



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:01 pm BST

PDB ID : 3FOK
Title : Crystal Structure of Cgl0159 From *Corynebacterium glutamicum* (*Brevibacterium flavum*). Northeast Structural Genomics Target CgR115
Authors : Seetharaman, J.; Neely, H.; Wang, H.; Janjua, H.; Foote, E.L.; Xiao, R.; Everett, J.K.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2008-12-30
Resolution : 2.50 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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 : 2.11
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

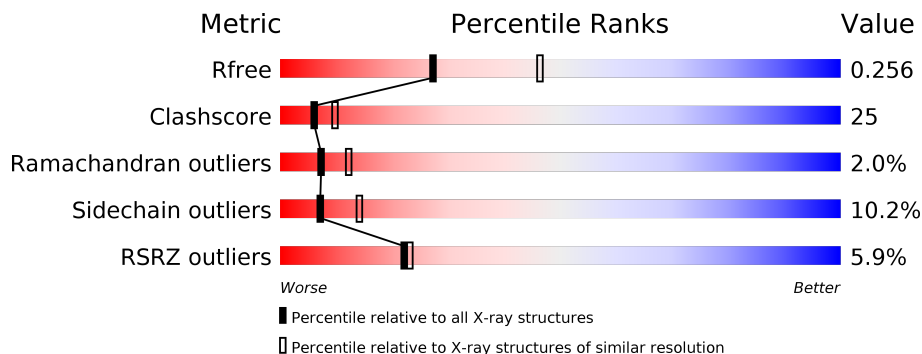
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



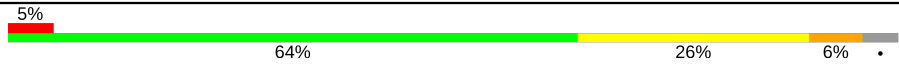

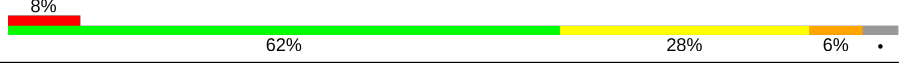
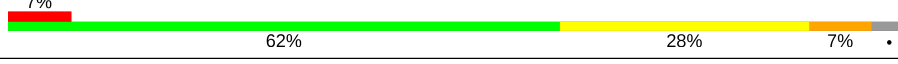
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	307	
1	B	307	
1	C	307	
1	D	307	
1	E	307	
1	F	307	

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Mol	Chain	Length	Quality of chain
1	G	307	
1	H	307	
1	I	307	
1	J	307	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 22795 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 uncharacterized protein Cgl0159.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	295	2208	1379	387	429	13	0	0	0
1	B	295	2208	1379	387	429	13	0	0	0
1	C	295	2208	1379	387	429	13	0	0	0
1	D	295	2208	1379	387	429	13	0	0	0
1	E	295	2208	1379	387	429	13	0	0	0
1	F	295	2208	1379	387	429	13	0	0	0
1	G	295	2208	1379	387	429	13	0	0	0
1	H	295	2208	1379	387	429	13	0	0	0
1	I	295	2208	1379	387	429	13	0	0	0
1	J	295	2208	1379	387	429	13	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	72	Total 72	O 72	0	0
2	B	90	Total 90	O 90	0	0
2	C	77	Total 77	O 77	0	0
2	D	95	Total 95	O 95	0	0

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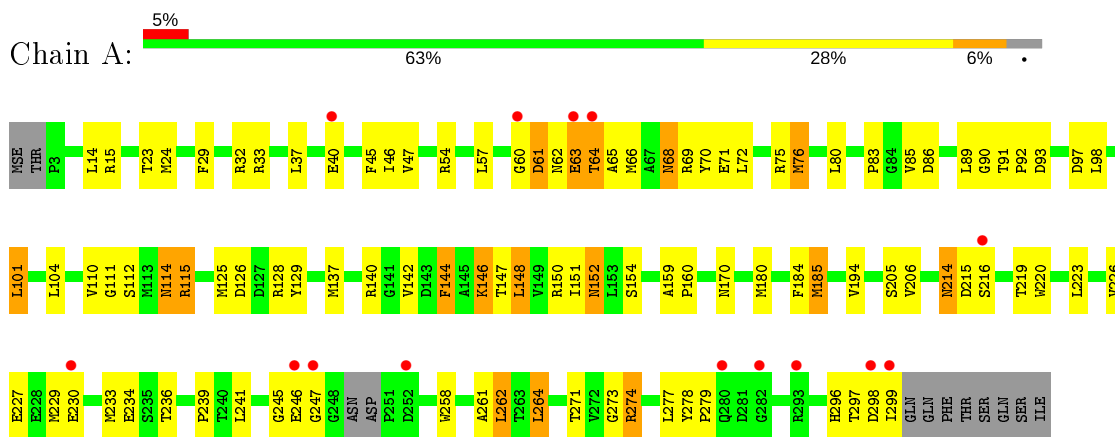
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	79	Total O 79 79	0	0
2	F	62	Total O 62 62	0	0
2	G	66	Total O 66 66	0	0
2	H	74	Total O 74 74	0	0
2	I	47	Total O 47 47	0	0
2	J	53	Total O 53 53	0	0

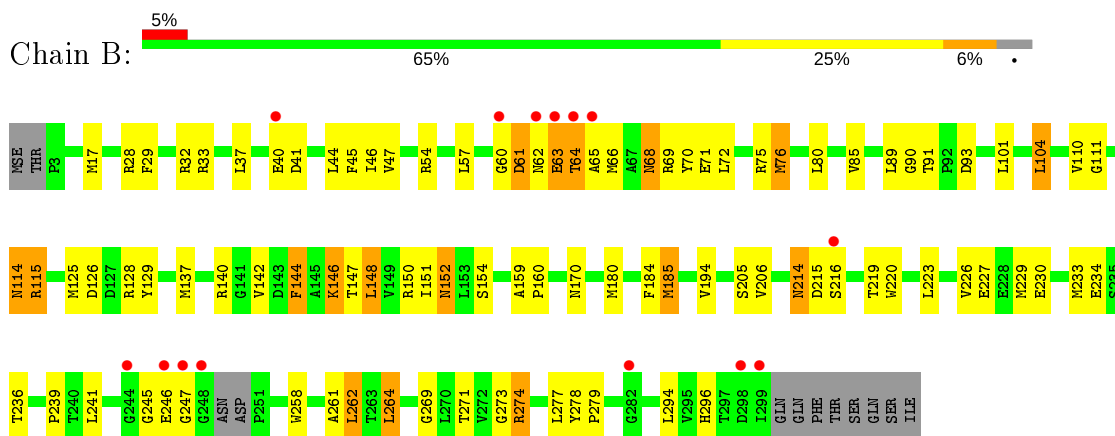
3 Residue-property plots [i](#)

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.

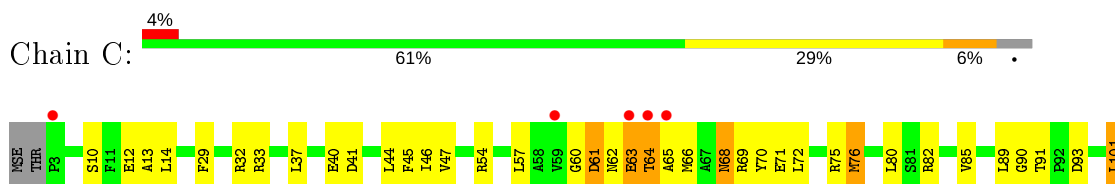
- Molecule 1: uncharacterized protein Cgl0159

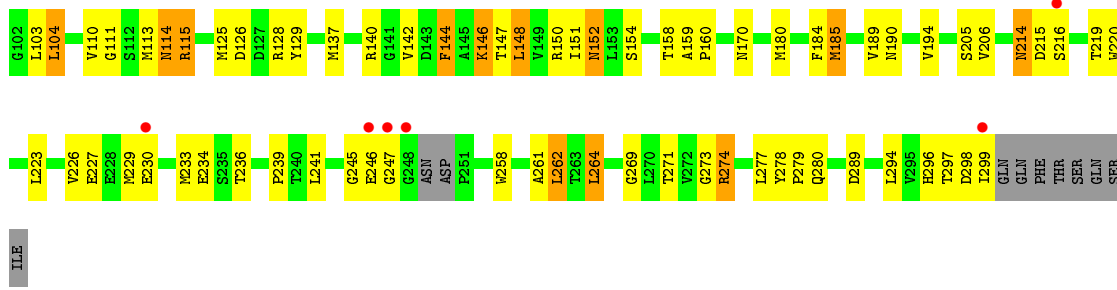


- Molecule 1: uncharacterized protein Cgl0159

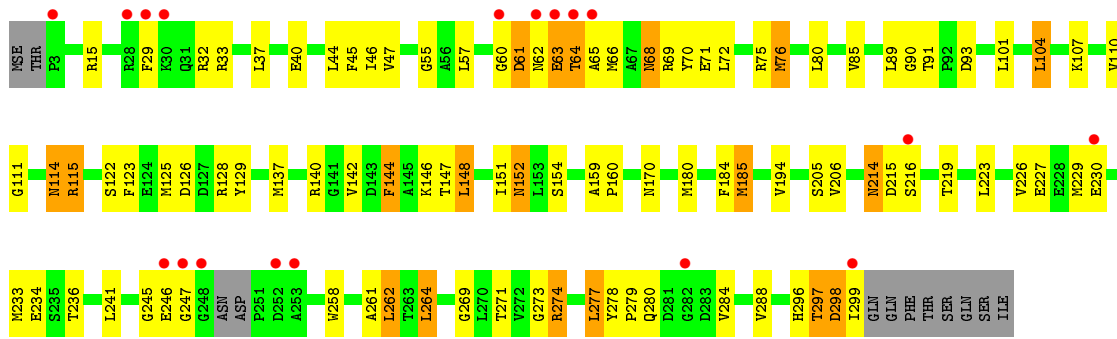


- Molecule 1: uncharacterized protein Cgl0159

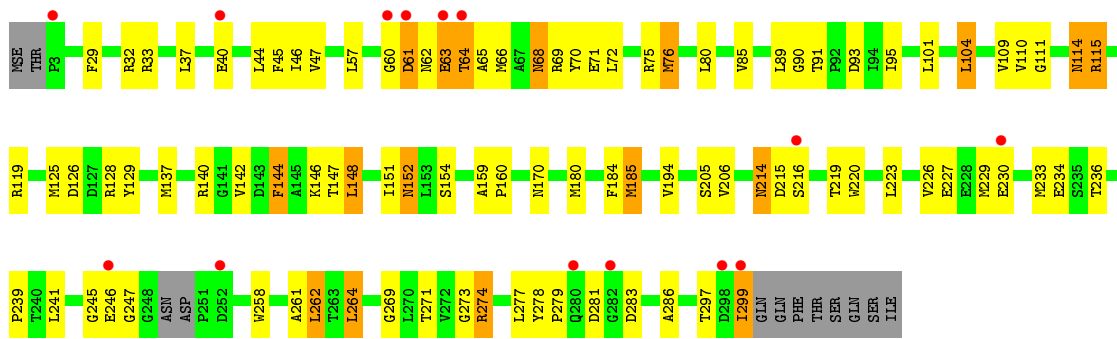




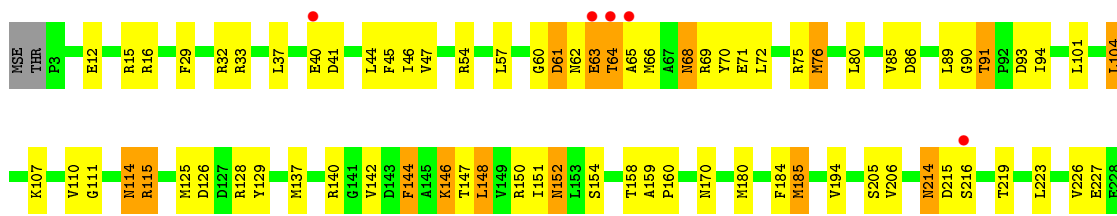
• Molecule 1: uncharacterized protein Cgl0159



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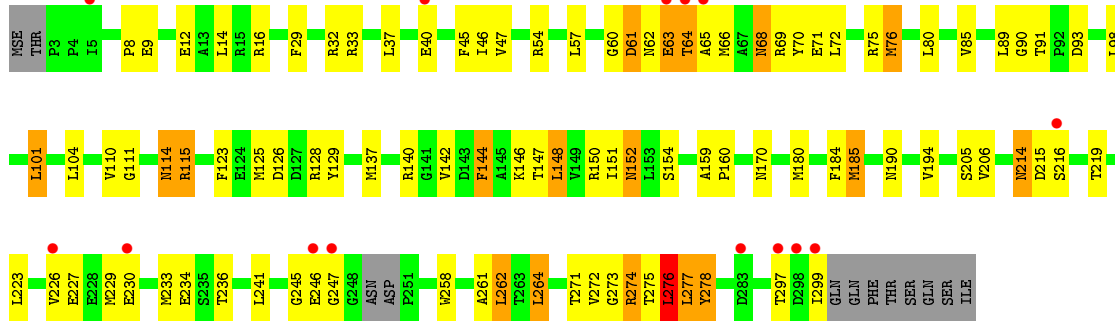


• Molecule 1: uncharacterized protein Cgl0159

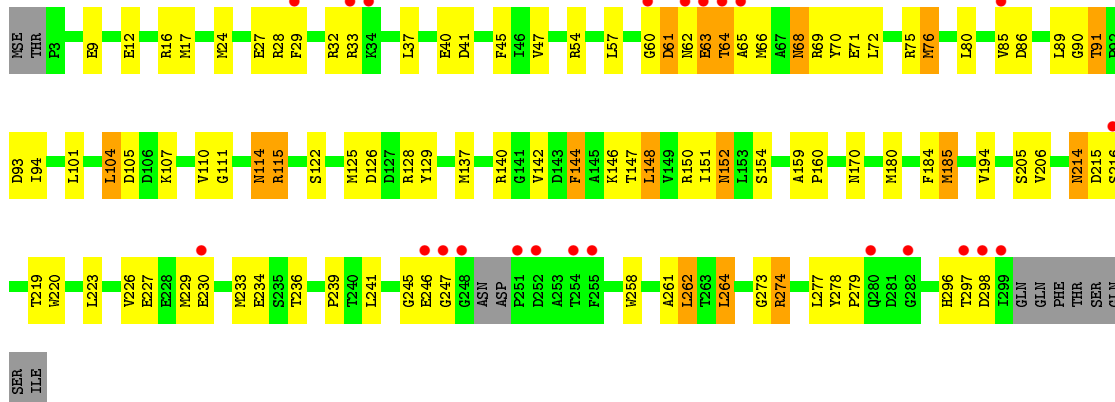




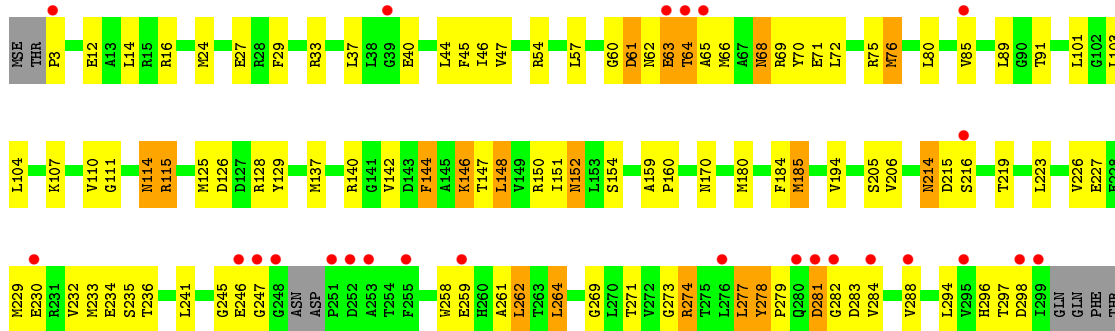
• Molecule 1: uncharacterized protein Cgl0159



• Molecule 1: uncharacterized protein Cgl0159

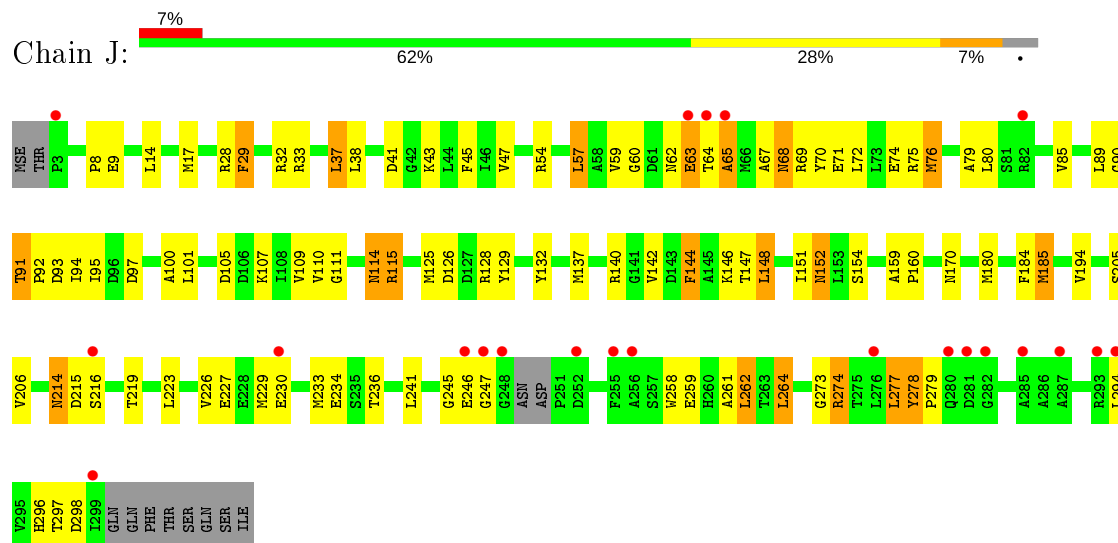


• Molecule 1: uncharacterized protein Cgl0159



SER
GLN
SER
ILE

• Molecule 1: uncharacterized protein Cgl0159



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	94.00Å 176.21Å 104.24Å 90.00° 101.94° 90.00°	Depositor
Resolution (Å)	39.00 – 2.50 49.50 – 2.39	Depositor EDS
% Data completeness (in resolution range)	94.9 (39.00-2.50) 97.4 (49.50-2.39)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.13 (at 2.39Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.225 , 0.254 0.228 , 0.256	Depositor DCC
R_{free} test set	9931 reflections (3.88%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtrriage
Anisotropy	0.457	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	22795	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.30	0/2230	0.68	1/3005 (0.0%)
1	B	0.30	0/2230	0.68	1/3005 (0.0%)
1	C	0.30	0/2230	0.68	1/3005 (0.0%)
1	D	0.31	0/2230	0.67	2/3005 (0.1%)
1	E	0.30	0/2230	0.67	1/3005 (0.0%)
1	F	0.30	0/2230	0.67	1/3005 (0.0%)
1	G	0.69	11/2230 (0.5%)	0.71	2/3005 (0.1%)
1	H	0.30	0/2230	0.67	1/3005 (0.0%)
1	I	0.57	7/2230 (0.3%)	0.70	3/3005 (0.1%)
1	J	0.76	10/2230 (0.4%)	0.69	2/3005 (0.1%)
All	All	0.45	28/22300 (0.1%)	0.68	15/30050 (0.0%)

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	278	TYR	CD1-CE1	-17.43	1.13	1.39
1	J	278	TYR	CD2-CE2	-16.39	1.14	1.39
1	G	278	TYR	CD1-CE1	-14.28	1.18	1.39
1	G	278	TYR	CD2-CE2	-12.96	1.20	1.39
1	J	278	TYR	CG-CD1	-11.49	1.24	1.39
1	J	278	TYR	CE2-CZ	-9.72	1.25	1.38
1	J	278	TYR	CE1-CZ	-9.47	1.26	1.38
1	I	278	TYR	CG-CD1	-9.09	1.27	1.39
1	I	278	TYR	CE2-CZ	-9.03	1.26	1.38
1	I	278	TYR	CD2-CE2	-8.61	1.26	1.39
1	G	278	TYR	CE2-CZ	-8.20	1.27	1.38
1	I	278	TYR	CD1-CE1	-8.16	1.27	1.39
1	G	277	LEU	CG-CD2	-7.78	1.23	1.51
1	G	278	TYR	CB-CG	-7.63	1.40	1.51
1	I	278	TYR	CE1-CZ	-6.61	1.29	1.38
1	J	278	TYR	CB-CG	-6.43	1.42	1.51
1	J	277	LEU	CG-CD1	-6.37	1.28	1.51
1	J	278	TYR	CG-CD2	-6.22	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	276	LEU	C-O	-6.07	1.11	1.23
1	I	278	TYR	CG-CD2	-5.99	1.31	1.39
1	G	277	LEU	CG-CD1	-5.97	1.29	1.51
1	G	278	TYR	CG-CD1	-5.82	1.31	1.39
1	G	278	TYR	CG-CD2	-5.56	1.31	1.39
1	G	276	LEU	CG-CD2	-5.43	1.31	1.51
1	J	277	LEU	CG-CD2	-5.20	1.32	1.51
1	J	278	TYR	C-O	-5.18	1.13	1.23
1	I	277	LEU	N-CA	-5.08	1.36	1.46
1	G	277	LEU	N-CA	-5.05	1.36	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	277	LEU	CA-CB-CG	7.91	133.49	115.30
1	I	277	LEU	CA-CB-CG	7.56	132.69	115.30
1	G	277	LEU	CB-CG-CD1	-6.85	99.36	111.00
1	I	277	LEU	N-CA-C	-5.93	94.99	111.00
1	D	277	LEU	N-CA-C	-5.57	95.96	111.00
1	C	185	MSE	N-CA-C	-5.29	96.71	111.00
1	A	185	MSE	N-CA-C	-5.29	96.73	111.00
1	G	185	MSE	N-CA-C	-5.27	96.78	111.00
1	J	185	MSE	N-CA-C	-5.26	96.80	111.00
1	H	185	MSE	N-CA-C	-5.25	96.82	111.00
1	I	185	MSE	N-CA-C	-5.25	96.83	111.00
1	D	185	MSE	N-CA-C	-5.24	96.85	111.00
1	F	185	MSE	N-CA-C	-5.23	96.89	111.00
1	E	185	MSE	N-CA-C	-5.22	96.90	111.00
1	B	185	MSE	N-CA-C	-5.21	96.93	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2208	0	2202	109	0
1	B	2208	0	2202	105	0
1	C	2208	0	2202	118	0
1	D	2208	0	2202	112	0
1	E	2208	0	2202	103	0
1	F	2208	0	2202	108	0
1	G	2208	0	2202	114	0
1	H	2208	0	2202	107	0
1	I	2208	0	2202	109	0
1	J	2208	0	2202	115	0
2	A	72	0	0	4	0
2	B	90	0	0	1	0
2	C	77	0	0	4	0
2	D	95	0	0	3	0
2	E	79	0	0	2	0
2	F	62	0	0	4	0
2	G	66	0	0	6	0
2	H	74	0	0	2	0
2	I	47	0	0	2	0
2	J	53	0	0	1	0
All	All	22795	0	22020	1090	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 25.

All (1090) 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:J:76:MSE:CE	1:J:277:LEU:HD21	1.71	1.20
1:C:137:MSE:HE2	1:C:142:VAL:HG21	1.20	1.16
1:F:137:MSE:HE2	1:F:142:VAL:HG21	1.22	1.15
1:A:137:MSE:HE2	1:A:142:VAL:HG21	1.22	1.14
1:J:137:MSE:HE2	1:J:142:VAL:HG21	1.23	1.12
1:G:137:MSE:HE2	1:G:142:VAL:HG21	1.22	1.11
1:I:137:MSE:HE2	1:I:142:VAL:HG21	1.23	1.11
1:D:137:MSE:HE2	1:D:142:VAL:HG21	1.23	1.11
1:B:137:MSE:HE2	1:B:142:VAL:HG21	1.21	1.10
1:H:137:MSE:HE2	1:H:142:VAL:HG21	1.21	1.10
1:E:137:MSE:HE2	1:E:142:VAL:HG21	1.22	1.09
1:C:190:ASN:OD1	1:H:122:SER:HA	1.54	1.08
1:J:76:MSE:HE3	1:J:277:LEU:HD21	1.39	0.99
1:J:76:MSE:HE2	1:J:277:LEU:HD21	1.47	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:ASN:OD1	1:H:122:SER:CA	2.19	0.90
1:C:111:GLY:HA3	1:C:137:MSE:HE3	1.52	0.90
1:C:189:VAL:HG12	1:C:190:ASN:ND2	1.86	0.90
1:J:114:ASN:HD22	1:J:114:ASN:H	1.20	0.89
1:E:111:GLY:HA3	1:E:137:MSE:HE3	1.54	0.89
1:I:76:MSE:HE3	1:I:277:LEU:HD21	1.56	0.88
1:A:111:GLY:HA3	1:A:137:MSE:HE3	1.56	0.87
1:G:76:MSE:HA	1:G:76:MSE:HE2	1.57	0.86
1:E:76:MSE:HA	1:E:76:MSE:HE2	1.58	0.86
1:A:76:MSE:HA	1:A:76:MSE:HE2	1.58	0.86
1:F:76:MSE:HA	1:F:76:MSE:HE2	1.57	0.86
1:H:76:MSE:HA	1:H:76:MSE:HE2	1.58	0.86
1:C:137:MSE:HE2	1:C:142:VAL:CG2	2.06	0.85
1:I:76:MSE:HA	1:I:76:MSE:HE2	1.57	0.85
1:D:122:SER:HA	1:G:190:ASN:OD1	1.76	0.85
1:C:76:MSE:HE2	1:C:76:MSE:HA	1.58	0.85
1:I:12:GLU:HG3	1:I:16:ARG:HH12	1.40	0.84
1:C:189:VAL:HG12	1:C:190:ASN:HD22	1.41	0.84
1:A:137:MSE:CE	1:A:142:VAL:HG21	2.07	0.84
1:A:114:ASN:HD22	1:A:114:ASN:H	1.24	0.84
1:H:75:ARG:HH21	1:H:278:TYR:HA	1.43	0.83
1:D:76:MSE:HA	1:D:76:MSE:HE2	1.58	0.83
1:E:137:MSE:HE2	1:E:142:VAL:CG2	2.07	0.83
1:B:137:MSE:CE	1:B:142:VAL:HG21	2.07	0.83
1:A:223:LEU:HD12	1:A:233:MSE:HE1	1.61	0.83
1:F:137:MSE:HE2	1:F:142:VAL:CG2	2.08	0.83
1:G:137:MSE:HE2	1:G:142:VAL:CG2	2.08	0.83
1:J:68:ASN:HD22	1:J:68:ASN:C	1.83	0.83
1:B:137:MSE:HE2	1:B:142:VAL:CG2	2.07	0.83
1:B:76:MSE:HE2	1:B:76:MSE:HA	1.57	0.82
1:H:137:MSE:HE2	1:H:142:VAL:CG2	2.07	0.82
1:B:223:LEU:HD12	1:B:233:MSE:HE1	1.61	0.82
1:I:137:MSE:HE2	1:I:142:VAL:CG2	2.09	0.82
1:B:274:ARG:H	1:B:274:ARG:HE	1.28	0.82
1:F:223:LEU:HD12	1:F:233:MSE:HE1	1.62	0.82
1:E:223:LEU:HD12	1:E:233:MSE:HE1	1.62	0.82
1:A:151:ILE:HD12	1:A:185:MSE:HE1	1.61	0.82
1:F:274:ARG:H	1:F:274:ARG:HE	1.27	0.82
1:G:111:GLY:HA3	1:G:137:MSE:HE3	1.62	0.82
1:I:137:MSE:CE	1:I:142:VAL:HG21	2.08	0.81
1:I:274:ARG:HE	1:I:274:ARG:H	1.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:MSE:HE2	1:A:142:VAL:CG2	2.08	0.81
1:H:137:MSE:CE	1:H:142:VAL:HG21	2.07	0.81
1:B:114:ASN:H	1:B:114:ASN:HD22	1.28	0.81
1:C:151:ILE:HD12	1:C:185:MSE:HE1	1.62	0.81
1:D:223:LEU:HD12	1:D:233:MSE:HE1	1.62	0.81
1:E:151:ILE:HD12	1:E:185:MSE:HE1	1.61	0.81
1:B:151:ILE:HD12	1:B:185:MSE:HE1	1.61	0.81
1:J:63:GLU:HG3	1:J:64:THR:H	1.44	0.81
1:F:151:ILE:HD12	1:F:185:MSE:HE1	1.62	0.81
1:C:137:MSE:CE	1:C:142:VAL:HG21	2.06	0.81
1:D:151:ILE:HD12	1:D:185:MSE:HE1	1.61	0.81
1:G:223:LEU:HD12	1:G:233:MSE:HE1	1.62	0.81
1:H:274:ARG:H	1:H:274:ARG:HE	1.27	0.81
1:G:114:ASN:HD22	1:G:114:ASN:H	1.29	0.81
1:D:274:ARG:H	1:D:274:ARG:HE	1.27	0.81
1:J:137:MSE:HB3	1:J:142:VAL:HG22	1.63	0.81
1:D:137:MSE:CE	1:D:142:VAL:HG21	2.09	0.80
1:F:137:MSE:HB3	1:F:142:VAL:HG22	1.63	0.80
1:C:223:LEU:HD12	1:C:233:MSE:HE1	1.62	0.80
1:F:114:ASN:HD21	1:F:148:LEU:H	1.25	0.80
1:D:137:MSE:HE2	1:D:142:VAL:CG2	2.09	0.80
1:J:274:ARG:H	1:J:274:ARG:HE	1.29	0.80
1:H:223:LEU:HD12	1:H:233:MSE:HE1	1.62	0.80
1:I:114:ASN:H	1:I:114:ASN:HD22	1.29	0.80
1:A:274:ARG:HE	1:A:274:ARG:H	1.27	0.80
1:B:137:MSE:HB3	1:B:142:VAL:HG22	1.63	0.80
1:H:151:ILE:HD12	1:H:185:MSE:HE1	1.61	0.80
1:J:137:MSE:HE2	1:J:142:VAL:CG2	2.09	0.80
1:J:151:ILE:HD12	1:J:185:MSE:HE1	1.62	0.80
1:C:125:MSE:HE2	1:C:152:ASN:HB2	1.64	0.80
1:D:137:MSE:HB3	1:D:142:VAL:HG22	1.64	0.80
1:G:137:MSE:HB3	1:G:142:VAL:HG22	1.63	0.80
1:I:125:MSE:HE2	1:I:152:ASN:HB2	1.63	0.80
1:F:137:MSE:CE	1:F:142:VAL:HG21	2.08	0.79
1:I:151:ILE:HD12	1:I:185:MSE:HE1	1.62	0.79
1:C:114:ASN:HD22	1:C:114:ASN:H	1.29	0.79
1:C:137:MSE:HB3	1:C:142:VAL:HG22	1.65	0.79
1:G:151:ILE:HD12	1:G:185:MSE:HE1	1.62	0.79
1:J:223:LEU:HD12	1:J:233:MSE:HE1	1.62	0.79
1:E:137:MSE:HB3	1:E:142:VAL:HG22	1.63	0.79
1:A:125:MSE:HE2	1:A:152:ASN:HB2	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:274:ARG:HE	1:C:274:ARG:H	1.27	0.79
1:G:125:MSE:HE2	1:G:152:ASN:HB2	1.64	0.79
1:H:137:MSE:HB3	1:H:142:VAL:HG22	1.63	0.79
1:I:137:MSE:HB3	1:I:142:VAL:HG22	1.64	0.79
1:G:137:MSE:CE	1:G:142:VAL:HG21	2.08	0.79
1:I:223:LEU:HD12	1:I:233:MSE:HE1	1.63	0.79
1:C:14:LEU:HD13	1:C:101:LEU:HD13	1.63	0.79
1:B:111:GLY:HA3	1:B:137:MSE:HE3	1.64	0.79
1:D:125:MSE:HE2	1:D:152:ASN:HB2	1.65	0.79
1:J:137:MSE:CE	1:J:142:VAL:HG21	2.09	0.79
1:F:125:MSE:HE2	1:F:152:ASN:HB2	1.64	0.78
1:J:125:MSE:HE2	1:J:152:ASN:HB2	1.64	0.78
1:H:111:GLY:HA3	1:H:137:MSE:HE3	1.64	0.78
1:H:125:MSE:HE2	1:H:152:ASN:HB2	1.63	0.78
1:J:71:GLU:O	1:J:75:ARG:HG3	1.83	0.78
1:A:137:MSE:HB3	1:A:142:VAL:HG22	1.63	0.78
1:G:274:ARG:H	1:G:274:ARG:HE	1.28	0.78
1:E:274:ARG:H	1:E:274:ARG:HE	1.28	0.77
1:E:137:MSE:CE	1:E:142:VAL:HG21	2.08	0.77
2:I:312:HOH:O	1:J:93:ASP:HA	1.84	0.77
1:A:185:MSE:HE3	1:A:205:SER:CB	2.14	0.77
1:D:114:ASN:H	1:D:114:ASN:HD22	1.32	0.77
1:I:76:MSE:CE	1:I:277:LEU:HD21	2.14	0.77
1:D:110:VAL:HG22	1:D:144:PHE:HB3	1.67	0.76
1:E:111:GLY:HA3	1:E:137:MSE:CE	2.15	0.76
1:E:185:MSE:HE3	1:E:205:SER:CB	2.15	0.76
1:F:111:GLY:HA3	1:F:137:MSE:HE3	1.66	0.76
1:G:114:ASN:HD21	1:G:148:LEU:H	1.32	0.76
1:H:185:MSE:HE3	1:H:205:SER:CB	2.15	0.76
1:B:125:MSE:HE2	1:B:152:ASN:HB2	1.65	0.76
1:D:114:ASN:HD21	1:D:148:LEU:H	1.32	0.76
1:D:32:ARG:HD2	1:D:104:LEU:HB3	1.67	0.76
1:E:125:MSE:HE2	1:E:152:ASN:HB2	1.65	0.76
1:E:63:GLU:HG3	1:E:64:THR:H	1.51	0.76
1:D:122:SER:CB	1:G:190:ASN:OD1	2.33	0.76
1:J:185:MSE:HE3	1:J:205:SER:CB	2.15	0.76
1:C:185:MSE:HE3	1:C:205:SER:CB	2.15	0.76
1:B:114:ASN:HD21	1:B:148:LEU:H	1.31	0.75
1:B:63:GLU:HG3	1:B:64:THR:H	1.51	0.75
1:G:185:MSE:HE3	1:G:205:SER:CB	2.15	0.75
1:F:63:GLU:HG3	1:F:64:THR:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:MSE:HE3	1:B:205:SER:CB	2.16	0.75
1:D:185:MSE:HE3	1:D:205:SER:CB	2.15	0.75
1:I:185:MSE:HE3	1:I:205:SER:CB	2.16	0.75
1:B:76:MSE:HE3	1:B:277:LEU:HD11	1.67	0.75
1:F:185:MSE:HE3	1:F:205:SER:CB	2.15	0.75
1:A:111:GLY:HA3	1:A:137:MSE:CE	2.17	0.75
1:D:63:GLU:HG3	1:D:64:THR:H	1.51	0.75
1:D:76:MSE:CE	1:D:277:LEU:HD21	2.17	0.74
1:A:63:GLU:HG3	1:A:64:THR:H	1.51	0.74
1:J:14:LEU:HD22	1:J:101:LEU:HD11	1.70	0.74
1:C:63:GLU:HG3	1:C:64:THR:H	1.52	0.74
1:C:111:GLY:HA3	1:C:137:MSE:CE	2.16	0.74
1:G:63:GLU:HG3	1:G:64:THR:H	1.52	0.73
1:F:41:ASP:OD2	1:F:296:HIS:HD2	1.71	0.73
1:G:272:VAL:HG13	2:G:549:HOH:O	1.87	0.73
1:H:63:GLU:HG3	1:H:64:THR:H	1.51	0.73
1:A:93:ASP:HA	2:A:308:HOH:O	1.87	0.73
1:I:63:GLU:HG3	1:I:64:THR:H	1.52	0.73
1:C:114:ASN:HD21	1:C:148:LEU:H	1.34	0.73
1:A:226:VAL:HG12	1:A:227:GLU:N	2.04	0.72
1:B:226:VAL:HG12	1:B:227:GLU:N	2.05	0.72
1:F:226:VAL:HG12	1:F:227:GLU:N	2.04	0.72
1:H:33:ARG:HH11	1:H:33:ARG:HG3	1.54	0.72
1:D:226:VAL:HG12	1:D:227:GLU:N	2.04	0.72
1:I:226:VAL:HG12	1:I:227:GLU:N	2.05	0.72
1:I:33:ARG:HH11	1:I:33:ARG:HG3	1.55	0.72
1:H:226:VAL:HG12	1:H:227:GLU:N	2.04	0.72
1:I:259:GLU:HB2	1:I:294:LEU:HD11	1.71	0.72
1:I:14:LEU:HD22	1:I:101:LEU:HD11	1.70	0.71
1:H:114:ASN:HD21	1:H:148:LEU:H	1.35	0.71
1:J:226:VAL:HG12	1:J:227:GLU:N	2.04	0.71
1:G:226:VAL:HG12	1:G:227:GLU:N	2.05	0.71
1:D:75:ARG:HH21	1:D:278:TYR:HA	1.55	0.71
1:C:226:VAL:HG12	1:C:227:GLU:N	2.04	0.71
1:J:111:GLY:HA3	1:J:137:MSE:HE3	1.73	0.71
1:I:71:GLU:O	1:I:75:ARG:HG3	1.91	0.71
1:F:33:ARG:HG3	1:F:33:ARG:HH11	1.56	0.71
1:H:68:ASN:HD22	1:H:68:ASN:C	1.95	0.71
1:C:68:ASN:HD22	1:C:68:ASN:C	1.94	0.70
1:E:226:VAL:HG12	1:E:227:GLU:N	2.04	0.70
1:E:33:ARG:HH11	1:E:33:ARG:HG3	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:GLY:HA3	1:D:137:MSE:HE3	1.71	0.70
2:G:308:HOH:O	1:H:93:ASP:HA	1.91	0.70
1:J:45:PHE:CE2	1:J:85:VAL:HG12	2.26	0.70
1:A:68:ASN:HD22	1:A:68:ASN:C	1.95	0.70
1:C:33:ARG:HG3	1:C:33:ARG:HH11	1.56	0.70
1:A:33:ARG:HH11	1:A:33:ARG:HG3	1.55	0.70
1:F:68:ASN:HD22	1:F:68:ASN:C	1.94	0.70
1:D:122:SER:CA	1:G:190:ASN:OD1	2.39	0.70
1:I:68:ASN:HD22	1:I:68:ASN:C	1.94	0.70
1:G:71:GLU:O	1:G:75:ARG:HG3	1.92	0.70
1:A:71:GLU:O	1:A:75:ARG:HG3	1.91	0.70
1:E:68:ASN:C	1:E:68:ASN:HD22	1.95	0.70
1:F:230:GLU:O	1:F:234:GLU:HG3	1.92	0.70
1:G:33:ARG:HG3	1:G:33:ARG:HH11	1.57	0.70
1:D:71:GLU:O	1:D:75:ARG:HG3	1.91	0.70
1:C:230:GLU:O	1:C:234:GLU:HG3	1.92	0.70
1:A:114:ASN:HD21	1:A:148:LEU:H	1.39	0.70
1:B:33:ARG:HG3	1:B:33:ARG:HH11	1.56	0.70
1:I:230:GLU:O	1:I:234:GLU:HG3	1.92	0.70
1:J:230:GLU:O	1:J:234:GLU:HG3	1.92	0.70
2:A:317:HOH:O	1:B:93:ASP:HA	1.91	0.69
1:H:71:GLU:O	1:H:75:ARG:HG3	1.92	0.69
1:H:230:GLU:O	1:H:234:GLU:HG3	1.92	0.69
1:A:230:GLU:O	1:A:234:GLU:HG3	1.92	0.69
1:B:230:GLU:O	1:B:234:GLU:HG3	1.91	0.69
1:B:68:ASN:C	1:B:68:ASN:HD22	1.96	0.69
1:E:230:GLU:O	1:E:234:GLU:HG3	1.92	0.69
1:G:230:GLU:O	1:G:234:GLU:HG3	1.92	0.69
1:D:68:ASN:C	1:D:68:ASN:HD22	1.95	0.69
1:D:33:ARG:HH11	1:D:33:ARG:HG3	1.56	0.69
1:J:114:ASN:HD22	1:J:114:ASN:N	1.91	0.69
1:D:230:GLU:O	1:D:234:GLU:HG3	1.92	0.69
1:G:68:ASN:C	1:G:68:ASN:HD22	1.95	0.69
1:F:114:ASN:HD22	1:F:114:ASN:H	1.40	0.69
1:A:76:MSE:HE3	1:A:277:LEU:HD21	1.75	0.69
1:E:71:GLU:O	1:E:75:ARG:HG3	1.93	0.69
1:D:76:MSE:HE3	1:D:277:LEU:HD21	1.75	0.68
1:F:71:GLU:O	1:F:75:ARG:HG3	1.92	0.68
1:C:80:LEU:HA	1:C:85:VAL:HG21	1.76	0.68
1:B:80:LEU:HA	1:B:85:VAL:HG21	1.76	0.68
1:C:71:GLU:O	1:C:75:ARG:HG3	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:93:ASP:HA	2:F:309:HOH:O	1.92	0.68
1:B:71:GLU:O	1:B:75:ARG:HG3	1.93	0.68
1:D:80:LEU:HA	1:D:85:VAL:HG21	1.76	0.68
1:J:76:MSE:HE3	1:J:277:LEU:HD11	1.76	0.68
1:I:111:GLY:HA3	1:I:137:MSE:HE3	1.75	0.68
1:I:80:LEU:HA	1:I:85:VAL:HG21	1.76	0.68
1:C:111:GLY:H	1:C:137:MSE:HE1	1.60	0.67
1:A:137:MSE:HB3	1:A:142:VAL:CG2	2.25	0.67
1:J:151:ILE:HB	1:J:185:MSE:CE	2.25	0.67
1:E:151:ILE:HB	1:E:185:MSE:CE	2.25	0.66
1:F:226:VAL:CG1	1:F:227:GLU:N	2.59	0.66
1:E:226:VAL:CG1	1:E:227:GLU:N	2.59	0.66
1:H:137:MSE:HB3	1:H:142:VAL:CG2	2.26	0.66
1:J:114:ASN:HD21	1:J:148:LEU:H	1.43	0.66
1:A:151:ILE:HB	1:A:185:MSE:CE	2.25	0.66
1:C:190:ASN:OD1	1:H:122:SER:CB	2.42	0.66
1:H:226:VAL:CG1	1:H:227:GLU:N	2.58	0.66
1:E:114:ASN:HD22	1:E:114:ASN:H	1.42	0.66
1:G:274:ARG:NH2	2:G:549:HOH:O	2.27	0.66
1:B:137:MSE:HB3	1:B:142:VAL:CG2	2.26	0.66
1:F:137:MSE:HB3	1:F:142:VAL:CG2	2.25	0.66
1:G:137:MSE:HB3	1:G:142:VAL:CG2	2.26	0.66
1:D:122:SER:HB2	1:G:190:ASN:OD1	1.95	0.66
1:A:80:LEU:HA	1:A:85:VAL:HG21	1.76	0.66
1:F:80:LEU:HA	1:F:85:VAL:HG21	1.77	0.66
1:G:80:LEU:HA	1:G:85:VAL:HG21	1.76	0.66
1:H:151:ILE:HB	1:H:185:MSE:CE	2.26	0.66
1:H:32:ARG:HD2	1:H:104:LEU:HB3	1.77	0.66
1:D:226:VAL:CG1	1:D:227:GLU:N	2.59	0.66
1:G:151:ILE:HB	1:G:185:MSE:CE	2.25	0.66
1:I:226:VAL:CG1	1:I:227:GLU:N	2.59	0.66
1:J:226:VAL:CG1	1:J:227:GLU:N	2.58	0.66
1:J:68:ASN:HD21	1:J:70:TYR:HB2	1.61	0.66
1:B:226:VAL:CG1	1:B:227:GLU:N	2.59	0.66
1:C:226:VAL:CG1	1:C:227:GLU:N	2.59	0.66
1:D:111:GLY:H	1:D:137:MSE:HE1	1.60	0.66
1:E:80:LEU:HA	1:E:85:VAL:HG21	1.76	0.66
1:C:151:ILE:HB	1:C:185:MSE:CE	2.26	0.65
1:F:151:ILE:HB	1:F:185:MSE:CE	2.26	0.65
1:D:110:VAL:HG22	1:D:144:PHE:CB	2.26	0.65
1:E:226:VAL:O	1:E:229:MSE:HG2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:VAL:CG1	1:A:227:GLU:N	2.59	0.65
1:G:226:VAL:CG1	1:G:227:GLU:N	2.59	0.65
1:H:75:ARG:NH2	1:H:278:TYR:HA	2.11	0.65
1:E:137:MSE:HB3	1:E:142:VAL:CG2	2.25	0.65
1:F:32:ARG:HD2	1:F:104:LEU:HB3	1.76	0.65
1:B:151:ILE:HB	1:B:185:MSE:CE	2.26	0.65
1:G:111:GLY:H	1:G:137:MSE:HE1	1.61	0.65
1:I:151:ILE:HB	1:I:185:MSE:CE	2.26	0.65
1:J:137:MSE:HB3	1:J:142:VAL:CG2	2.26	0.65
1:H:80:LEU:HA	1:H:85:VAL:HG21	1.76	0.65
1:B:111:GLY:H	1:B:137:MSE:HE1	1.62	0.65
1:B:151:ILE:CD1	1:B:185:MSE:HE1	2.27	0.65
1:D:151:ILE:HB	1:D:185:MSE:CE	2.26	0.65
1:F:226:VAL:O	1:F:229:MSE:HG2	1.97	0.65
2:F:310:HOH:O	1:G:93:ASP:HA	1.96	0.65
1:I:125:MSE:HE2	1:I:152:ASN:CB	2.27	0.65
1:I:226:VAL:O	1:I:229:MSE:HG2	1.97	0.65
1:H:151:ILE:CD1	1:H:185:MSE:HE1	2.27	0.65
1:A:76:MSE:CE	1:A:277:LEU:HD21	2.27	0.65
1:H:76:MSE:CE	1:H:277:LEU:HD21	2.27	0.64
1:D:151:ILE:CD1	1:D:185:MSE:HE1	2.28	0.64
1:E:151:ILE:CD1	1:E:185:MSE:HE1	2.27	0.64
1:A:151:ILE:CD1	1:A:185:MSE:HE1	2.28	0.64
1:F:151:ILE:CD1	1:F:185:MSE:HE1	2.28	0.64
1:D:226:VAL:O	1:D:229:MSE:HG2	1.96	0.64
1:G:151:ILE:CD1	1:G:185:MSE:HE1	2.27	0.64
1:I:151:ILE:CD1	1:I:185:MSE:HE1	2.28	0.64
1:J:125:MSE:HE2	1:J:152:ASN:CB	2.27	0.64
1:B:226:VAL:O	1:B:229:MSE:HG2	1.97	0.64
1:D:137:MSE:HB3	1:D:142:VAL:CG2	2.26	0.64
1:F:125:MSE:HE2	1:F:152:ASN:CB	2.27	0.64
1:J:226:VAL:O	1:J:229:MSE:HG2	1.98	0.64
1:C:76:MSE:HE3	1:C:277:LEU:HD11	1.80	0.64
1:G:125:MSE:HE2	1:G:152:ASN:CB	2.27	0.64
1:A:114:ASN:N	1:A:114:ASN:HD22	1.94	0.64
1:C:151:ILE:CD1	1:C:185:MSE:HE1	2.28	0.64
1:D:125:MSE:HE2	1:D:152:ASN:CB	2.28	0.64
1:E:93:ASP:HA	2:J:308:HOH:O	1.97	0.64
1:C:137:MSE:HB3	1:C:142:VAL:CG2	2.26	0.64
1:D:278:TYR:N	1:D:279:PRO:HD3	2.12	0.64
1:I:137:MSE:HB3	1:I:142:VAL:CG2	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:VAL:O	1:C:229:MSE:HG2	1.98	0.64
1:A:125:MSE:HE2	1:A:152:ASN:CB	2.28	0.63
1:H:226:VAL:O	1:H:229:MSE:HG2	1.98	0.63
1:B:125:MSE:HE2	1:B:152:ASN:CB	2.28	0.63
1:J:151:ILE:CD1	1:J:185:MSE:HE1	2.28	0.63
1:H:125:MSE:HE2	1:H:152:ASN:CB	2.27	0.63
1:A:226:VAL:O	1:A:229:MSE:HG2	1.98	0.63
1:G:111:GLY:HA3	1:G:137:MSE:CE	2.28	0.63
1:I:278:TYR:N	1:I:279:PRO:HD3	2.13	0.63
1:C:125:MSE:HE2	1:C:152:ASN:CB	2.28	0.63
1:E:125:MSE:HE2	1:E:152:ASN:CB	2.28	0.63
1:F:111:GLY:H	1:F:137:MSE:HE1	1.64	0.62
1:A:185:MSE:HE3	1:A:205:SER:HB3	1.81	0.62
1:G:226:VAL:O	1:G:229:MSE:HG2	1.98	0.62
1:H:111:GLY:H	1:H:137:MSE:HE1	1.65	0.62
1:D:93:ASP:HA	2:D:310:HOH:O	1.97	0.62
1:G:54:ARG:HH21	1:G:150:ARG:HH12	1.46	0.62
1:H:111:GLY:HA3	1:H:137:MSE:CE	2.28	0.62
1:B:151:ILE:HD12	1:B:185:MSE:CE	2.30	0.62
1:D:277:LEU:O	1:D:278:TYR:HB2	1.98	0.62
1:H:114:ASN:HD22	1:H:114:ASN:H	1.46	0.62
1:C:93:ASP:HA	2:E:308:HOH:O	1.99	0.62
1:E:278:TYR:N	1:E:279:PRO:HD3	2.14	0.62
1:G:151:ILE:HD12	1:G:185:MSE:CE	2.30	0.62
1:C:185:MSE:HE3	1:C:205:SER:HB3	1.81	0.61
1:D:151:ILE:HD12	1:D:185:MSE:CE	2.29	0.61
1:J:97:ASP:O	1:J:101:LEU:HD13	2.00	0.61
1:F:185:MSE:HE3	1:F:205:SER:HB3	1.82	0.61
1:B:185:MSE:HE3	1:B:205:SER:HB3	1.82	0.61
1:F:151:ILE:HD12	1:F:185:MSE:CE	2.30	0.61
1:G:185:MSE:HE3	1:G:205:SER:HB3	1.82	0.61
1:J:63:GLU:HG3	1:J:64:THR:N	2.13	0.61
1:B:111:GLY:HA3	1:B:137:MSE:CE	2.29	0.61
1:E:114:ASN:HD21	1:E:148:LEU:H	1.47	0.61
1:H:110:VAL:HG13	1:H:144:PHE:HB3	1.82	0.61
1:H:185:MSE:HE3	1:H:205:SER:HB3	1.81	0.61
1:I:111:GLY:H	1:I:137:MSE:HE1	1.65	0.61
1:E:151:ILE:HD12	1:E:185:MSE:CE	2.30	0.60
1:D:185:MSE:HE3	1:D:205:SER:HB3	1.81	0.60
1:E:76:MSE:HE3	1:E:277:LEU:HD21	1.82	0.60
1:H:76:MSE:HE3	1:H:277:LEU:HD21	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ASN:N	1:C:114:ASN:HD22	1.98	0.60
1:G:246:GLU:HG2	1:G:247:GLY:H	1.67	0.60
1:J:151:ILE:HD12	1:J:185:MSE:CE	2.31	0.60
1:J:185:MSE:HE3	1:J:205:SER:HB3	1.82	0.60
1:C:151:ILE:HD12	1:C:185:MSE:CE	2.31	0.60
1:C:76:MSE:CE	1:C:277:LEU:HD21	2.30	0.60
1:E:185:MSE:HE3	1:E:205:SER:HB3	1.82	0.60
1:E:246:GLU:HG2	1:E:247:GLY:H	1.67	0.60
1:E:76:MSE:CE	1:E:277:LEU:HD21	2.31	0.60
1:F:75:ARG:HH21	1:F:278:TYR:HA	1.67	0.60
1:H:151:ILE:HD12	1:H:185:MSE:CE	2.29	0.60
1:J:151:ILE:HB	1:J:185:MSE:HE2	1.84	0.60
1:D:246:GLU:HG2	1:D:247:GLY:H	1.67	0.60
1:H:24:MSE:HE1	1:H:27:GLU:OE1	2.01	0.60
1:A:151:ILE:HB	1:A:185:MSE:HE2	1.82	0.60
1:F:110:VAL:HG22	1:F:144:PHE:HB3	1.84	0.60
1:F:246:GLU:HG2	1:F:247:GLY:H	1.67	0.60
1:J:68:ASN:ND2	1:J:68:ASN:C	2.55	0.60
1:B:76:MSE:CE	1:B:277:LEU:HD21	2.31	0.60
1:I:151:ILE:HD12	1:I:185:MSE:CE	2.30	0.60
1:A:151:ILE:HD12	1:A:185:MSE:CE	2.30	0.59
1:C:47:VAL:HG11	1:C:76:MSE:HE1	1.84	0.59
1:G:32:ARG:HD2	1:G:104:LEU:HB3	1.83	0.59
1:J:47:VAL:HB	1:J:76:MSE:HE1	1.84	0.59
1:B:273:GLY:N	1:B:274:ARG:HH21	2.00	0.59
1:C:85:VAL:HG23	1:C:85:VAL:O	2.03	0.59
1:E:151:ILE:HB	1:E:185:MSE:HE2	1.83	0.59
1:E:75:ARG:HH21	1:E:278:TYR:HA	1.67	0.59
1:F:111:GLY:HA3	1:F:137:MSE:CE	2.31	0.59
1:H:47:VAL:HG11	1:H:76:MSE:HE1	1.84	0.59
1:I:185:MSE:HE3	1:I:205:SER:HB3	1.83	0.59
1:H:246:GLU:HG2	1:H:247:GLY:H	1.67	0.59
1:I:246:GLU:HG2	1:I:247:GLY:H	1.67	0.59
1:C:273:GLY:H	1:C:274:ARG:HH21	1.51	0.59
1:D:226:VAL:CG1	1:D:227:GLU:H	2.16	0.59
1:I:85:VAL:O	1:I:85:VAL:HG23	2.03	0.59
1:B:274:ARG:O	1:B:277:LEU:O	2.21	0.59
1:H:273:GLY:H	1:H:274:ARG:HH21	1.51	0.59
1:C:151:ILE:HB	1:C:185:MSE:HE2	1.85	0.59
1:C:273:GLY:N	1:C:274:ARG:HH21	2.01	0.59
1:E:261:ALA:HA	1:E:264:LEU:HD22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:273:GLY:N	1:F:274:ARG:HH21	2.00	0.59
1:C:190:ASN:OD1	1:H:122:SER:HB2	2.03	0.59
1:J:226:VAL:CG1	1:J:227:GLU:H	2.16	0.59
1:J:80:LEU:HA	1:J:85:VAL:HG21	1.85	0.59
1:A:111:GLY:H	1:A:137:MSE:HE1	1.67	0.59
1:A:246:GLU:HG2	1:A:247:GLY:H	1.67	0.59
1:D:151:ILE:HB	1:D:185:MSE:HE2	1.85	0.59
1:J:246:GLU:HG2	1:J:247:GLY:H	1.67	0.59
1:E:46:ILE:HD13	1:E:110:VAL:HG21	1.83	0.58
1:E:152:ASN:HD22	1:E:152:ASN:C	2.06	0.58
1:F:151:ILE:HB	1:F:185:MSE:HE2	1.84	0.58
1:E:226:VAL:CG1	1:E:227:GLU:H	2.16	0.58
1:I:151:ILE:HB	1:I:185:MSE:HE2	1.85	0.58
1:I:226:VAL:CG1	1:I:227:GLU:H	2.16	0.58
1:B:278:TYR:N	1:B:279:PRO:HD3	2.18	0.58
1:G:85:VAL:O	1:G:85:VAL:HG23	2.03	0.58
1:J:76:MSE:HE2	1:J:277:LEU:CD2	2.26	0.58
1:C:261:ALA:HA	1:C:264:LEU:HD22	1.86	0.58
1:F:226:VAL:CG1	1:F:227:GLU:H	2.16	0.58
1:I:152:ASN:C	1:I:152:ASN:HD22	2.07	0.58
1:A:226:VAL:CG1	1:A:227:GLU:H	2.16	0.58
1:F:47:VAL:HG11	1:F:76:MSE:HE1	1.85	0.58
1:I:273:GLY:N	1:I:274:ARG:HH21	2.02	0.58
1:C:246:GLU:HG2	1:C:247:GLY:H	1.67	0.58
1:G:151:ILE:HB	1:G:185:MSE:HE2	1.84	0.58
1:H:261:ALA:HA	1:H:264:LEU:HD22	1.86	0.58
1:C:226:VAL:CG1	1:C:227:GLU:H	2.16	0.58
1:D:261:ALA:HA	1:D:264:LEU:HD22	1.85	0.58
1:E:47:VAL:HG11	1:E:76:MSE:HE1	1.86	0.58
1:F:85:VAL:O	1:F:85:VAL:HG23	2.03	0.58
1:H:85:VAL:O	1:H:85:VAL:HG23	2.03	0.58
1:B:151:ILE:HB	1:B:185:MSE:HE2	1.85	0.58
1:B:246:GLU:HG2	1:B:247:GLY:H	1.67	0.58
1:B:274:ARG:H	1:B:274:ARG:NE	2.01	0.58
1:C:54:ARG:HH21	1:C:150:ARG:HH12	1.52	0.58
1:G:261:ALA:HA	1:G:264:LEU:HD22	1.85	0.58
1:B:261:ALA:HA	1:B:264:LEU:HD22	1.86	0.57
1:D:273:GLY:N	1:D:274:ARG:HH21	2.02	0.57
1:H:273:GLY:N	1:H:274:ARG:HH21	2.01	0.57
1:I:114:ASN:HD21	1:I:148:LEU:H	1.52	0.57
1:B:152:ASN:C	1:B:152:ASN:HD22	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:VAL:O	1:B:85:VAL:HG23	2.04	0.57
1:C:111:GLY:CA	1:C:137:MSE:CE	2.82	0.57
1:C:75:ARG:HH21	1:C:278:TYR:HA	1.69	0.57
1:E:85:VAL:HG23	1:E:85:VAL:O	2.03	0.57
1:F:273:GLY:H	1:F:274:ARG:HH21	1.51	0.57
1:G:152:ASN:C	1:G:152:ASN:HD22	2.06	0.57
1:H:226:VAL:CG1	1:H:227:GLU:H	2.16	0.57
1:H:274:ARG:NE	1:H:274:ARG:H	2.01	0.57
1:A:76:MSE:HA	1:A:76:MSE:CE	2.33	0.57
1:B:47:VAL:HG11	1:B:76:MSE:HE1	1.86	0.57
1:C:152:ASN:C	1:C:152:ASN:HD22	2.07	0.57
1:H:151:ILE:HB	1:H:185:MSE:HE2	1.85	0.57
1:H:41:ASP:OD2	1:H:296:HIS:HD2	1.86	0.57
1:J:76:MSE:HE2	1:J:76:MSE:HA	1.86	0.57
1:A:273:GLY:N	1:A:274:ARG:HH21	2.02	0.57
1:B:110:VAL:HG13	1:B:144:PHE:HB3	1.87	0.57
1:F:152:ASN:C	1:F:152:ASN:HD22	2.06	0.57
1:B:273:GLY:H	1:B:274:ARG:HH21	1.51	0.57
1:F:76:MSE:HA	1:F:76:MSE:CE	2.33	0.57
1:I:47:VAL:HG11	1:I:76:MSE:HE1	1.85	0.57
1:J:152:ASN:C	1:J:152:ASN:HD22	2.07	0.57
1:F:12:GLU:OE1	1:F:16:ARG:NH2	2.36	0.57
1:G:226:VAL:CG1	1:G:227:GLU:H	2.17	0.57
1:G:47:VAL:HG11	1:G:76:MSE:HE1	1.86	0.57
1:I:261:ALA:HA	1:I:264:LEU:HD22	1.86	0.57
1:A:152:ASN:C	1:A:152:ASN:HD22	2.08	0.57
1:D:85:VAL:HG23	1:D:85:VAL:O	2.04	0.57
1:G:114:ASN:HD22	1:G:114:ASN:N	1.98	0.57
1:D:47:VAL:HG11	1:D:76:MSE:HE1	1.86	0.57
1:F:261:ALA:HA	1:F:264:LEU:HD22	1.86	0.57
1:H:76:MSE:HA	1:H:76:MSE:CE	2.34	0.57
1:I:274:ARG:H	1:I:274:ARG:NE	2.01	0.57
1:A:47:VAL:HG11	1:A:76:MSE:HE1	1.86	0.57
1:E:273:GLY:H	1:E:274:ARG:HH21	1.53	0.57
1:E:273:GLY:N	1:E:274:ARG:HH21	2.02	0.57
1:F:283:ASP:HB3	1:F:286:ALA:HB3	1.85	0.57
1:J:261:ALA:HA	1:J:264:LEU:HD22	1.86	0.57
1:B:226:VAL:CG1	1:B:227:GLU:H	2.17	0.56
1:I:274:ARG:O	1:I:277:LEU:O	2.23	0.56
1:A:261:ALA:HA	1:A:264:LEU:HD22	1.86	0.56
1:A:85:VAL:HG23	1:A:85:VAL:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:273:GLY:H	1:D:274:ARG:HH21	1.52	0.56
1:F:86:ASP:OD2	1:F:296:HIS:HE1	1.88	0.56
1:J:273:GLY:N	1:J:274:ARG:HH21	2.02	0.56
1:B:185:MSE:HE3	1:B:205:SER:HA	1.88	0.56
1:D:152:ASN:C	1:D:152:ASN:HD22	2.07	0.56
1:C:110:VAL:HG22	1:C:144:PHE:HB3	1.87	0.56
1:E:32:ARG:HD2	1:E:104:LEU:HB3	1.87	0.56
1:G:76:MSE:HA	1:G:76:MSE:CE	2.33	0.56
1:I:110:VAL:HG22	1:I:144:PHE:HB3	1.87	0.56
1:A:273:GLY:H	1:A:274:ARG:HH21	1.52	0.56
1:A:274:ARG:H	1:A:274:ARG:NE	2.01	0.56
1:F:278:TYR:N	1:F:279:PRO:HD3	2.21	0.56
1:H:152:ASN:C	1:H:152:ASN:HD22	2.07	0.56
1:I:54:ARG:HH21	1:I:150:ARG:HH12	1.54	0.56
1:B:185:MSE:HE3	1:B:205:SER:CA	2.36	0.55
1:E:76:MSE:CE	1:E:76:MSE:HA	2.34	0.55
1:J:111:GLY:H	1:J:137:MSE:HE1	1.71	0.55
1:A:97:ASP:O	1:A:101:LEU:HD22	2.06	0.55
1:D:76:MSE:HA	1:D:76:MSE:CE	2.34	0.55
1:D:76:MSE:HE2	1:D:277:LEU:HD21	1.88	0.55
1:G:274:ARG:H	1:G:274:ARG:NE	2.02	0.55
1:H:185:MSE:HE3	1:H:205:SER:HA	1.89	0.55
1:I:273:GLY:H	1:I:274:ARG:HH21	1.53	0.55
1:D:45:PHE:CE2	1:D:85:VAL:HG12	2.42	0.55
1:J:273:GLY:H	1:J:274:ARG:HH21	1.53	0.55
1:F:110:VAL:HG22	1:F:144:PHE:CB	2.37	0.55
1:G:185:MSE:HE3	1:G:205:SER:CA	2.37	0.55
1:G:273:GLY:N	1:G:274:ARG:HH21	2.05	0.55
1:C:113:MSE:HE3	2:C:704:HOH:O	2.07	0.55
1:H:105:ASP:O	1:H:107:LYS:HG2	2.07	0.55
1:J:75:ARG:HH21	1:J:278:TYR:HA	1.72	0.55
1:B:76:MSE:HA	1:B:76:MSE:CE	2.33	0.55
1:C:185:MSE:HE3	1:C:205:SER:CA	2.37	0.55
1:C:185:MSE:HE3	1:C:205:SER:HA	1.88	0.55
1:D:185:MSE:HE3	1:D:205:SER:CA	2.37	0.55
1:E:45:PHE:CE2	1:E:85:VAL:HG12	2.42	0.55
1:J:185:MSE:HE3	1:J:205:SER:HA	1.89	0.55
1:J:89:LEU:HD12	1:J:90:GLY:N	2.22	0.55
1:A:45:PHE:CE2	1:A:85:VAL:HG12	2.42	0.55
1:B:45:PHE:CE2	1:B:85:VAL:HG12	2.42	0.55
1:J:9:GLU:N	1:J:9:GLU:OE1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:ASP:OD2	1:B:296:HIS:HD2	1.90	0.54
1:C:45:PHE:CE2	1:C:85:VAL:HG12	2.42	0.54
1:F:185:MSE:HE3	1:F:205:SER:CA	2.38	0.54
1:G:185:MSE:HE3	1:G:205:SER:HA	1.89	0.54
1:J:185:MSE:HE3	1:J:205:SER:CA	2.37	0.54
1:A:278:TYR:N	1:A:279:PRO:HD3	2.23	0.54
1:E:185:MSE:HE3	1:E:205:SER:HA	1.90	0.54
1:H:45:PHE:CE2	1:H:85:VAL:HG12	2.42	0.54
1:I:185:MSE:HE3	1:I:205:SER:HA	1.88	0.54
1:I:76:MSE:HA	1:I:76:MSE:CE	2.33	0.54
1:C:76:MSE:HA	1:C:76:MSE:CE	2.34	0.54
1:I:14:LEU:HD22	1:I:101:LEU:CD1	2.37	0.54
1:I:185:MSE:HE3	1:I:205:SER:CA	2.37	0.54
1:I:259:GLU:CB	1:I:294:LEU:HD11	2.35	0.54
1:J:110:VAL:HG22	1:J:144:PHE:HB3	1.90	0.54
1:C:111:GLY:N	1:C:137:MSE:HE1	2.21	0.54
1:E:170:ASN:ND2	1:E:214:ASN:H	2.06	0.54
1:H:185:MSE:HE3	1:H:205:SER:CA	2.37	0.54
1:F:45:PHE:CE2	1:F:85:VAL:HG12	2.42	0.54
1:E:126:ASP:OD2	1:E:128:ARG:NH1	2.40	0.54
1:I:45:PHE:CE2	1:I:85:VAL:HG12	2.42	0.54
1:D:185:MSE:HE3	1:D:205:SER:HA	1.89	0.54
1:E:274:ARG:H	1:E:274:ARG:NE	2.02	0.54
1:F:185:MSE:HE3	1:F:205:SER:HA	1.89	0.54
1:G:45:PHE:CE2	1:G:85:VAL:HG12	2.43	0.53
1:J:29:PHE:O	1:J:32:ARG:HB3	2.07	0.53
1:D:297:THR:O	1:D:299:ILE:N	2.41	0.53
2:C:569:HOH:O	1:D:55:GLY:HA2	2.07	0.53
1:D:75:ARG:NH2	1:D:278:TYR:HA	2.23	0.53
1:G:273:GLY:H	1:G:274:ARG:HH21	1.56	0.53
1:H:33:ARG:NH1	1:H:33:ARG:HG3	2.23	0.53
1:D:274:ARG:H	1:D:274:ARG:NE	2.00	0.53
1:B:54:ARG:HH21	1:B:150:ARG:HH12	1.54	0.53
1:F:114:ASN:O	1:F:115:ARG:HD2	2.08	0.53
1:J:170:ASN:ND2	1:J:214:ASN:H	2.07	0.53
1:A:110:VAL:HG13	1:A:144:PHE:HB3	1.91	0.53
1:F:170:ASN:ND2	1:F:214:ASN:H	2.07	0.53
1:E:185:MSE:HE3	1:E:205:SER:CA	2.38	0.53
1:H:126:ASP:OD2	1:H:128:ARG:NH1	2.41	0.53
1:H:274:ARG:O	1:H:277:LEU:O	2.27	0.53
1:I:229:MSE:O	1:I:264:LEU:HD23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:LEU:O	1:B:278:TYR:HB2	2.09	0.53
1:B:46:ILE:HD13	1:B:110:VAL:HG21	1.91	0.53
1:G:170:ASN:ND2	1:G:214:ASN:H	2.07	0.53
1:H:278:TYR:N	1:H:279:PRO:HD3	2.24	0.53
1:H:64:THR:O	1:H:65:ALA:HB3	2.09	0.53
1:J:47:VAL:CG1	1:J:76:MSE:HE1	2.39	0.52
1:F:12:GLU:OE2	1:F:15:ARG:NH2	2.42	0.52
1:F:229:MSE:O	1:F:264:LEU:HD23	2.09	0.52
1:G:64:THR:O	1:G:65:ALA:HB3	2.10	0.52
1:A:111:GLY:CA	1:A:137:MSE:CE	2.86	0.52
1:A:24:MSE:HG3	2:A:316:HOH:O	2.08	0.52
1:E:114:ASN:N	1:E:114:ASN:HD22	2.06	0.52
1:E:111:GLY:CA	1:E:137:MSE:CE	2.86	0.52
1:I:170:ASN:ND2	1:I:214:ASN:H	2.07	0.52
1:J:274:ARG:NE	1:J:274:ARG:H	2.01	0.52
1:F:110:VAL:HG13	1:F:144:PHE:HB3	1.91	0.52
1:F:114:ASN:O	1:F:115:ARG:CD	2.58	0.52
1:I:64:THR:O	1:I:65:ALA:HB3	2.09	0.52
1:J:64:THR:O	1:J:65:ALA:HB3	2.09	0.52
1:B:33:ARG:NH1	1:B:33:ARG:HG3	2.25	0.52
1:A:296:HIS:C	1:A:298:ASP:H	2.13	0.52
1:A:64:THR:O	1:A:65:ALA:HB3	2.09	0.52
1:D:68:ASN:CG	1:D:71:GLU:HG3	2.30	0.52
1:H:47:VAL:HG11	1:H:76:MSE:CE	2.40	0.52
1:A:185:MSE:HE3	1:A:205:SER:CA	2.38	0.52
1:C:126:ASP:OD2	1:C:128:ARG:NH1	2.41	0.52
1:D:64:THR:O	1:D:65:ALA:HB3	2.10	0.52
1:F:64:THR:O	1:F:65:ALA:HB3	2.10	0.52
1:H:229:MSE:O	1:H:264:LEU:HD23	2.10	0.52
1:A:274:ARG:O	1:A:277:LEU:O	2.27	0.52
1:H:170:ASN:ND2	1:H:214:ASN:H	2.08	0.52
1:J:45:PHE:HE2	1:J:85:VAL:HG12	1.73	0.52
1:D:297:THR:C	1:D:299:ILE:H	2.13	0.52
1:E:68:ASN:CG	1:E:71:GLU:HG3	2.30	0.52
1:J:69:ARG:HH11	1:J:72:LEU:HD13	1.75	0.52
1:A:185:MSE:HE3	1:A:205:SER:HA	1.90	0.51
1:A:170:ASN:ND2	1:A:214:ASN:H	2.08	0.51
1:B:64:THR:O	1:B:65:ALA:HB3	2.10	0.51
1:B:76:MSE:HE2	1:B:277:LEU:HD21	1.92	0.51
1:C:64:THR:O	1:C:65:ALA:HB3	2.09	0.51
1:F:274:ARG:H	1:F:274:ARG:NE	2.00	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:47:VAL:CG1	1:H:76:MSE:HE1	2.40	0.51
1:J:65:ALA:C	1:J:67:ALA:H	2.13	0.51
1:B:170:ASN:ND2	1:B:214:ASN:H	2.08	0.51
1:C:297:THR:O	1:C:298:ASP:HB2	2.11	0.51
1:B:180:MSE:HE2	1:B:241:LEU:HD12	1.92	0.51
1:C:229:MSE:O	1:C:264:LEU:HD23	2.11	0.51
1:D:111:GLY:HA3	1:D:137:MSE:CE	2.40	0.51
1:E:229:MSE:O	1:E:264:LEU:HD23	2.11	0.51
1:B:126:ASP:OD2	1:B:128:ARG:NH1	2.41	0.51
1:E:64:THR:O	1:E:65:ALA:HB3	2.09	0.51
1:G:229:MSE:O	1:G:264:LEU:HD23	2.10	0.51
1:G:68:ASN:CG	1:G:71:GLU:HG3	2.30	0.51
1:H:111:GLY:N	1:H:137:MSE:HE1	2.25	0.51
1:I:68:ASN:HD21	1:I:70:TYR:HB2	1.76	0.51
1:A:111:GLY:N	1:A:137:MSE:HE1	2.26	0.51
1:B:32:ARG:HD2	1:B:104:LEU:HB3	1.92	0.51
1:C:33:ARG:HG3	1:C:33:ARG:NH1	2.25	0.51
1:C:47:VAL:CG1	1:C:76:MSE:HE1	2.40	0.51
1:D:114:ASN:N	1:D:114:ASN:HD22	2.04	0.51
1:D:170:ASN:ND2	1:D:214:ASN:H	2.08	0.51
1:F:274:ARG:O	1:F:277:LEU:O	2.29	0.51
1:J:129:TYR:OH	1:J:147:THR:HG21	2.11	0.51
1:A:75:ARG:HH21	1:A:278:TYR:HA	1.74	0.51
1:F:47:VAL:HG11	1:F:76:MSE:CE	2.41	0.51
1:G:47:VAL:HG11	1:G:76:MSE:CE	2.41	0.51
1:B:75:ARG:HH21	1:B:278:TYR:HA	1.75	0.51
1:C:68:ASN:CG	1:C:71:GLU:HG3	2.31	0.51
1:J:229:MSE:O	1:J:264:LEU:HD23	2.10	0.51
1:D:180:MSE:HE2	1:D:241:LEU:HD12	1.93	0.51
1:E:297:THR:OG1	1:E:299:ILE:HG12	2.11	0.51
1:I:68:ASN:CG	1:I:71:GLU:HG3	2.31	0.51
1:C:180:MSE:HE2	1:C:241:LEU:HD12	1.93	0.51
1:C:47:VAL:HG11	1:C:76:MSE:CE	2.40	0.51
1:I:47:VAL:HG11	1:I:76:MSE:CE	2.41	0.51
1:A:46:ILE:HD13	1:A:110:VAL:HG21	1.93	0.51
1:B:68:ASN:CG	1:B:71:GLU:HG3	2.31	0.51
1:D:229:MSE:O	1:D:264:LEU:HD23	2.10	0.51
1:D:33:ARG:HG3	1:D:33:ARG:NH1	2.25	0.51
1:E:129:TYR:OH	1:E:147:THR:HG21	2.11	0.51
1:G:275:THR:HG22	1:G:276:LEU:HD23	1.93	0.51
1:I:33:ARG:NH1	1:I:33:ARG:HG3	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:MSE:O	1:A:264:LEU:HD23	2.10	0.50
1:B:68:ASN:HD21	1:B:70:TYR:HB2	1.76	0.50
1:C:170:ASN:ND2	1:C:214:ASN:H	2.08	0.50
1:I:110:VAL:HG22	1:I:144:PHE:CB	2.42	0.50
1:A:126:ASP:OD2	1:A:128:ARG:NH1	2.41	0.50
1:A:47:VAL:HG11	1:A:76:MSE:CE	2.41	0.50
1:D:47:VAL:HG11	1:D:76:MSE:CE	2.40	0.50
1:E:47:VAL:HG11	1:E:76:MSE:CE	2.41	0.50
1:G:129:TYR:OH	1:G:147:THR:HG21	2.11	0.50
1:G:274:ARG:O	1:G:277:LEU:O	2.29	0.50
1:H:57:LEU:O	1:H:65:ALA:O	2.30	0.50
1:F:68:ASN:HD21	1:F:70:TYR:HB2	1.77	0.50
1:I:114:ASN:HD22	1:I:114:ASN:N	1.99	0.50
1:I:129:TYR:OH	1:I:147:THR:HG21	2.12	0.50
1:B:47:VAL:CG1	1:B:76:MSE:HE1	2.42	0.50
1:D:89:LEU:HD13	1:D:110:VAL:HG12	1.92	0.50
1:F:126:ASP:OD2	1:F:128:ARG:NH1	2.41	0.50
1:G:110:VAL:HG22	1:G:144:PHE:HB3	1.92	0.50
1:G:68:ASN:HD21	1:G:70:TYR:HB2	1.76	0.50
1:G:47:VAL:CG1	1:G:76:MSE:HE1	2.42	0.50
1:A:180:MSE:HE2	1:A:241:LEU:HD12	1.93	0.50
1:B:66:MSE:HG2	1:B:278:TYR:CE2	2.46	0.50
1:C:278:TYR:N	1:C:279:PRO:HD3	2.27	0.50
1:E:180:MSE:HE2	1:E:241:LEU:HD12	1.93	0.50
1:A:68:ASN:CG	1:A:71:GLU:HG3	2.31	0.50
1:B:111:GLY:N	1:B:137:MSE:HE1	2.25	0.50
1:C:110:VAL:HG22	1:C:144:PHE:CB	2.42	0.50
1:C:57:LEU:O	1:C:65:ALA:O	2.30	0.50
1:G:126:ASP:OD2	1:G:128:ARG:NH1	2.41	0.50
1:H:12:GLU:OE1	1:H:16:ARG:NH2	2.42	0.50
1:J:17:MSE:HE1	1:J:28:ARG:HE	1.75	0.50
1:B:47:VAL:HG11	1:B:76:MSE:CE	2.41	0.50
1:C:68:ASN:HD21	1:C:70:TYR:HB2	1.77	0.50
1:F:180:MSE:HE2	1:F:241:LEU:HD12	1.92	0.50
1:F:68:ASN:CG	1:F:71:GLU:HG3	2.32	0.50
1:J:111:GLY:HA3	1:J:137:MSE:CE	2.40	0.50
1:C:111:GLY:CA	1:C:137:MSE:HE1	2.42	0.50
1:D:126:ASP:OD2	1:D:128:ARG:NH1	2.41	0.50
1:G:12:GLU:OE1	1:G:16:ARG:NH2	2.45	0.50
1:H:68:ASN:HD21	1:H:70:TYR:HB2	1.76	0.50
1:A:47:VAL:CG1	1:A:76:MSE:HE1	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:MSE:O	1:B:264:LEU:HD23	2.10	0.49
1:D:68:ASN:HD21	1:D:70:TYR:HB2	1.76	0.49
1:E:33:ARG:HG3	1:E:33:ARG:NH1	2.25	0.49
1:E:68:ASN:HD21	1:E:70:TYR:HB2	1.76	0.49
1:F:129:TYR:OH	1:F:147:THR:HG21	2.12	0.49
1:F:76:MSE:CE	1:F:277:LEU:HD21	2.42	0.49
1:G:114:ASN:O	1:G:115:ARG:HD2	2.13	0.49
1:H:180:MSE:HE2	1:H:241:LEU:HD12	1.93	0.49
1:I:296:HIS:O	1:I:298:ASP:N	2.45	0.49
1:J:68:ASN:HD22	1:J:69:ARG:N	2.10	0.49
1:D:47:VAL:CG1	1:D:76:MSE:HE1	2.42	0.49
1:J:180:MSE:HE2	1:J:241:LEU:HD12	1.93	0.49
1:J:41:ASP:O	1:J:43:LYS:HD3	2.12	0.49
1:A:129:TYR:OH	1:A:147:THR:HG21	2.12	0.49
1:B:129:TYR:OH	1:B:147:THR:HG21	2.11	0.49
1:B:57:LEU:O	1:B:65:ALA:O	2.30	0.49
1:F:47:VAL:CG1	1:F:76:MSE:HE1	2.42	0.49
1:F:76:MSE:HE3	1:F:277:LEU:HD11	1.94	0.49
1:I:47:VAL:CG1	1:I:76:MSE:HE1	2.41	0.49
1:J:259:GLU:HB2	1:J:294:LEU:HD11	1.94	0.49
1:A:63:GLU:O	1:A:64:THR:O	2.31	0.49
1:C:274:ARG:NE	1:C:274:ARG:H	2.01	0.49
1:H:129:TYR:OH	1:H:147:THR:HG21	2.12	0.49
1:J:92:PRO:HG3	1:J:132:TYR:CD2	2.47	0.49
1:J:85:VAL:HG23	1:J:85:VAL:O	2.13	0.49
1:J:95:ILE:HD12	1:J:109:VAL:HG13	1.95	0.49
1:C:129:TYR:OH	1:C:147:THR:HG21	2.12	0.49
1:F:114:ASN:HD22	1:F:114:ASN:N	2.09	0.49
1:I:110:VAL:HG13	1:I:144:PHE:HB3	1.95	0.49
1:J:91:THR:OG1	1:J:93:ASP:OD1	2.25	0.49
1:A:111:GLY:CA	1:A:137:MSE:HE1	2.43	0.49
1:A:57:LEU:O	1:A:65:ALA:O	2.31	0.49
1:C:32:ARG:HD2	1:C:104:LEU:HB3	1.94	0.49
1:E:46:ILE:HD13	1:E:110:VAL:CG2	2.43	0.49
1:G:76:MSE:HE3	1:G:277:LEU:HD21	1.94	0.49
1:I:57:LEU:O	1:I:65:ALA:O	2.31	0.49
1:B:17:MSE:HE1	1:B:28:ARG:NE	2.27	0.49
1:D:129:TYR:OH	1:D:147:THR:HG21	2.11	0.49
1:F:33:ARG:HG3	1:F:33:ARG:NH1	2.24	0.49
1:G:8:PRO:HG2	1:G:9:GLU:OE1	2.13	0.49
1:H:68:ASN:CG	1:H:71:GLU:HG3	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:180:MSE:HE2	1:I:241:LEU:HD12	1.94	0.49
1:A:68:ASN:HD21	1:A:70:TYR:HB2	1.77	0.48
1:C:82:ARG:NH2	1:C:289:ASP:OD2	2.44	0.48
1:I:296:HIS:C	1:I:298:ASP:H	2.16	0.48
1:C:274:ARG:O	1:C:277:LEU:O	2.30	0.48
1:E:47:VAL:CG1	1:E:76:MSE:HE1	2.42	0.48
1:F:57:LEU:O	1:F:65:ALA:O	2.31	0.48
1:G:33:ARG:HG3	1:G:33:ARG:NH1	2.26	0.48
1:J:278:TYR:N	1:J:279:PRO:HD3	2.28	0.48
1:J:63:GLU:CG	1:J:64:THR:H	2.19	0.48
1:B:63:GLU:O	1:B:64:THR:O	2.31	0.48
1:C:76:MSE:HE2	1:C:277:LEU:HD21	1.95	0.48
1:D:214:ASN:HD22	1:D:214:ASN:C	2.17	0.48
1:I:152:ASN:HD22	1:I:154:SER:H	1.62	0.48
1:J:79:ALA:O	1:J:85:VAL:HG21	2.13	0.48
1:C:214:ASN:C	1:C:214:ASN:HD22	2.16	0.48
1:G:57:LEU:O	1:G:65:ALA:O	2.31	0.48
1:I:103:LEU:O	1:I:104:LEU:HD12	2.14	0.48
1:J:151:ILE:HB	1:J:185:MSE:HE1	1.96	0.48
1:A:214:ASN:HD22	1:A:214:ASN:C	2.17	0.48
1:D:63:GLU:O	1:D:64:THR:O	2.31	0.48
1:E:111:GLY:H	1:E:137:MSE:HE1	1.77	0.48
1:E:63:GLU:O	1:E:64:THR:O	2.32	0.48
1:E:57:LEU:O	1:E:65:ALA:O	2.31	0.48
1:G:214:ASN:C	1:G:214:ASN:HD22	2.16	0.48
1:G:180:MSE:HE2	1:G:241:LEU:HD12	1.94	0.48
1:H:151:ILE:HB	1:H:185:MSE:HE1	1.96	0.48
1:H:152:ASN:HD22	1:H:154:SER:H	1.62	0.48
1:D:111:GLY:N	1:D:137:MSE:HE1	2.29	0.47
1:F:115:ARG:HA	1:F:115:ARG:HD2	1.58	0.47
1:H:214:ASN:C	1:H:214:ASN:HD22	2.17	0.47
1:I:214:ASN:C	1:I:214:ASN:HD22	2.17	0.47
1:I:63:GLU:O	1:I:64:THR:O	2.32	0.47
1:E:110:VAL:HG13	1:E:144:PHE:HB3	1.96	0.47
1:E:214:ASN:HD22	1:E:214:ASN:C	2.17	0.47
1:F:214:ASN:C	1:F:214:ASN:HD22	2.16	0.47
1:G:14:LEU:HD13	1:G:101:LEU:HD13	1.95	0.47
1:A:15:ARG:HD3	1:A:70:TYR:OH	2.14	0.47
1:H:17:MSE:HE1	1:H:28:ARG:NE	2.30	0.47
1:I:111:GLY:HA3	1:I:137:MSE:CE	2.42	0.47
1:A:68:ASN:ND2	1:A:68:ASN:C	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:ASN:HD22	1:C:154:SER:H	1.63	0.47
1:F:151:ILE:HB	1:F:185:MSE:HE1	1.97	0.47
1:G:63:GLU:O	1:G:64:THR:O	2.31	0.47
1:H:63:GLU:O	1:H:64:THR:O	2.31	0.47
1:F:273:GLY:H	1:F:274:ARG:NH2	2.12	0.47
1:H:273:GLY:H	1:H:274:ARG:NH2	2.13	0.47
1:J:126:ASP:OD2	1:J:128:ARG:NH1	2.40	0.47
1:J:214:ASN:HD22	1:J:214:ASN:C	2.17	0.47
1:A:54:ARG:HH21	1:A:150:ARG:HH12	1.62	0.47
1:A:273:GLY:H	1:A:274:ARG:NH2	2.13	0.47
1:C:63:GLU:O	1:C:64:THR:O	2.32	0.47
1:D:151:ILE:HB	1:D:185:MSE:HE1	1.97	0.47
1:A:86:ASP:OD2	1:A:296:HIS:HE1	1.97	0.47
1:D:273:GLY:H	1:D:274:ARG:NH2	2.12	0.47
1:F:63:GLU:O	1:F:64:THR:O	2.31	0.47
1:F:85:VAL:HG23	1:F:107:LYS:HE3	1.96	0.47
1:G:152:ASN:HD22	1:G:154:SER:H	1.63	0.47
1:I:40:GLU:N	1:I:40:GLU:OE2	2.45	0.47
1:J:273:GLY:H	1:J:274:ARG:NH2	2.13	0.47
1:J:32:ARG:NH1	1:J:109:VAL:HG23	2.30	0.47
1:B:227:GLU:HB2	2:B:578:HOH:O	2.15	0.47
1:J:47:VAL:CB	1:J:76:MSE:HE1	2.44	0.47
1:D:284:VAL:O	1:D:288:VAL:HG23	2.14	0.47
1:A:14:LEU:HD22	1:A:101:LEU:HD11	1.97	0.46
1:A:23:THR:OG1	1:A:24:MSE:HE2	2.15	0.46
1:D:57:LEU:O	1:D:65:ALA:O	2.31	0.46
1:G:111:GLY:N	1:G:137:MSE:HE1	2.27	0.46
1:I:273:GLY:H	1:I:274:ARG:NH2	2.13	0.46
1:I:46:ILE:O	1:I:271:THR:HA	2.15	0.46
1:A:152:ASN:HD22	1:A:154:SER:H	1.62	0.46
1:B:152:ASN:HD22	1:B:154:SER:H	1.63	0.46
1:E:152:ASN:HD22	1:E:154:SER:H	1.62	0.46
1:G:54:ARG:NH2	1:G:150:ARG:HH12	2.12	0.46
1:I:115:ARG:HD2	1:I:115:ARG:HA	1.56	0.46
1:A:115:ARG:HA	1:A:115:ARG:HD2	1.58	0.46
1:C:273:GLY:H	1:C:274:ARG:NH2	2.13	0.46
1:H:54:ARG:HH21	1:H:150:ARG:HH12	1.62	0.46
1:B:214:ASN:C	1:B:214:ASN:HD22	2.18	0.46
1:D:15:ARG:HD3	1:D:70:TYR:OH	2.15	0.46
1:E:273:GLY:H	1:E:274:ARG:NH2	2.14	0.46
1:E:68:ASN:C	1:E:68:ASN:ND2	2.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:ARG:HD2	1:D:115:ARG:HA	1.57	0.46
1:E:111:GLY:CA	1:E:137:MSE:HE1	2.45	0.46
1:J:63:GLU:O	1:J:67:ALA:HB2	2.16	0.46
1:B:273:GLY:H	1:B:274:ARG:NH2	2.12	0.46
1:D:68:ASN:C	1:D:68:ASN:ND2	2.67	0.46
1:G:151:ILE:HB	1:G:185:MSE:HE1	1.96	0.46
1:J:152:ASN:HD22	1:J:154:SER:H	1.63	0.46
1:B:111:GLY:CA	1:B:137:MSE:CE	2.93	0.46
1:E:89:LEU:HA	1:E:110:VAL:HB	1.97	0.46
1:E:75:ARG:NH2	1:E:278:TYR:HA	2.29	0.46
1:H:111:GLY:CA	1:H:137:MSE:CE	2.93	0.46
1:I:126:ASP:OD2	1:I:128:ARG:NH1	2.41	0.46
1:D:152:ASN:HD22	1:D:154:SER:H	1.63	0.46
1:G:111:GLY:CA	1:G:137:MSE:CE	2.93	0.46
1:B:46:ILE:O	1:B:271:THR:HA	2.16	0.45
1:E:151:ILE:HB	1:E:185:MSE:HE1	1.97	0.45
1:F:111:GLY:CA	1:F:137:MSE:CE	2.93	0.45
1:H:68:ASN:C	1:H:68:ASN:ND2	2.67	0.45
1:J:296:HIS:C	1:J:298:ASP:H	2.20	0.45
1:F:146:LYS:HE3	2:F:308:HOH:O	2.16	0.45
1:G:297:THR:OG1	1:G:299:ILE:HG13	2.16	0.45
1:I:151:ILE:HB	1:I:185:MSE:HE1	1.96	0.45
1:I:24:MSE:HE1	1:I:27:GLU:OE1	2.15	0.45
1:F:111:GLY:N	1:F:137:MSE:HE1	2.30	0.45
1:F:152:ASN:HD22	1:F:154:SER:H	1.63	0.45
1:G:115:ARG:HD2	1:G:115:ARG:HA	1.58	0.45
1:G:273:GLY:H	1:G:274:ARG:NH2	2.15	0.45
1:C:151:ILE:HB	1:C:185:MSE:HE1	1.97	0.45
1:C:76:MSE:HE3	1:C:277:LEU:HD21	1.98	0.45
1:G:68:ASN:ND2	1:G:71:GLU:H	2.15	0.45
1:H:296:HIS:C	1:H:298:ASP:H	2.19	0.45
1:I:68:ASN:ND2	1:I:68:ASN:C	2.67	0.45
1:E:115:ARG:HD2	1:E:115:ARG:HA	1.56	0.45
1:I:284:VAL:O	1:I:288:VAL:HG23	2.17	0.45
1:E:283:ASP:HB3	1:E:286:ALA:HB3	1.99	0.45
1:H:115:ARG:HA	1:H:115:ARG:HD2	1.55	0.45
1:A:33:ARG:HG3	1:A:33:ARG:NH1	2.24	0.45
1:G:75:ARG:HH21	1:G:278:TYR:HA	1.81	0.45
1:H:68:ASN:ND2	1:H:71:GLU:H	2.15	0.45
1:C:41:ASP:OD2	1:C:296:HIS:HD2	2.00	0.45
1:I:68:ASN:ND2	1:I:71:GLU:H	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:ASP:OD2	1:F:296:HIS:CD2	2.61	0.44
1:G:114:ASN:O	1:G:115:ARG:CD	2.65	0.44
1:G:16:ARG:HD2	2:G:489:HOH:O	2.16	0.44
1:G:76:MSE:CE	1:G:277:LEU:HD21	2.47	0.44
1:H:76:MSE:HE2	1:H:277:LEU:HD21	1.97	0.44
1:A:98:LEU:HB3	1:A:104:LEU:HD11	1.99	0.44
1:B:151:ILE:HB	1:B:185:MSE:HE1	1.96	0.44
1:D:68:ASN:ND2	1:D:71:GLU:H	2.15	0.44
1:G:110:VAL:HG22	1:G:144:PHE:CB	2.48	0.44
1:J:8:PRO:HG2	1:J:9:GLU:OE1	2.18	0.44
1:C:46:ILE:O	1:C:271:THR:HA	2.17	0.44
1:D:85:VAL:HG23	1:D:107:LYS:NZ	2.32	0.44
1:A:68:ASN:ND2	1:A:71:GLU:H	2.16	0.44
1:I:111:GLY:N	1:I:137:MSE:HE1	2.33	0.44
1:B:40:GLU:N	1:B:40:GLU:OE2	2.46	0.44
1:C:103:LEU:HD22	2:C:522:HOH:O	2.16	0.44
1:J:85:VAL:HG23	1:J:107:LYS:NZ	2.33	0.44
1:D:247:GLY:HA3	2:D:361:HOH:O	2.18	0.44
1:A:246:GLU:HG2	1:A:247:GLY:N	2.33	0.44
1:A:63:GLU:HB3	2:H:637:HOH:O	2.16	0.44
1:B:114:ASN:N	1:B:114:ASN:HD22	1.97	0.44
1:B:159:ALA:HB3	1:B:160:PRO:CD	2.48	0.44
1:F:40:GLU:N	1:F:40:GLU:OE2	2.45	0.44
1:A:61:ASP:OD1	1:A:61:ASP:C	2.56	0.43
1:J:159:ALA:HB3	1:J:160:PRO:CD	2.48	0.43
1:A:159:ALA:HB3	1:A:160:PRO:CD	2.49	0.43
1:B:44:LEU:O	1:B:269:GLY:HA3	2.18	0.43
1:C:115:ARG:HD2	1:C:115:ARG:HA	1.57	0.43
1:C:12:GLU:OE1	1:C:12:GLU:HA	2.18	0.43
1:C:44:LEU:O	1:C:269:GLY:HA3	2.17	0.43
1:G:246:GLU:HG2	1:G:247:GLY:N	2.33	0.43
1:H:61:ASP:OD1	1:H:61:ASP:C	2.57	0.43
1:D:65:ALA:O	1:D:66:MSE:HB2	2.18	0.43
1:F:75:ARG:NH2	1:F:278:TYR:HA	2.33	0.43
1:G:98:LEU:HB3	1:G:104:LEU:CD1	2.49	0.43
1:G:68:ASN:C	1:G:68:ASN:ND2	2.67	0.43
1:J:110:VAL:HG22	1:J:144:PHE:CB	2.48	0.43
1:A:151:ILE:HB	1:A:185:MSE:HE1	1.97	0.43
1:B:114:ASN:O	1:B:115:ARG:HD2	2.18	0.43
1:B:68:ASN:ND2	1:B:71:GLU:H	2.15	0.43
1:C:89:LEU:HD11	1:C:146:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:ASN:O	1:D:115:ARG:HD2	2.17	0.43
1:E:274:ARG:O	1:E:277:LEU:O	2.37	0.43
1:F:68:ASN:ND2	1:F:71:GLU:H	2.16	0.43
1:G:46:ILE:O	1:G:271:THR:HA	2.19	0.43
1:I:85:VAL:HG23	1:I:107:LYS:NZ	2.34	0.43
1:C:65:ALA:O	1:C:66:MSE:HB2	2.19	0.43
1:G:40:GLU:N	1:G:40:GLU:OE2	2.46	0.43
1:J:68:ASN:ND2	1:J:70:TYR:N	2.67	0.43
1:B:61:ASP:OD1	1:B:61:ASP:C	2.57	0.43
1:C:158:THR:HB	1:D:123:PHE:CE2	2.54	0.43
1:C:214:ASN:HD22	1:C:215:ASP:N	2.17	0.43
1:F:184:PHE:O	1:F:185:MSE:HE2	2.19	0.43
1:G:65:ALA:O	1:G:66:MSE:HB2	2.19	0.43
1:I:159:ALA:HB3	1:I:160:PRO:CD	2.49	0.43
1:I:277:LEU:O	1:I:278:TYR:HB2	2.17	0.43
1:I:65:ALA:O	1:I:66:MSE:HB2	2.19	0.43
1:A:46:ILE:HD13	1:A:110:VAL:CG2	2.49	0.43
1:B:246:GLU:HG2	1:B:247:GLY:N	2.34	0.43
1:D:277:LEU:O	1:D:278:TYR:CB	2.62	0.43
1:E:61:ASP:C	1:E:61:ASP:OD1	2.57	0.43
1:F:61:ASP:C	1:F:61:ASP:OD1	2.57	0.43
1:H:40:GLU:N	1:H:40:GLU:OE2	2.46	0.43
1:C:125:MSE:CE	1:C:152:ASN:HB2	2.44	0.43
1:C:61:ASP:C	1:C:61:ASP:OD1	2.57	0.43
1:E:65:ALA:O	1:E:66:MSE:HB2	2.19	0.43
1:F:206:VAL:CG1	1:F:236:THR:HG23	2.49	0.43
1:F:236:THR:HG22	2:G:520:HOH:O	2.17	0.43
1:H:65:ALA:O	1:H:66:MSE:HB2	2.19	0.43
1:D:44:LEU:O	1:D:269:GLY:HA3	2.19	0.43
1:E:159:ALA:HB3	1:E:160:PRO:CD	2.49	0.43
1:E:214:ASN:HD22	1:E:215:ASP:N	2.17	0.43
1:F:159:ALA:HB3	1:F:160:PRO:CD	2.49	0.43
1:J:184:PHE:O	1:J:185:MSE:HE2	2.19	0.43
1:J:223:LEU:CD1	1:J:233:MSE:HE1	2.43	0.43
1:A:40:GLU:OE2	1:A:40:GLU:N	2.45	0.43
1:C:214:ASN:C	1:C:214:ASN:ND2	2.73	0.43
1:C:246:GLU:HG2	1:C:247:GLY:N	2.33	0.43
1:C:68:ASN:ND2	1:C:71:GLU:H	2.16	0.43
1:E:68:ASN:ND2	1:E:71:GLU:H	2.16	0.43
1:C:115:ARG:HB2	2:C:313:HOH:O	2.18	0.42
1:C:159:ALA:HB3	1:C:160:PRO:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:281:ASP:OD2	1:E:281:ASP:C	2.58	0.42
1:H:86:ASP:OD2	1:H:296:HIS:HE1	2.02	0.42
1:J:274:ARG:O	1:J:277:LEU:O	2.37	0.42
1:A:65:ALA:O	1:A:66:MSE:HB2	2.19	0.42
1:E:111:GLY:N	1:E:137:MSE:HE1	2.34	0.42
1:H:184:PHE:O	1:H:185:MSE:HE2	2.19	0.42
1:I:214:ASN:HD22	1:I:215:ASP:N	2.17	0.42
1:J:214:ASN:HD22	1:J:215:ASP:N	2.17	0.42
1:D:61:ASP:OD1	1:D:61:ASP:C	2.57	0.42
1:F:214:ASN:HD22	1:F:215:ASP:N	2.16	0.42
1:G:194:VAL:O	1:G:194:VAL:HG23	2.20	0.42
1:I:44:LEU:O	1:I:269:GLY:HA3	2.19	0.42
1:C:184:PHE:O	1:C:185:MSE:HE2	2.19	0.42
1:C:40:GLU:OE2	1:C:40:GLU:N	2.46	0.42
1:F:54:ARG:HH21	1:F:150:ARG:HH12	1.66	0.42
1:G:272:VAL:HA	2:G:549:HOH:O	2.19	0.42
1:H:159:ALA:HB3	1:H:160:PRO:CD	2.49	0.42
1:H:214:ASN:HD22	1:H:215:ASP:N	2.18	0.42
1:J:45:PHE:HD2	1:J:85:VAL:HA	1.82	0.42
1:A:214:ASN:HD22	1:A:215:ASP:N	2.17	0.42
1:B:76:MSE:HE3	1:B:277:LEU:HD21	2.00	0.42
1:D:159:ALA:HB3	1:D:160:PRO:CD	2.50	0.42
1:E:262:LEU:HD12	1:E:262:LEU:HA	1.93	0.42
1:F:125:MSE:CE	1:F:152:ASN:HB2	2.45	0.42
1:H:214:ASN:ND2	1:H:214:ASN:C	2.73	0.42
1:I:61:ASP:OD1	1:I:61:ASP:C	2.57	0.42
1:J:28:ARG:HD3	1:J:100:ALA:HA	2.01	0.42
1:B:206:VAL:CG1	1:B:236:THR:HG23	2.50	0.42
1:C:114:ASN:O	1:C:115:ARG:HD2	2.20	0.42
1:C:33:ARG:HH11	1:C:33:ARG:CG	2.29	0.42
1:D:194:VAL:HG23	1:D:194:VAL:O	2.20	0.42
1:D:89:LEU:HD12	1:D:90:GLY:N	2.35	0.42
1:E:214:ASN:ND2	1:E:214:ASN:C	2.73	0.42
1:E:206:VAL:CG1	1:E:236:THR:HG23	2.50	0.42
1:G:214:ASN:HD22	1:G:215:ASP:N	2.17	0.42
1:G:61:ASP:OD1	1:G:61:ASP:C	2.57	0.42
1:H:246:GLU:HG2	1:H:247:GLY:N	2.33	0.42
1:H:89:LEU:HD12	1:H:90:GLY:N	2.35	0.42
1:D:115:ARG:HB2	2:D:356:HOH:O	2.19	0.42
1:D:214:ASN:HD22	1:D:215:ASP:N	2.17	0.42
1:D:46:ILE:O	1:D:271:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:46:ILE:O	1:E:271:THR:HA	2.20	0.42
1:I:184:PHE:O	1:I:185:MSE:HE2	2.20	0.42
1:J:206:VAL:CG1	1:J:236:THR:HG23	2.50	0.42
1:J:45:PHE:CD2	1:J:85:VAL:HA	2.55	0.42
1:J:57:LEU:N	1:J:57:LEU:HD22	2.35	0.42
1:A:112:SER:HA	1:A:146:LYS:HG3	2.01	0.42
1:A:32:ARG:HD2	1:A:104:LEU:HB3	2.01	0.42
1:A:92:PRO:HB2	2:H:468:HOH:O	2.19	0.42
1:C:194:VAL:HG23	1:C:194:VAL:O	2.20	0.42
1:D:246:GLU:HG2	1:D:247:GLY:N	2.33	0.42
1:F:44:LEU:O	1:F:269:GLY:HA3	2.19	0.42
1:I:194:VAL:O	1:I:194:VAL:HG23	2.20	0.42
1:B:65:ALA:O	1:B:66:MSE:HB2	2.19	0.42
1:C:10:SER:O	1:C:13:ALA:HB3	2.20	0.42
1:C:258:TRP:O	1:C:262:LEU:HB2	2.20	0.42
1:D:223:LEU:CD1	1:D:233:MSE:HE1	2.43	0.42
1:E:40:GLU:OE2	1:E:40:GLU:N	2.46	0.42
1:F:296:HIS:C	1:F:298:ASP:H	2.23	0.42
1:F:91:THR:HG23	1:F:94:ILE:HG12	2.01	0.42
1:J:194:VAL:HG23	1:J:194:VAL:O	2.20	0.42
1:J:47:VAL:HG11	1:J:76:MSE:HE1	2.02	0.42
1:A:223:LEU:CD1	1:A:233:MSE:HE1	2.43	0.42
1:G:184:PHE:O	1:G:185:MSE:HE2	2.20	0.42
1:I:206:VAL:CG1	1:I:236:THR:HG23	2.50	0.42
1:J:258:TRP:O	1:J:262:LEU:HB2	2.20	0.42
1:B:114:ASN:ND2	1:B:114:ASN:N	2.68	0.41
1:E:246:GLU:HG2	1:E:247:GLY:N	2.33	0.41
1:F:66:MSE:HG2	1:F:278:TYR:CE2	2.55	0.41
1:G:159:ALA:HB3	1:G:160:PRO:CD	2.50	0.41
1:J:214:ASN:ND2	1:J:214:ASN:C	2.73	0.41
1:B:194:VAL:O	1:B:194:VAL:HG23	2.20	0.41
1:E:258:TRP:O	1:E:262:LEU:HB2	2.20	0.41
1:E:89:LEU:HD12	1:E:90:GLY:N	2.36	0.41
1:G:206:VAL:CG1	1:G:236:THR:HG23	2.50	0.41
1:H:194:VAL:O	1:H:194:VAL:HG23	2.19	0.41
1:I:12:GLU:HG3	1:I:16:ARG:NH1	2.21	0.41
1:J:125:MSE:CE	1:J:152:ASN:HB2	2.44	0.41
1:C:206:VAL:CG1	1:C:236:THR:HG23	2.50	0.41
1:D:184:PHE:O	1:D:185:MSE:HE2	2.20	0.41
1:D:296:HIS:C	1:D:298:ASP:H	2.21	0.41
1:E:44:LEU:O	1:E:269:GLY:HA3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:125:MSE:CE	1:H:152:ASN:HB2	2.44	0.41
1:H:206:VAL:CG1	1:H:236:THR:HG23	2.50	0.41
1:H:91:THR:HG23	1:H:94:ILE:HG12	2.03	0.41
1:I:3:PRO:HA	2:I:486:HOH:O	2.20	0.41
1:A:46:ILE:O	1:A:271:THR:HA	2.20	0.41
1:A:89:LEU:HD12	1:A:90:GLY:N	2.35	0.41
1:B:89:LEU:HD11	1:B:146:LYS:HG2	2.02	0.41
1:D:214:ASN:C	1:D:214:ASN:ND2	2.73	0.41
1:D:40:GLU:OE2	1:D:40:GLU:N	2.45	0.41
1:F:214:ASN:ND2	1:F:214:ASN:C	2.72	0.41
1:I:152:ASN:ND2	1:I:154:SER:H	2.18	0.41
1:A:98:LEU:HB3	1:A:104:LEU:CD1	2.51	0.41
1:B:214:ASN:HD22	1:B:215:ASP:N	2.18	0.41
1:E:125:MSE:CE	1:E:152:ASN:HB2	2.43	0.41
1:E:184:PHE:O	1:E:185:MSE:HE2	2.20	0.41
1:F:89:LEU:HD12	1:F:90:GLY:N	2.35	0.41
2:F:548:HOH:O	1:G:115:ARG:HB2	2.20	0.41
1:H:33:ARG:CG	1:H:33:ARG:NH1	2.83	0.41
1:A:184:PHE:O	1:A:185:MSE:HE2	2.20	0.41
1:A:194:VAL:HG23	1:A:194:VAL:O	2.21	0.41
1:C:297:THR:OG1	1:C:299:ILE:HG13	2.20	0.41
1:F:65:ALA:O	1:F:66:MSE:HB2	2.19	0.41
1:G:214:ASN:ND2	1:G:214:ASN:C	2.73	0.41
1:G:223:LEU:CD1	1:G:233:MSE:HE1	2.43	0.41
1:H:66:MSE:HG2	1:H:278:TYR:CE2	2.56	0.41
1:J:37:LEU:HD13	1:J:38:LEU:HG	2.02	0.41
1:C:47:VAL:CB	1:C:76:MSE:HE1	2.50	0.41
1:C:89:LEU:HD12	1:C:90:GLY:N	2.35	0.41
1:F:194:VAL:O	1:F:194:VAL:HG23	2.21	0.41
1:I:258:TRP:O	1:I:262:LEU:HB2	2.20	0.41
1:B:125:MSE:CE	1:B:152:ASN:HB2	2.44	0.41
1:B:214:ASN:C	1:B:214:ASN:ND2	2.73	0.41
1:D:114:ASN:O	1:D:115:ARG:CD	2.69	0.41
1:G:152:ASN:ND2	1:G:154:SER:H	2.19	0.41
1:J:63:GLU:CG	1:J:64:THR:N	2.80	0.41
1:A:206:VAL:CG1	1:A:236:THR:HG23	2.50	0.41
1:A:214:ASN:ND2	1:A:214:ASN:C	2.73	0.41
1:B:54:ARG:NH2	1:B:150:ARG:HH12	2.18	0.41
1:B:258:TRP:O	1:B:262:LEU:HB2	2.20	0.41
1:D:206:VAL:CG1	1:D:236:THR:HG23	2.50	0.41
1:F:46:ILE:O	1:F:271:THR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:158:THR:HB	1:G:123:PHE:CE2	2.56	0.41
1:G:110:VAL:HG13	1:G:144:PHE:HB3	2.03	0.41
1:G:89:LEU:HD12	1:G:90:GLY:N	2.36	0.41
1:J:229:MSE:O	1:J:233:MSE:HG2	2.21	0.41
1:B:220:TRP:CE3	1:B:239:PRO:HB2	2.56	0.41
1:E:119:ARG:HD3	2:E:324:HOH:O	2.21	0.41
1:E:223:LEU:CD1	1:E:233:MSE:HE1	2.43	0.41
1:A:258:TRP:O	1:A:262:LEU:HB2	2.21	0.41
1:D:125:MSE:CE	1:D:152:ASN:HB2	2.44	0.41
1:H:47:VAL:CB	1:H:76:MSE:HE1	2.51	0.41
1:I:214:ASN:ND2	1:I:214:ASN:C	2.74	0.41
1:I:232:VAL:O	1:I:235:SER:HB2	2.21	0.41
1:A:47:VAL:CB	1:A:76:MSE:HE1	2.51	0.40
1:B:184:PHE:O	1:B:185:MSE:HE2	2.20	0.40
1:D:47:VAL:CB	1:D:76:MSE:HE1	2.51	0.40
1:F:152:ASN:ND2	1:F:154:SER:H	2.19	0.40
1:F:68:ASN:ND2	1:F:68:ASN:C	2.67	0.40
1:G:258:TRP:O	1:G:262:LEU:HB2	2.20	0.40
1:I:89:LEU:HD11	1:I:146:LYS:HG2	2.03	0.40
1:I:33:ARG:NH1	1:I:33:ARG:CG	2.84	0.40
1:A:220:TRP:CE3	1:A:239:PRO:HB2	2.56	0.40
1:B:47:VAL:CB	1:B:76:MSE:HE1	2.51	0.40
1:C:220:TRP:CE3	1:C:239:PRO:HB2	2.56	0.40
1:G:101:LEU:HA	1:G:101:LEU:HD12	1.91	0.40
1:H:114:ASN:ND2	1:H:147:THR:HG23	2.37	0.40
1:H:220:TRP:CE3	1:H:239:PRO:HB2	2.57	0.40
1:I:12:GLU:OE1	1:I:16:ARG:NH2	2.55	0.40
1:J:105:ASP:O	1:J:107:LYS:HG2	2.20	0.40
1:J:65:ALA:C	1:J:67:ALA:N	2.74	0.40
1:A:83:PRO:HG2	2:A:319:HOH:O	2.22	0.40
1:B:115:ARG:HD2	1:B:115:ARG:HA	1.57	0.40
1:C:110:VAL:HG13	1:C:144:PHE:HB3	2.02	0.40
1:E:194:VAL:O	1:E:194:VAL:HG23	2.20	0.40
1:G:33:ARG:CG	1:G:33:ARG:HH11	2.29	0.40
1:G:98:LEU:HB3	1:G:104:LEU:HD11	2.03	0.40
1:A:75:ARG:NH2	1:A:278:TYR:HA	2.37	0.40
1:I:281:ASP:O	1:I:283:ASP:N	2.54	0.40
1:I:296:HIS:C	1:I:298:ASP:N	2.74	0.40
1:I:85:VAL:HG23	1:I:107:LYS:HZ2	1.86	0.40
1:J:129:TYR:OH	1:J:147:THR:CG2	2.70	0.40
1:B:47:VAL:HB	1:B:76:MSE:HE1	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:LEU:HD12	1:B:90:GLY:N	2.36	0.40
1:C:229:MSE:O	1:C:233:MSE:HG2	2.22	0.40
1:D:258:TRP:O	1:D:262:LEU:HB2	2.21	0.40
1:E:95:ILE:HD12	1:E:109:VAL:HG13	2.03	0.40
1:E:220:TRP:CE3	1:E:239:PRO:HB2	2.57	0.40
1:H:258:TRP:O	1:H:262:LEU:HB2	2.21	0.40
1:I:103:LEU:C	1:I:104:LEU:HD12	2.42	0.40
1:J:115:ARG:HD2	1:J:115:ARG:HA	1.56	0.40
1:J:246:GLU:HG2	1:J:247:GLY:N	2.33	0.40
1:J:94:ILE:HD13	1:J:94:ILE:HA	1.98	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	291/307 (95%)	266 (91%)	19 (6%)	6 (2%)	7	11
1	B	291/307 (95%)	269 (92%)	17 (6%)	5 (2%)	9	16
1	C	291/307 (95%)	269 (92%)	17 (6%)	5 (2%)	9	16
1	D	291/307 (95%)	266 (91%)	18 (6%)	7 (2%)	6	9
1	E	291/307 (95%)	267 (92%)	19 (6%)	5 (2%)	9	16
1	F	291/307 (95%)	266 (91%)	19 (6%)	6 (2%)	7	11
1	G	291/307 (95%)	268 (92%)	18 (6%)	5 (2%)	9	16
1	H	291/307 (95%)	266 (91%)	19 (6%)	6 (2%)	7	11
1	I	291/307 (95%)	268 (92%)	16 (6%)	7 (2%)	6	9
1	J	291/307 (95%)	265 (91%)	19 (6%)	7 (2%)	6	9
All	All	2910/3070 (95%)	2670 (92%)	181 (6%)	59 (2%)	7	12

All (59) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	THR
1	B	64	THR
1	C	64	THR
1	D	64	THR
1	D	298	ASP
1	E	64	THR
1	F	64	THR
1	G	64	THR
1	H	64	THR
1	I	64	THR
1	J	62	ASN
1	A	62	ASN
1	A	63	GLU
1	A	245	GLY
1	B	62	ASN
1	B	63	GLU
1	B	245	GLY
1	C	62	ASN
1	C	63	GLU
1	C	245	GLY
1	D	62	ASN
1	D	63	GLU
1	D	245	GLY
1	E	62	ASN
1	E	63	GLU
1	E	245	GLY
1	F	62	ASN
1	F	63	GLU
1	F	245	GLY
1	G	62	ASN
1	G	63	GLU
1	G	245	GLY
1	H	62	ASN
1	H	63	GLU
1	H	245	GLY
1	I	62	ASN
1	I	63	GLU
1	I	245	GLY
1	I	282	GLY
1	I	297	THR
1	J	245	GLY
1	A	297	THR

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Mol	Chain	Res	Type
1	D	297	THR
1	F	297	THR
1	J	59	VAL
1	J	297	THR
1	A	60	GLY
1	B	60	GLY
1	C	60	GLY
1	D	60	GLY
1	E	60	GLY
1	F	60	GLY
1	G	60	GLY
1	H	60	GLY
1	H	297	THR
1	I	60	GLY
1	J	63	GLU
1	J	65	ALA
1	J	60	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	230/229 (100%)	207 (90%)	23 (10%)	7	15
1	B	230/229 (100%)	206 (90%)	24 (10%)	7	13
1	C	230/229 (100%)	205 (89%)	25 (11%)	6	12
1	D	230/229 (100%)	206 (90%)	24 (10%)	7	13
1	E	230/229 (100%)	206 (90%)	24 (10%)	7	13
1	F	230/229 (100%)	206 (90%)	24 (10%)	7	13
1	G	230/229 (100%)	207 (90%)	23 (10%)	7	15
1	H	230/229 (100%)	206 (90%)	24 (10%)	7	13
1	I	230/229 (100%)	208 (90%)	22 (10%)	8	16
1	J	230/229 (100%)	208 (90%)	22 (10%)	8	16
All	All	2300/2290 (100%)	2065 (90%)	235 (10%)	7	14

All (235) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	PHE
1	A	37	LEU
1	A	61	ASP
1	A	68	ASN
1	A	69	ARG
1	A	72	LEU
1	A	76	MSE
1	A	91	THR
1	A	101	LEU
1	A	114	ASN
1	A	115	ARG
1	A	140	ARG
1	A	144	PHE
1	A	146	LYS
1	A	148	LEU
1	A	152	ASN
1	A	214	ASN
1	A	216	SER
1	A	219	THR
1	A	262	LEU
1	A	264	LEU
1	A	274	ARG
1	A	299	ILE
1	B	29	PHE
1	B	37	LEU
1	B	61	ASP
1	B	68	ASN
1	B	69	ARG
1	B	72	LEU
1	B	76	MSE
1	B	91	THR
1	B	101	LEU
1	B	104	LEU
1	B	114	ASN
1	B	115	ARG
1	B	140	ARG
1	B	144	PHE
1	B	146	LYS
1	B	148	LEU
1	B	152	ASN
1	B	214	ASN
1	B	216	SER

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Mol	Chain	Res	Type
1	B	219	THR
1	B	262	LEU
1	B	264	LEU
1	B	274	ARG
1	B	294	LEU
1	C	29	PHE
1	C	37	LEU
1	C	61	ASP
1	C	68	ASN
1	C	69	ARG
1	C	72	LEU
1	C	76	MSE
1	C	91	THR
1	C	101	LEU
1	C	104	LEU
1	C	114	ASN
1	C	115	ARG
1	C	140	ARG
1	C	144	PHE
1	C	146	LYS
1	C	148	LEU
1	C	152	ASN
1	C	214	ASN
1	C	216	SER
1	C	219	THR
1	C	262	LEU
1	C	264	LEU
1	C	274	ARG
1	C	280	GLN
1	C	294	LEU
1	D	29	PHE
1	D	37	LEU
1	D	61	ASP
1	D	68	ASN
1	D	69	ARG
1	D	72	LEU
1	D	76	MSE
1	D	91	THR
1	D	101	LEU
1	D	104	LEU
1	D	114	ASN
1	D	115	ARG

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Mol	Chain	Res	Type
1	D	140	ARG
1	D	144	PHE
1	D	146	LYS
1	D	148	LEU
1	D	152	ASN
1	D	214	ASN
1	D	216	SER
1	D	219	THR
1	D	262	LEU
1	D	264	LEU
1	D	274	ARG
1	D	280	GLN
1	E	29	PHE
1	E	37	LEU
1	E	61	ASP
1	E	68	ASN
1	E	69	ARG
1	E	72	LEU
1	E	76	MSE
1	E	91	THR
1	E	101	LEU
1	E	104	LEU
1	E	114	ASN
1	E	115	ARG
1	E	140	ARG
1	E	144	PHE
1	E	146	LYS
1	E	148	LEU
1	E	152	ASN
1	E	214	ASN
1	E	216	SER
1	E	219	THR
1	E	262	LEU
1	E	264	LEU
1	E	274	ARG
1	E	299	ILE
1	F	29	PHE
1	F	37	LEU
1	F	61	ASP
1	F	68	ASN
1	F	69	ARG
1	F	72	LEU

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Mol	Chain	Res	Type
1	F	76	MSE
1	F	91	THR
1	F	101	LEU
1	F	104	LEU
1	F	114	ASN
1	F	115	ARG
1	F	140	ARG
1	F	144	PHE
1	F	146	LYS
1	F	148	LEU
1	F	152	ASN
1	F	214	ASN
1	F	216	SER
1	F	219	THR
1	F	262	LEU
1	F	264	LEU
1	F	274	ARG
1	F	283	ASP
1	G	29	PHE
1	G	37	LEU
1	G	61	ASP
1	G	68	ASN
1	G	69	ARG
1	G	72	LEU
1	G	76	MSE
1	G	91	THR
1	G	101	LEU
1	G	114	ASN
1	G	115	ARG
1	G	140	ARG
1	G	144	PHE
1	G	146	LYS
1	G	148	LEU
1	G	152	ASN
1	G	214	ASN
1	G	216	SER
1	G	219	THR
1	G	262	LEU
1	G	264	LEU
1	G	274	ARG
1	G	276	LEU
1	H	9	GLU

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Mol	Chain	Res	Type
1	H	29	PHE
1	H	37	LEU
1	H	61	ASP
1	H	68	ASN
1	H	69	ARG
1	H	72	LEU
1	H	76	MSE
1	H	91	THR
1	H	101	LEU
1	H	104	LEU
1	H	114	ASN
1	H	115	ARG
1	H	140	ARG
1	H	144	PHE
1	H	146	LYS
1	H	148	LEU
1	H	152	ASN
1	H	214	ASN
1	H	216	SER
1	H	219	THR
1	H	262	LEU
1	H	264	LEU
1	H	274	ARG
1	I	29	PHE
1	I	37	LEU
1	I	61	ASP
1	I	68	ASN
1	I	69	ARG
1	I	72	LEU
1	I	76	MSE
1	I	91	THR
1	I	114	ASN
1	I	115	ARG
1	I	140	ARG
1	I	144	PHE
1	I	146	LYS
1	I	148	LEU
1	I	152	ASN
1	I	214	ASN
1	I	216	SER
1	I	219	THR
1	I	262	LEU

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Mol	Chain	Res	Type
1	I	264	LEU
1	I	274	ARG
1	I	281	ASP
1	J	29	PHE
1	J	33	ARG
1	J	37	LEU
1	J	54	ARG
1	J	57	LEU
1	J	68	ASN
1	J	74	GLU
1	J	76	MSE
1	J	91	THR
1	J	114	ASN
1	J	115	ARG
1	J	140	ARG
1	J	144	PHE
1	J	146	LYS
1	J	148	LEU
1	J	152	ASN
1	J	214	ASN
1	J	216	SER
1	J	219	THR
1	J	262	LEU
1	J	264	LEU
1	J	274	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	68	ASN
1	A	114	ASN
1	A	152	ASN
1	A	167	HIS
1	A	170	ASN
1	A	176	GLN
1	A	204	GLN
1	A	214	ASN
1	A	280	GLN
1	A	296	HIS
1	B	31	GLN
1	B	68	ASN

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Mol	Chain	Res	Type
1	B	114	ASN
1	B	152	ASN
1	B	167	HIS
1	B	170	ASN
1	B	176	GLN
1	B	204	GLN
1	B	214	ASN
1	B	280	GLN
1	B	296	HIS
1	C	68	ASN
1	C	114	ASN
1	C	152	ASN
1	C	167	HIS
1	C	170	ASN
1	C	176	GLN
1	C	204	GLN
1	C	214	ASN
1	C	280	GLN
1	C	296	HIS
1	D	68	ASN
1	D	114	ASN
1	D	152	ASN
1	D	167	HIS
1	D	170	ASN
1	D	176	GLN
1	D	190	ASN
1	D	204	GLN
1	D	214	ASN
1	D	296	HIS
1	E	31	GLN
1	E	68	ASN
1	E	114	ASN
1	E	152	ASN
1	E	170	ASN
1	E	176	GLN
1	E	190	ASN
1	E	204	GLN
1	E	214	ASN
1	E	260	HIS
1	E	280	GLN
1	E	296	HIS
1	F	31	GLN

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Mol	Chain	Res	Type
1	F	68	ASN
1	F	114	ASN
1	F	152	ASN
1	F	167	HIS
1	F	170	ASN
1	F	176	GLN
1	F	190	ASN
1	F	204	GLN
1	F	214	ASN
1	F	260	HIS
1	F	280	GLN
1	F	296	HIS
1	G	31	GLN
1	G	68	ASN
1	G	114	ASN
1	G	152	ASN
1	G	167	HIS
1	G	170	ASN
1	G	176	GLN
1	G	204	GLN
1	G	214	ASN
1	G	280	GLN
1	G	296	HIS
1	H	31	GLN
1	H	68	ASN
1	H	114	ASN
1	H	152	ASN
1	H	167	HIS
1	H	170	ASN
1	H	176	GLN
1	H	204	GLN
1	H	214	ASN
1	H	280	GLN
1	H	296	HIS
1	I	68	ASN
1	I	114	ASN
1	I	152	ASN
1	I	167	HIS
1	I	170	ASN
1	I	176	GLN
1	I	204	GLN
1	I	214	ASN

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Mol	Chain	Res	Type
1	I	280	GLN
1	I	296	HIS
1	J	31	GLN
1	J	68	ASN
1	J	114	ASN
1	J	152	ASN
1	J	167	HIS
1	J	170	ASN
1	J	176	GLN
1	J	204	GLN
1	J	214	ASN
1	J	260	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	282/307 (91%)	0.34	14 (4%) 28 30	10, 23, 47, 62	0
1	B	282/307 (91%)	0.21	14 (4%) 28 30	12, 22, 43, 65	0
1	C	282/307 (91%)	0.18	11 (3%) 39 42	10, 23, 43, 61	0
1	D	282/307 (91%)	0.30	18 (6%) 19 20	12, 23, 45, 67	0
1	E	282/307 (91%)	0.24	14 (4%) 28 30	11, 24, 48, 65	0
1	F	282/307 (91%)	0.21	11 (3%) 39 42	12, 25, 48, 66	0
1	G	282/307 (91%)	0.24	14 (4%) 28 30	13, 26, 45, 67	0
1	H	282/307 (91%)	0.43	23 (8%) 11 11	11, 24, 45, 70	0
1	I	282/307 (91%)	0.46	25 (8%) 9 9	13, 27, 51, 73	0
1	J	282/307 (91%)	0.33	22 (7%) 13 13	12, 29, 51, 68	0
All	All	2820/3070 (91%)	0.30	166 (5%) 22 23	10, 24, 49, 73	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	299	ILE	16.2
1	E	299	ILE	12.1
1	I	299	ILE	10.8
1	H	299	ILE	10.6
1	C	299	ILE	9.0
1	F	299	ILE	8.8
1	H	282	GLY	7.8
1	D	299	ILE	7.8
1	A	299	ILE	7.8
1	A	282	GLY	7.5
1	G	299	ILE	7.2
1	J	282	GLY	6.7
1	D	282	GLY	6.4

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Mol	Chain	Res	Type	RSRZ
1	I	64	THR	5.8
1	B	247	GLY	5.6
1	J	299	ILE	5.5
1	D	247	GLY	5.3
1	C	247	GLY	5.2
1	F	282	GLY	5.2
1	D	64	THR	5.1
1	H	63	GLU	4.9
1	I	247	GLY	4.8
1	D	246	GLU	4.7
1	B	282	GLY	4.7
1	B	64	THR	4.5
1	I	63	GLU	4.5
1	C	64	THR	4.4
1	F	63	GLU	4.4
1	A	64	THR	4.4
1	B	63	GLU	4.4
1	H	64	THR	4.2
1	F	247	GLY	4.1
1	I	248	GLY	4.0
1	B	216	SER	3.8
1	C	63	GLU	3.8
1	A	298	ASP	3.8
1	G	64	THR	3.7
1	A	246	GLU	3.7
1	I	298	ASP	3.7
1	A	63	GLU	3.6
1	H	251	PRO	3.6
1	I	252	ASP	3.6
1	D	65	ALA	3.6
1	E	282	GLY	3.6
1	F	64	THR	3.6
1	J	247	GLY	3.6
1	H	298	ASP	3.6
1	G	298	ASP	3.5
1	F	246	GLU	3.5
1	E	216	SER	3.5
1	H	255	PHE	3.4
1	A	280	GLN	3.4
1	J	64	THR	3.4
1	I	255	PHE	3.4
1	G	63	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	I	288	VAL	3.4
1	C	248	GLY	3.3
1	F	216	SER	3.3
1	G	247	GLY	3.3
1	H	247	GLY	3.3
1	I	216	SER	3.3
1	H	216	SER	3.2
1	D	63	GLU	3.2
1	E	63	GLU	3.2
1	B	248	GLY	3.2
1	A	216	SER	3.2
1	J	3	PRO	3.1
1	H	33	ARG	3.1
1	J	246	GLU	3.1
1	J	63	GLU	3.1
1	E	280	GLN	3.1
1	C	3	PRO	3.0
1	E	40	GLU	3.0
1	D	29	PHE	3.0
1	C	65	ALA	2.9
1	B	40	GLU	2.9
1	A	247	GLY	2.9
1	D	60	GLY	2.9
1	E	60	GLY	2.9
1	A	40	GLU	2.9
1	E	3	PRO	2.9
1	H	60	GLY	2.8
1	I	253	ALA	2.8
1	F	230	GLU	2.8
1	A	293	ARG	2.8
1	D	230	GLU	2.8
1	I	282	GLY	2.8
1	D	252	ASP	2.8
1	B	65	ALA	2.7
1	C	216	SER	2.7
1	J	276	LEU	2.7
1	H	246	GLU	2.7
1	J	216	SER	2.7
1	A	230	GLU	2.7
1	I	230	GLU	2.7
1	D	28	ARG	2.7
1	E	246	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	I	3	PRO	2.6
1	C	246	GLU	2.6
1	F	65	ALA	2.6
1	H	297	THR	2.6
1	H	254	THR	2.6
1	I	251	PRO	2.6
1	B	246	GLU	2.6
1	G	297	THR	2.5
1	D	216	SER	2.5
1	J	293	ARG	2.5
1	C	59	VAL	2.5
1	H	65	ALA	2.5
1	H	252	ASP	2.5
1	I	281	ASP	2.5
1	E	64	THR	2.5
1	H	29	PHE	2.4
1	I	246	GLU	2.4
1	H	280	GLN	2.4
1	J	281	ASP	2.4
1	D	3	PRO	2.4
1	E	230	GLU	2.4
1	G	40	GLU	2.4
1	J	252	ASP	2.4
1	B	60	GLY	2.4
1	H	85	VAL	2.3
1	H	34	LYS	2.3
1	G	216	SER	2.3
1	I	85	VAL	2.3
1	G	5	ILE	2.3
1	J	287	ALA	2.3
1	G	65	ALA	2.3
1	H	230	GLU	2.3
1	I	65	ALA	2.3
1	I	280	GLN	2.3
1	G	246	GLU	2.3
1	J	294	LEU	2.3
1	D	62	ASN	2.2
1	H	62	ASN	2.2
1	A	252	ASP	2.2
1	B	298	ASP	2.2
1	D	30	LYS	2.2
1	H	248	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	284	VAL	2.2
1	I	259	GLU	2.2
1	J	65	ALA	2.2
1	E	298	ASP	2.2
1	J	255	PHE	2.2
1	A	60	GLY	2.2
1	J	82	ARG	2.2
1	I	276	LEU	2.2
1	J	230	GLU	2.2
1	J	248	GLY	2.1
1	E	61	ASP	2.1
1	I	295	VAL	2.1
1	E	252	ASP	2.1
1	F	248	GLY	2.1
1	J	280	GLN	2.1
1	D	253	ALA	2.1
1	J	285	ALA	2.1
1	G	283	ASP	2.1
1	B	62	ASN	2.1
1	C	230	GLU	2.1
1	D	248	GLY	2.1
1	B	244	GLY	2.0
1	J	256	ALA	2.0
1	G	226	VAL	2.0
1	G	230	GLU	2.0
1	I	39	GLY	2.0
1	F	40	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.