0.43
1:F:205:THR:O	1:F:235:HIS:ND1	2.51	0.43
1:E:282:VAL:HG21	1:E:296:LEU:HD13	2.00	0.43
1:E:316:SER:O	1:E:320:GLN:HG3	2.18	0.43
1:A:60:ILE:HD13	1:A:73:THR:HG23	1.99	0.43
1:B:306:ILE:HG13	1:B:310:LEU:HD23	1.99	0.43
1:D:90:GLU:CD	1:D:90:GLU:H	2.22	0.43
1:E:268:TYR:N	1:E:268:TYR:CD1	2.87	0.43
1:F:78:SER:C	1:F:80:LYS:N	2.72	0.43
1:F:133:LEU:HB2	1:F:177:GLU:HG3	1.99	0.43
1:E:270:GLN:O	1:E:272:ALA:N	2.51	0.43
1:D:147:PHE:HZ	1:D:188:VAL:HG13	1.83	0.43
1:F:82:VAL:HG13	1:F:82:VAL:O	2.18	0.43
1:A:41:MET:SD	1:A:106:LEU:CD1	3.04	0.43
1:A:110:LEU:O	1:A:114:GLU:HG3	2.18	0.43
1:B:232:VAL:HG22	1:B:234:CYS:SG	2.59	0.43
1:A:70:VAL:HA	1:A:102:ASN:O	2.18	0.42
1:F:106:LEU:HD12	1:F:106:LEU:C	2.39	0.42
1:F:139:ILE:O	1:F:140:ASN:CB	2.65	0.42
1:A:33:VAL:HG23	1:A:290:ILE:HG21	2.01	0.42
1:D:31:LYS:HD3	1:D:31:LYS:N	2.33	0.42
1:D:31:LYS:HE2	1:D:31:LYS:H	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:MET:CE	1:B:232:VAL:HG21	2.48	0.42
1:B:260:VAL:O	1:B:279:GLU:OE1	2.38	0.42
1:B:276:LEU:HD21	1:B:281:LEU:HB2	2.02	0.42
1:D:41:MET:HE3	1:D:42:ASP:HA	2.01	0.42
1:D:53:THR:N	1:D:54:PRO:HD2	2.35	0.42
1:F:141:CYS:O	1:F:142:SER:C	2.57	0.42
1:B:232:VAL:CG2	1:B:234:CYS:SG	3.08	0.42
1:C:32:ARG:NH1	1:C:291:HIS:CD2	2.85	0.42
1:F:46:ASN:ND2	1:F:267:PRO:CG	2.80	0.42
1:B:77:VAL:HG12	1:B:108:PRO:HG3	2.02	0.42
1:C:154:LEU:CD2	1:C:164:VAL:HG11	2.49	0.42
1:E:74:THR:OG1	1:E:88:HIS:HB3	2.20	0.42
1:E:87:ASP:O	1:E:91:VAL:HG23	2.20	0.42
1:E:288:LEU:CD1	1:F:211:PRO:HD2	2.47	0.42
1:F:157:ALA:HB1	1:F:162:ILE:O	2.19	0.42
1:F:215:LYS:O	1:F:219:SER:HB2	2.19	0.42
1:C:80:LYS:HA	1:C:80:LYS:HD3	1.86	0.42
1:B:49:ASN:HD22	1:B:49:ASN:H	1.63	0.42
1:B:251:MET:HE2	1:B:251:MET:HA	2.02	0.42
1:E:266:CYS:HA	1:E:267:PRO:HD3	1.85	0.42
1:B:142:SER:HB3	1:B:145:GLU:HG3	2.01	0.42
1:C:36:VAL:HA	1:C:70:VAL:CG2	2.44	0.42
1:C:208:VAL:HG12	1:C:238:TYR:CE2	2.54	0.42
1:D:219:SER:O	1:D:223:GLN:HG2	2.20	0.42
1:E:221:VAL:HG12	1:E:230:LEU:HD21	2.02	0.42
1:F:58:LYS:HB3	1:F:305:PHE:CE2	2.54	0.42
1:F:246:LEU:O	1:F:250:GLN:HG3	2.20	0.42
1:F:135:THR:OG1	1:F:143:ILE:HG12	2.20	0.42
1:F:150:PHE:O	1:F:154:LEU:HG	2.20	0.42
1:B:77:VAL:HG21	1:B:82:VAL:HG11	2.02	0.42
1:B:123:GLU:HG3	1:B:163:SER:OG	2.19	0.42
1:C:42:ASP:CG	1:C:275:ASN:HD21	2.24	0.42
1:E:117:VAL:HG22	1:E:162:ILE:CD1	2.50	0.42
1:C:48:LYS:HD2	1:C:48:LYS:N	2.29	0.41
1:E:191:LYS:HG3	1:E:195:MET:CE	2.49	0.41
1:F:167:TYR:HE2	1:F:233:HIS:ND1	2.18	0.41
1:A:107:THR:CG2	1:A:113:PHE:HA	2.50	0.41
1:B:161:ASN:HD22	1:B:161:ASN:HA	1.59	0.41
1:D:52:SER:OG	1:D:55:VAL:HG23	2.21	0.41
1:E:300:LEU:HD13	1:E:322:THR:HG21	2.02	0.41
1:F:151:ASP:HA	1:F:154:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:ALA:HB1	1:B:276:LEU:HB2	2.02	0.41
1:C:279:GLU:O	1:C:282:VAL:HG22	2.20	0.41
1:A:272:ALA:O	1:A:273:SER:O	2.38	0.41
1:B:45:GLN:HE22	2:B:401:HMG:C3P	2.29	0.41
1:C:78:SER:C	1:C:80:LYS:H	2.24	0.41
1:D:278:THR:HG22	1:D:299:LEU:HD11	2.01	0.41
1:E:276:LEU:HA	4:E:736:HOH:O	2.20	0.41
1:F:231:ALA:HA	1:F:255:VAL:HG13	2.01	0.41
1:A:231:ALA:HA	1:A:255:VAL:O	2.20	0.41
1:A:312:ARG:HD3	1:A:313:LYS:O	2.21	0.41
1:B:306:ILE:CD1	1:B:310:LEU:HD21	2.50	0.41
1:C:308:GLN:C	1:C:310:LEU:H	2.23	0.41
1:D:73:THR:OG1	1:D:103:TYR:HB3	2.20	0.41
1:E:98:PHE:HB2	1:E:101:ILE:HD12	2.02	0.41
1:C:174:CYS:SG	1:C:175:PRO:HD2	2.60	0.41
1:F:53:THR:O	1:F:57:ILE:HG13	2.20	0.41
1:F:79:PRO:HG3	1:F:86:GLY:HA2	2.02	0.41
1:A:77:VAL:HG11	1:A:82:VAL:HG11	2.02	0.41
1:B:260:VAL:HG13	1:B:299:LEU:CD2	2.51	0.41
1:D:74:THR:OG1	1:D:88:HIS:HB3	2.20	0.41
1:F:36:VAL:HA	1:F:70:VAL:HG13	2.02	0.41
1:B:41:MET:O	1:B:45:GLN:HB2	2.20	0.41
1:B:234:CYS:HB3	4:B:580:HOH:O	2.21	0.41
1:B:260:VAL:C	1:B:262:GLY:H	2.25	0.41
1:C:60:ILE:CD1	1:C:73:THR:HG23	2.51	0.41
1:C:91:VAL:O	1:C:95:ILE:HG23	2.21	0.41
1:D:205:THR:O	1:D:235:HIS:ND1	2.44	0.41
1:B:159:SER:O	1:B:160:ALA:CB	2.69	0.41
1:D:37:GLU:OE2	1:D:260:VAL:N	2.51	0.41
1:E:169:SER:O	1:E:170:CYS:HB2	2.21	0.41
1:E:279:GLU:HG2	1:E:300:LEU:CD2	2.51	0.41
1:F:66:ALA:HA	1:F:298:LYS:HB2	2.02	0.41
1:F:132:GLU:OE2	1:F:132:GLU:HA	2.21	0.41
1:C:111:LYS:HE2	1:C:111:LYS:HB3	1.94	0.40
1:A:259:SER:O	1:A:260:VAL:C	2.59	0.40
1:B:87:ASP:O	1:B:91:VAL:HG23	2.20	0.40
1:E:272:ALA:HA	1:F:320:GLN:HE21	1.86	0.40
1:F:77:VAL:HG11	1:F:82:VAL:HG11	2.02	0.40
1:F:132:GLU:N	1:F:143:ILE:HD11	2.37	0.40
1:F:114:GLU:OE1	1:F:114:GLU:HA	2.21	0.40
1:C:127:PHE:CD1	1:C:127:PHE:N	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:VAL:CG1	1:D:234:CYS:SG	3.10	0.40
1:F:78:SER:C	1:F:80:LYS:H	2.24	0.40
1:A:287:GLY:HA3	1:B:210:THR:HG21	2.04	0.40
1:B:41:MET:C	1:B:41:MET:SD	3.00	0.40
1:C:137:LYS:HD2	1:C:176:TYR:CE1	2.57	0.40
1:D:78:SER:HA	1:D:79:PRO:HD3	1.95	0.40
1:F:139:ILE:HG13	1:F:140:ASN:N	2.36	0.40
1:F:308:GLN:HE21	1:F:308:GLN:HA	1.87	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	294/298 (99%)	281 (96%)	10 (3%)	3 (1%)	15	13
1	B	294/298 (99%)	283 (96%)	8 (3%)	3 (1%)	15	13
1	C	284/298 (95%)	265 (93%)	16 (6%)	3 (1%)	14	10
1	D	290/298 (97%)	275 (95%)	14 (5%)	1 (0%)	41	46
1	E	294/298 (99%)	282 (96%)	9 (3%)	3 (1%)	15	13
1	F	290/298 (97%)	258 (89%)	28 (10%)	4 (1%)	11	7
All	All	1746/1788 (98%)	1644 (94%)	85 (5%)	17 (1%)	15	13

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	260	VAL
1	A	273	SER
1	B	160	ALA
1	B	260	VAL

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Mol	Chain	Res	Type
1	C	260	VAL
1	D	260	VAL
1	E	260	VAL
1	E	271	GLY
1	F	77	VAL
1	F	142	SER
1	A	271	GLY
1	C	322	THR
1	E	273	SER
1	F	108	PRO
1	B	261	ALA
1	F	260	VAL
1	C	45	GLN

### 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	238/240 (99%)	228 (96%)	10 (4%)	30	34
1	B	238/240 (99%)	223 (94%)	15 (6%)	18	17
1	C	234/240 (98%)	223 (95%)	11 (5%)	26	29
1	D	237/240 (99%)	221 (93%)	16 (7%)	16	14
1	E	238/240 (99%)	225 (94%)	13 (6%)	21	21
1	F	237/240 (99%)	224 (94%)	13 (6%)	21	21
All	All	1422/1440 (99%)	1344 (94%)	78 (6%)	21	21

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	41	MET
1	A	44	LEU
1	A	70	VAL
1	A	230	LEU

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Mol	Chain	Res	Type
1	A	255	VAL
1	A	288	LEU
1	A	297	GLN
1	A	299	LEU
1	A	312	ARG
1	B	31	LYS
1	B	44	LEU
1	B	46	ASN
1	B	49	ASN
1	B	50	ILE
1	B	111	LYS
1	B	114	GLU
1	B	161	ASN
1	B	165	ARG
1	B	230	LEU
1	B	246	LEU
1	B	255	VAL
1	B	299	LEU
1	B	311	ASN
1	B	312	ARG
1	C	70	VAL
1	C	84	GLN
1	C	140	ASN
1	C	158	GLN
1	C	167	TYR
1	C	246	LEU
1	C	255	VAL
1	C	256	VAL
1	C	299	LEU
1	C	311	ASN
1	C	312	ARG
1	D	41	MET
1	D	74	THR
1	D	82	VAL
1	D	85	MET
1	D	90	GLU
1	D	158	GLN
1	D	165	ARG
1	D	205	THR
1	D	230	LEU
1	D	232	VAL
1	D	246	LEU

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Mol	Chain	Res	Type
1	D	255	VAL
1	D	256	VAL
1	D	299	LEU
1	D	310	LEU
1	D	312	ARG
1	E	41	MET
1	E	42	ASP
1	E	44	LEU
1	E	84	GLN
1	E	90	GLU
1	E	139	ILE
1	E	165	ARG
1	E	205	THR
1	E	230	LEU
1	E	255	VAL
1	E	256	VAL
1	E	299	LEU
1	E	312	ARG
1	F	41	MET
1	F	44	LEU
1	F	70	VAL
1	F	114	GLU
1	F	140	ASN
1	F	232	VAL
1	F	255	VAL
1	F	288	LEU
1	F	297	GLN
1	F	299	LEU
1	F	308	GLN
1	F	311	ASN
1	F	312	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (58) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	102	ASN
1	A	140	ASN
1	A	161	ASN
1	A	223	GLN
1	A	244	ASN
1	A	250	GLN

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Mol	Chain	Res	Type
1	A	291	HIS
1	A	297	GLN
1	A	304	ASN
1	A	308	GLN
1	B	45	GLN
1	B	46	ASN
1	B	49	ASN
1	B	161	ASN
1	B	223	GLN
1	B	235	HIS
1	B	244	ASN
1	B	250	GLN
1	B	291	HIS
1	B	297	GLN
1	B	311	ASN
1	C	84	GLN
1	C	140	ASN
1	C	223	GLN
1	C	244	ASN
1	C	250	GLN
1	C	275	ASN
1	C	291	HIS
1	C	297	GLN
1	C	311	ASN
1	C	320	GLN
1	D	161	ASN
1	D	223	GLN
1	D	244	ASN
1	D	250	GLN
1	D	291	HIS
1	D	297	GLN
1	D	308	GLN
1	E	84	GLN
1	E	102	ASN
1	E	140	ASN
1	E	223	GLN
1	E	244	ASN
1	E	250	GLN
1	E	291	HIS
1	E	297	GLN
1	E	311	ASN
1	F	45	GLN

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Mol	Chain	Res	Type
1	F	46	ASN
1	F	223	GLN
1	F	244	ASN
1	F	250	GLN
1	F	297	GLN
1	F	304	ASN
1	F	308	GLN
1	F	311	ASN
1	F	320	GLN

### 5.3.3 RNA [i](#)

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 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	$\# Z  > 2$
2	HMG	B	401	3	49,60,60	3.93	22 (44%)	59,90,90	2.42	17 (28%)

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
2	HMG	B	401	3	-	20/54/77/77	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	HMG	C2A-N3A	15.09	1.56	1.32
2	B	401	HMG	C4A-N3A	13.44	1.54	1.35
2	B	401	HMG	C5P-N4P	6.98	1.49	1.33
2	B	401	HMG	C2A-N1A	6.69	1.46	1.33
2	B	401	HMG	O7-C3	-6.02	1.35	1.44
2	B	401	HMG	C6A-N1A	5.52	1.61	1.37
2	B	401	HMG	P3B-O3B	4.79	1.68	1.59
2	B	401	HMG	C5A-C4A	4.38	1.52	1.40
2	B	401	HMG	C6A-C5A	4.12	1.58	1.43
2	B	401	HMG	O4B-C1B	3.57	1.46	1.41
2	B	401	HMG	O5P-C5P	3.48	1.30	1.23
2	B	401	HMG	C2B-C3B	2.93	1.59	1.52
2	B	401	HMG	P2A-O5A	2.82	1.60	1.50
2	B	401	HMG	C6P-C5P	2.75	1.56	1.51
2	B	401	HMG	C7P-N8P	-2.62	1.40	1.46
2	B	401	HMG	C9P-N8P	2.62	1.39	1.33
2	B	401	HMG	C6-C3	-2.57	1.49	1.52
2	B	401	HMG	CEP-CBP	-2.54	1.48	1.53
2	B	401	HMG	O9P-C9P	2.38	1.28	1.23
2	B	401	HMG	O2-C1	2.24	1.24	1.21
2	B	401	HMG	C2B-C1B	2.04	1.56	1.53
2	B	401	HMG	C2P-C3P	-2.00	1.42	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	HMG	O2-C1-S1P	-7.54	112.83	122.61
2	B	401	HMG	O6A-CCP-CBP	7.01	121.82	110.55
2	B	401	HMG	C2-C1-S1P	6.95	122.22	113.63
2	B	401	HMG	N3A-C2A-N1A	-5.98	119.34	128.68
2	B	401	HMG	C2P-S1P-C1	5.57	119.20	101.87
2	B	401	HMG	C1B-N9A-C4A	-3.61	120.29	126.64
2	B	401	HMG	O5P-C5P-N4P	3.34	129.32	123.01
2	B	401	HMG	O5B-C5B-C4B	3.14	119.81	108.99
2	B	401	HMG	CDP-CBP-CCP	-2.96	103.41	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	HMG	C7P-N8P-C9P	2.89	127.74	122.59
2	B	401	HMG	O4B-C1B-C2B	-2.86	102.75	106.93
2	B	401	HMG	C3P-N4P-C5P	-2.41	118.36	122.84
2	B	401	HMG	O4B-C4B-C5B	-2.30	101.79	109.37
2	B	401	HMG	O5P-C5P-C6P	-2.24	117.92	122.02
2	B	401	HMG	C6P-C5P-N4P	-2.18	112.75	116.42
2	B	401	HMG	C2P-C3P-N4P	-2.16	107.88	112.42
2	B	401	HMG	C4A-C5A-N7A	2.15	111.64	109.40

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	HMG	P1A-O3A-P2A-O6A
2	B	401	HMG	CCP-O6A-P2A-O5A
2	B	401	HMG	CCP-O6A-P2A-O4A
2	B	401	HMG	CCP-O6A-P2A-O3A
2	B	401	HMG	C5B-O5B-P1A-O3A
2	B	401	HMG	C5B-O5B-P1A-O2A
2	B	401	HMG	CAP-CBP-CCP-O6A
2	B	401	HMG	O9P-C9P-CAP-OAP
2	B	401	HMG	N8P-C9P-CAP-OAP
2	B	401	HMG	C5P-C6P-C7P-N8P
2	B	401	HMG	O7-C3-C4-C5
2	B	401	HMG	C3B-C4B-C5B-O5B
2	B	401	HMG	C2-C3-C4-C5
2	B	401	HMG	O4B-C4B-C5B-O5B
2	B	401	HMG	CDP-CBP-CCP-O6A
2	B	401	HMG	CEP-CBP-CCP-O6A
2	B	401	HMG	O9P-C9P-CAP-CBP
2	B	401	HMG	N8P-C9P-CAP-CBP
2	B	401	HMG	C5B-O5B-P1A-O1A
2	B	401	HMG	S1P-C2P-C3P-N4P

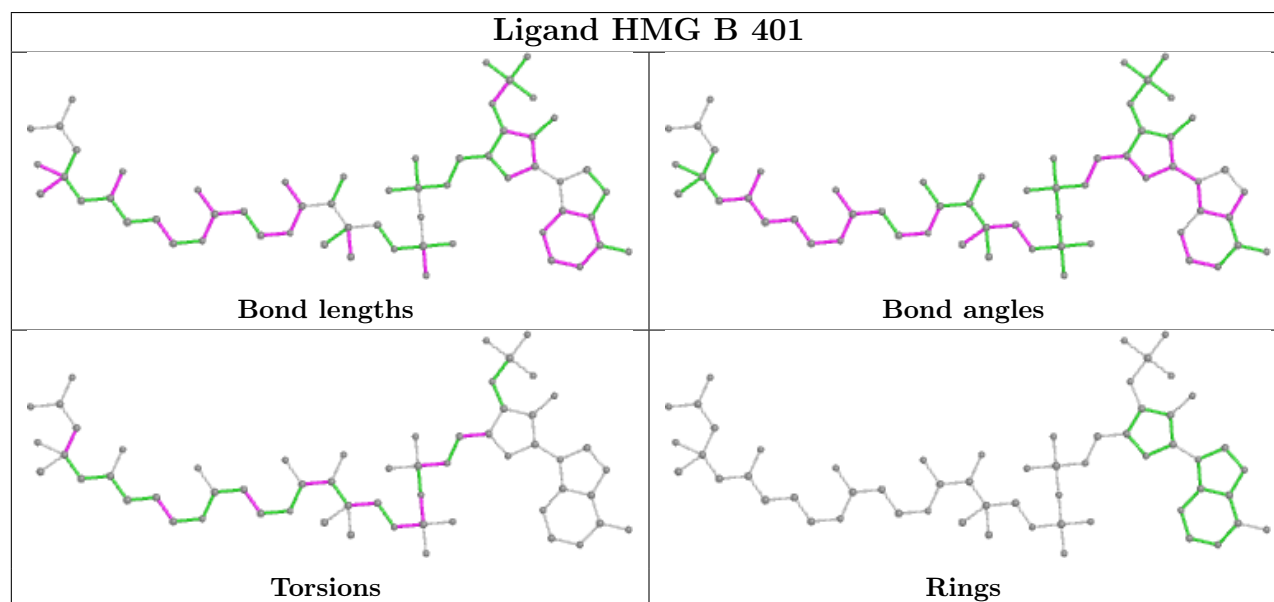
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	HMG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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, 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	296/298 (99%)	0.02	11 (3%) 41 44	14, 25, 49, 65	0
1	B	296/298 (99%)	0.39	20 (6%) 17 18	17, 32, 56, 64	0
1	C	288/298 (96%)	0.71	33 (11%) 4 4	22, 43, 65, 73	0
1	D	294/298 (98%)	0.11	15 (5%) 28 30	16, 32, 54, 70	0
1	E	296/298 (99%)	0.12	11 (3%) 41 44	18, 31, 56, 69	0
1	F	294/298 (98%)	0.91	52 (17%) 1 1	24, 50, 68, 78	0
All	All	1764/1788 (98%)	0.37	142 (8%) 12 13	14, 34, 62, 78	0

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	140	ASN	9.3
1	E	271	GLY	7.1
1	F	118	ALA	6.3
1	D	268	TYR	5.7
1	C	50	ILE	5.5
1	F	266	CYS	5.2
1	B	271	GLY	5.2
1	E	268	TYR	5.1
1	F	139	ILE	5.1
1	D	266	CYS	5.1
1	C	176	TYR	4.9
1	C	77	VAL	4.9
1	C	81	TRP	4.9
1	B	268	TYR	4.9
1	C	48	LYS	4.7
1	C	323	CYS	4.7
1	F	323	CYS	4.6
1	A	323	CYS	4.5
1	F	133	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	137	LYS	4.5
1	D	323	CYS	4.4
1	C	49	ASN	4.2
1	C	311	ASN	3.9
1	F	271	GLY	3.8
1	B	323	CYS	3.8
1	F	141	CYS	3.7
1	D	322	THR	3.6
1	F	95	ILE	3.6
1	F	155	LYS	3.6
1	A	271	GLY	3.6
1	D	269	ALA	3.5
1	E	270	GLN	3.5
1	E	272	ALA	3.5
1	B	270	GLN	3.5
1	F	83	PRO	3.4
1	C	110	LEU	3.4
1	E	269	ALA	3.4
1	D	48	LYS	3.4
1	C	139	ILE	3.4
1	F	119	ALA	3.3
1	F	267	PRO	3.3
1	C	51	VAL	3.3
1	F	115	ALA	3.2
1	C	313	LYS	3.2
1	F	92	LEU	3.2
1	B	269	ALA	3.2
1	F	154	LEU	3.2
1	F	110	LEU	3.2
1	B	272	ALA	3.2
1	A	80	LYS	3.1
1	D	272	ALA	3.1
1	C	38	VAL	3.0
1	B	266	CYS	3.0
1	A	81	TRP	3.0
1	F	93	LYS	3.0
1	B	260	VAL	2.9
1	E	323	CYS	2.9
1	A	269	ALA	2.9
1	C	111	LYS	2.9
1	F	167	TYR	2.9
1	F	48	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	195	MET	2.9
1	F	81	TRP	2.9
1	C	118	ALA	2.8
1	F	28	THR	2.8
1	C	291	HIS	2.8
1	E	267	PRO	2.8
1	A	272	ALA	2.8
1	C	138	ASN	2.8
1	C	140	ASN	2.8
1	C	175	PRO	2.8
1	B	267	PRO	2.7
1	B	106	LEU	2.7
1	D	267	PRO	2.7
1	F	322	THR	2.7
1	C	308	GLN	2.7
1	F	160	ALA	2.7
1	C	232	VAL	2.6
1	F	75	SER	2.6
1	D	28	THR	2.6
1	A	322	THR	2.5
1	F	100	GLY	2.5
1	F	270	GLN	2.5
1	A	268	TYR	2.5
1	A	267	PRO	2.5
1	F	260	VAL	2.4
1	B	159	SER	2.4
1	F	125	VAL	2.4
1	F	176	TYR	2.4
1	C	159	SER	2.4
1	F	161	ASN	2.4
1	F	159	SER	2.4
1	F	243	ALA	2.4
1	F	142	SER	2.4
1	D	50	ILE	2.4
1	C	178	GLY	2.4
1	F	111	LYS	2.4
1	B	322	THR	2.4
1	F	258	SER	2.4
1	F	65	GLU	2.4
1	F	158	GLN	2.4
1	F	179	LYS	2.3
1	C	114	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	117	VAL	2.3
1	F	127	PHE	2.3
1	B	263	LEU	2.3
1	E	127	PHE	2.3
1	B	176	TYR	2.3
1	D	243	ALA	2.3
1	B	147	PHE	2.3
1	B	28	THR	2.3
1	B	311	ASN	2.3
1	F	272	ALA	2.3
1	B	136	LYS	2.2
1	B	36	VAL	2.2
1	C	55	VAL	2.2
1	C	134	PHE	2.2
1	F	90	GLU	2.2
1	A	161	ASN	2.2
1	D	49	ASN	2.2
1	F	138	ASN	2.2
1	E	133	LEU	2.2
1	F	49	ASN	2.1
1	C	243	ALA	2.1
1	E	243	ALA	2.1
1	F	157	ALA	2.1
1	B	141	CYS	2.1
1	C	36	VAL	2.1
1	C	167	TYR	2.1
1	F	77	VAL	2.1
1	F	136	LYS	2.1
1	D	260	VAL	2.1
1	C	78	SER	2.1
1	F	85	MET	2.1
1	C	312	ARG	2.1
1	F	121	ALA	2.1
1	D	313	LYS	2.1
1	E	176	TYR	2.1
1	F	134	PHE	2.1
1	A	260	VAL	2.0
1	C	98	PHE	2.0
1	D	148	GLN	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](#)

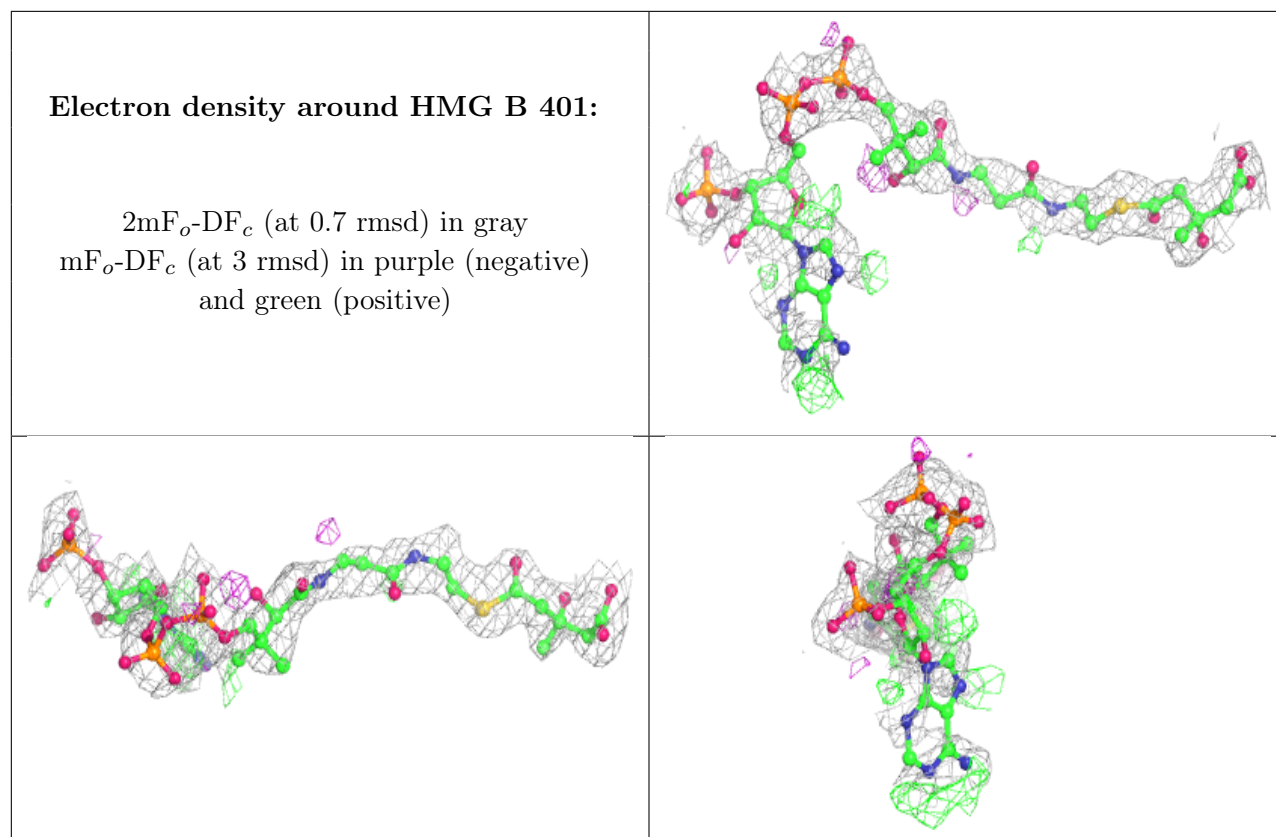
There are no monosaccharides in this entry.

## 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( $\text{\AA}^2$ )	Q<0.9
2	HMG	B	401	58/58	0.64	0.31	54,78,88,88	0
3	MG	C	403	1/1	0.81	0.32	42,42,42,42	0
3	MG	B	402	1/1	0.94	0.19	29,29,29,29	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.