



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3CRC / pdb_00003crc
Title : Crystal Structure of Escherichia coli MazG, the Regulator of Nutritional Stress Response
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Deposited on : 2008-04-05
Resolution : 3.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

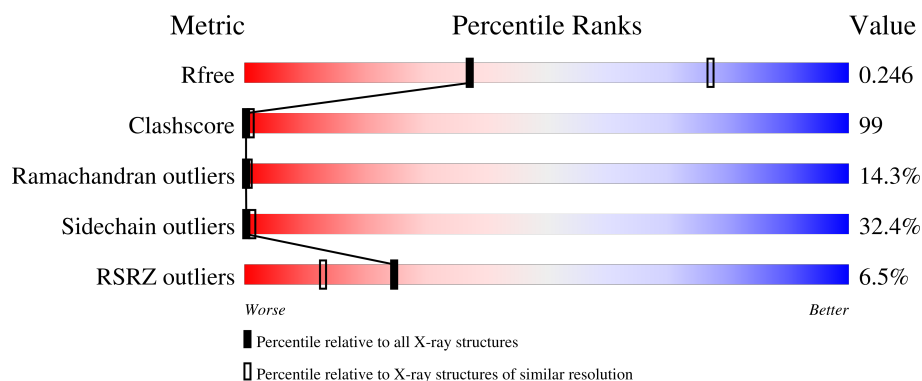
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 ≥ 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	265	6% 9% 30% 33% 13% 15%
1	B	265	5% 7% 27% 35% 14% 17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ATP	B	265	X	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3658 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 Protein mazG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1829	1145	318	356	10			
1	B	220	Total	C	N	O	S	0	0	0
			1784	1121	307	347	9			

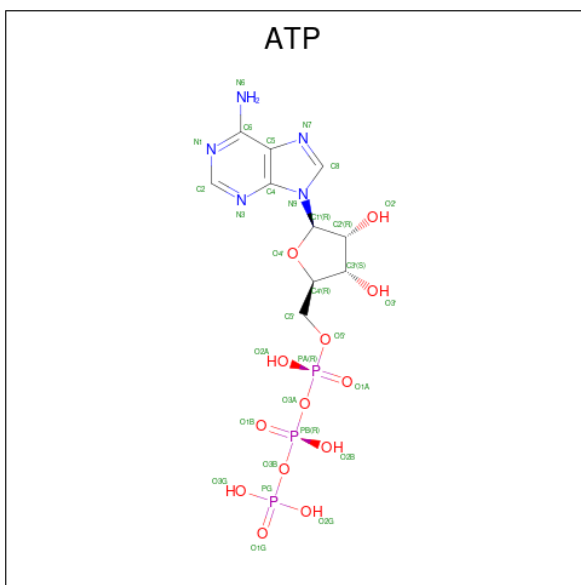
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P0AEY3
A	0	HIS	-	expression tag	UNP P0AEY3
A	257	ALA	LYS	conflict	UNP P0AEY3
B	-1	GLY	-	expression tag	UNP P0AEY3
B	0	HIS	-	expression tag	UNP P0AEY3
B	257	ALA	LYS	conflict	UNP P0AEY3

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

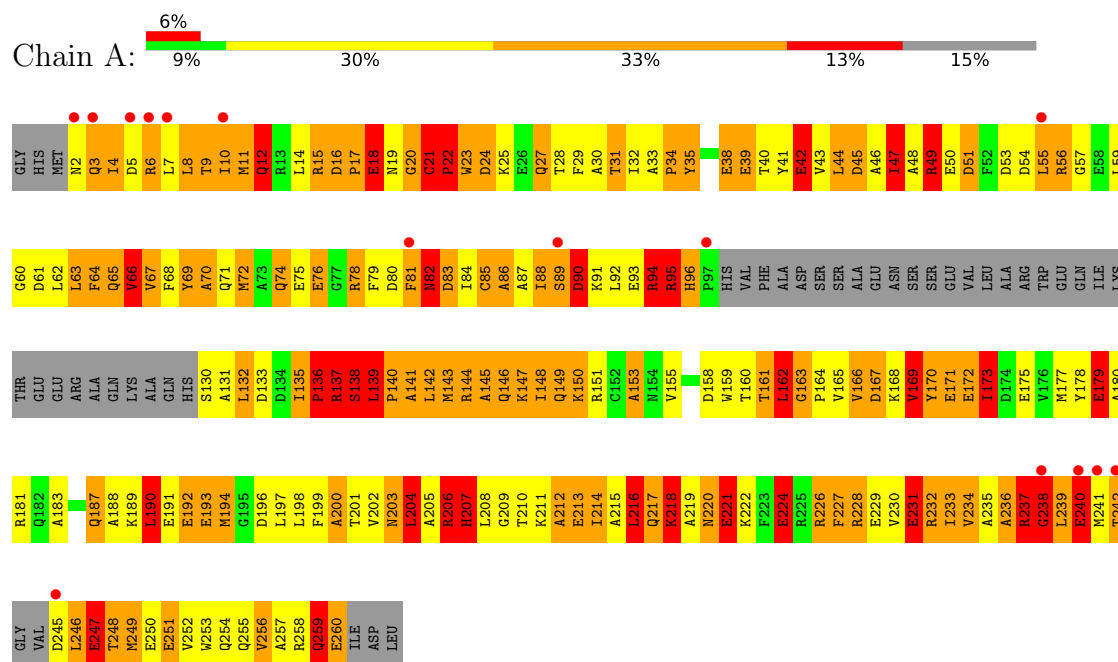
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total O 5 5	0	0
4	B	8	Total O 8 8	0	0

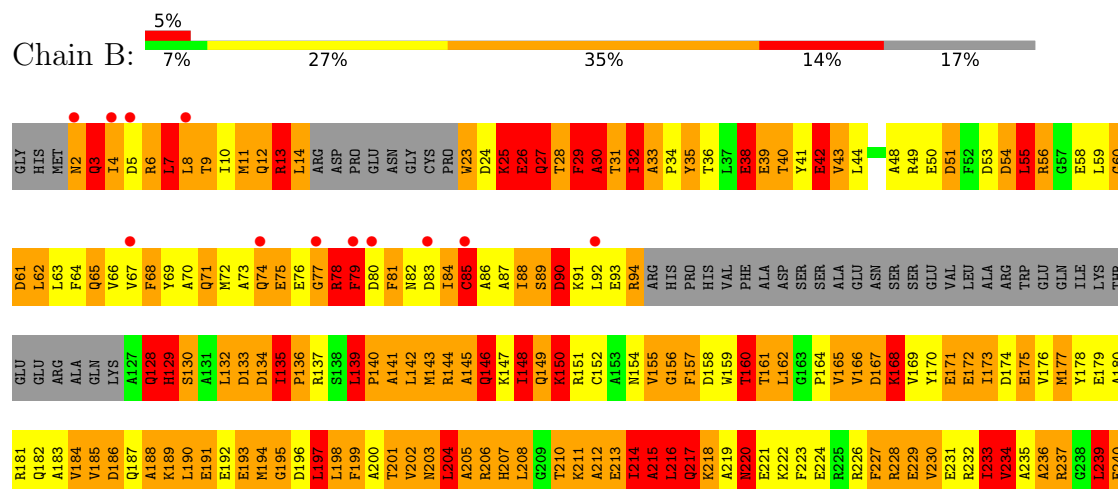
3 Residue-property plots

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: Protein mazG



• Molecule 1: Protein mazG



M241	T242	G243	Y244	D245	I246	E247	T248	M249	E250	E251	V252	W253	Q254	Q255	V256	A257	R258	Q259	E260	I261	ASP	LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.23Å 66.91Å 140.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.79 – 3.00 33.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	93.9 (33.79-3.00) 95.7 (33.79-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.216 , 0.345 (Not available) , 0.246	Depositor DCC
R_{free} test set	579 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3658	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% 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

5.1 Standard geometry

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

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	2.13	54/1856 (2.9%)	2.21	91/2503 (3.6%)
1	B	2.46	87/1808 (4.8%)	2.38	99/2437 (4.1%)
All	All	2.30	141/3664 (3.8%)	2.29	190/4940 (3.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	6
1	B	1	11
All	All	3	17

All (141) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	203	ASN	C-O	14.77	1.43	1.24
1	B	204	LEU	CA-C	14.23	1.70	1.52
1	B	212	ALA	CA-CB	-12.80	1.33	1.53
1	B	219	ALA	CA-CB	-12.60	1.33	1.53
1	B	203	ASN	N-CA	-12.13	1.30	1.46
1	B	217	GLN	CA-C	-11.42	1.38	1.52
1	B	215	ALA	CA-CB	-10.73	1.35	1.53
1	B	145	ALA	CA-CB	-10.36	1.37	1.53
1	B	214	ILE	C-O	9.88	1.35	1.24
1	A	153	ALA	CA-CB	-9.76	1.37	1.53
1	A	141	ALA	CA-CB	-9.72	1.38	1.53
1	A	135	ILE	CA-CB	9.57	1.63	1.53
1	A	173	ILE	CA-CB	-9.38	1.41	1.54
1	B	216	LEU	N-CA	-9.30	1.33	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	218	LYS	C-O	9.17	1.36	1.24
1	B	142	LEU	N-CA	-9.17	1.35	1.46
1	B	36	THR	CA-CB	-9.11	1.38	1.53
1	B	26	GLU	CA-C	8.67	1.64	1.52
1	B	35	TYR	CA-C	-8.47	1.43	1.52
1	B	233	ILE	CA-CB	-8.38	1.43	1.54
1	B	213	GLU	C-O	8.34	1.33	1.24
1	B	157	PHE	CA-C	8.29	1.61	1.53
1	B	205	ALA	N-CA	-8.21	1.35	1.46
1	A	234	VAL	CA-CB	-7.86	1.44	1.54
1	B	207	HIS	C-O	-7.62	1.14	1.24
1	A	212	ALA	CA-CB	-7.57	1.41	1.53
1	B	211	LYS	C-O	7.57	1.33	1.24
1	A	209	GLY	C-O	-7.56	1.13	1.23
1	B	145	ALA	CA-C	7.52	1.62	1.52
1	A	202	VAL	C-O	7.46	1.33	1.24
1	A	169	VAL	CA-CB	-7.45	1.44	1.54
1	B	141	ALA	CA-CB	-7.44	1.41	1.53
1	B	143	MET	CA-C	-7.41	1.43	1.52
1	B	216	LEU	CB-CG	7.34	1.68	1.53
1	B	202	VAL	CA-CB	-7.32	1.45	1.54
1	B	227	PHE	N-CA	-7.24	1.37	1.46
1	A	218	LYS	N-CA	7.12	1.55	1.46
1	B	143	MET	C-O	-7.02	1.16	1.24
1	B	188	ALA	CA-CB	-7.01	1.41	1.53
1	A	167	ASP	C-O	6.96	1.32	1.24
1	A	200	ALA	CA-C	-6.93	1.42	1.52
1	B	183	ALA	CA-CB	-6.88	1.42	1.53
1	B	54	ASP	CA-C	-6.83	1.44	1.52
1	B	210	THR	CA-CB	-6.82	1.41	1.54
1	B	148	ILE	N-CA	6.81	1.54	1.46
1	A	190	LEU	CA-C	6.80	1.61	1.52
1	A	35	TYR	CA-C	-6.69	1.43	1.52
1	A	187	GLN	N-CA	6.68	1.54	1.46
1	A	84	ILE	N-CA	6.67	1.54	1.46
1	A	198	LEU	CA-C	-6.67	1.43	1.52
1	B	205	ALA	CA-CB	-6.64	1.42	1.53
1	B	230	VAL	C-O	-6.58	1.16	1.24
1	B	206	ARG	N-CA	6.58	1.54	1.46
1	B	199	PHE	CA-CB	-6.58	1.42	1.53
1	B	156	GLY	C-O	-6.50	1.15	1.23
1	B	202	VAL	N-CA	-6.48	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	215	ALA	C-N	6.47	1.42	1.33
1	A	160	THR	CA-CB	6.47	1.63	1.53
1	B	168	LYS	CA-CB	-6.46	1.43	1.53
1	A	167	ASP	N-CA	-6.41	1.38	1.46
1	A	66	VAL	CA-CB	-6.37	1.45	1.54
1	A	89	SER	C-O	-6.26	1.16	1.24
1	A	238	GLY	C-N	6.25	1.42	1.33
1	B	150	LYS	CA-CB	-6.25	1.43	1.53
1	B	74	GLN	C-O	6.23	1.31	1.24
1	B	186	ASP	C-O	6.21	1.31	1.23
1	B	168	LYS	N-CA	-6.19	1.38	1.46
1	B	220	ASN	N-CA	6.15	1.54	1.46
1	B	204	LEU	C-O	6.14	1.31	1.24
1	B	216	LEU	CG-CD1	-6.12	1.32	1.52
1	B	161	THR	CA-CB	-6.05	1.42	1.54
1	A	142	LEU	N-CA	-6.04	1.39	1.46
1	B	215	ALA	C-N	-6.01	1.25	1.33
1	B	205	ALA	C-N	6.00	1.41	1.33
1	A	140	PRO	CB-CG	5.99	1.79	1.49
1	B	216	LEU	CA-C	-5.99	1.44	1.52
1	A	87	ALA	CA-C	5.88	1.60	1.52
1	B	203	ASN	CG-OD1	5.88	1.34	1.23
1	B	148	ILE	CA-C	5.87	1.60	1.52
1	B	142	LEU	CA-C	-5.87	1.45	1.52
1	B	140	PRO	C-O	5.81	1.30	1.23
1	B	183	ALA	CA-C	-5.77	1.45	1.52
1	A	51	ASP	CA-C	5.70	1.60	1.53
1	A	214	ILE	CA-CB	-5.69	1.46	1.54
1	B	42	GLU	C-O	5.68	1.30	1.24
1	A	86	ALA	C-O	-5.67	1.16	1.24
1	B	146	GLN	N-CA	5.67	1.53	1.46
1	B	134	ASP	CA-C	-5.65	1.46	1.53
1	B	9	THR	CA-CB	5.64	1.63	1.53
1	A	219	ALA	CA-C	-5.62	1.45	1.52
1	A	169	VAL	C-O	-5.61	1.17	1.24
1	A	169	VAL	CA-C	-5.59	1.45	1.52
1	A	82	ASN	CA-C	5.56	1.59	1.52
1	B	193	GLU	C-O	5.55	1.30	1.24
1	B	213	GLU	CA-C	5.51	1.59	1.52
1	A	38	GLU	CG-CD	5.50	1.65	1.52
1	B	218	LYS	CA-C	5.47	1.60	1.52
1	B	136	PRO	C-O	5.46	1.30	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	202	VAL	C-N	-5.45	1.26	1.33
1	A	178	TYR	C-O	5.44	1.30	1.24
1	A	144	ARG	N-CA	-5.42	1.39	1.46
1	A	85	CYS	C-O	5.41	1.30	1.24
1	B	177	MET	C-O	5.39	1.30	1.24
1	B	214	ILE	CA-C	5.39	1.59	1.52
1	A	140	PRO	C-O	5.35	1.30	1.23
1	B	204	LEU	C-N	5.35	1.41	1.33
1	B	143	MET	CA-CB	-5.31	1.45	1.53
1	B	55	LEU	CA-C	5.28	1.59	1.52
1	B	51	ASP	CA-CB	-5.27	1.46	1.52
1	B	206	ARG	C-O	-5.26	1.18	1.24
1	B	79	PHE	CA-C	5.26	1.59	1.52
1	A	188	ALA	CA-CB	5.24	1.61	1.53
1	B	77	GLY	N-CA	5.24	1.52	1.45
1	B	40	THR	N-CA	-5.19	1.40	1.46
1	B	240	GLU	CA-C	5.19	1.60	1.53
1	A	136	PRO	CA-C	5.18	1.59	1.52
1	B	236	ALA	CA-C	5.18	1.59	1.52
1	A	34	PRO	C-O	-5.18	1.17	1.24
1	B	181	ARG	CA-C	5.17	1.59	1.52
1	A	188	ALA	N-CA	5.16	1.52	1.46
1	B	9	THR	N-CA	5.15	1.52	1.46
1	B	78	ARG	CA-C	5.14	1.59	1.52
1	A	81	PHE	CA-C	-5.14	1.45	1.52
1	A	33	ALA	CA-CB	-5.13	1.45	1.53
1	B	132	LEU	N-CA	-5.13	1.39	1.46
1	A	171	GLU	C-O	-5.10	1.17	1.24
1	B	7	LEU	CA-C	5.10	1.59	1.52
1	A	150	LYS	CA-CB	-5.10	1.45	1.53
1	B	160	THR	CA-CB	-5.09	1.45	1.53
1	B	168	LYS	C-O	5.08	1.30	1.24
1	A	95	ARG	N-CA	5.05	1.52	1.46
1	A	259	GLN	CA-C	5.05	1.59	1.52
1	A	247	GLU	CA-C	5.04	1.58	1.53
1	B	150	LYS	CB-CG	-5.03	1.37	1.52
1	A	180	ALA	N-CA	-5.02	1.39	1.46
1	A	204	LEU	N-CA	-5.01	1.40	1.46
1	A	173	ILE	C-O	-5.01	1.18	1.24
1	A	136	PRO	N-CA	5.01	1.53	1.47
1	B	139	LEU	CA-C	-5.01	1.47	1.53
1	A	145	ALA	CA-CB	-5.00	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	197	LEU	CA-CB	-5.00	1.45	1.53

All (190) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	139	LEU	CA-C-N	-14.95	105.66	120.31
1	B	139	LEU	C-N-CA	-14.95	105.66	120.31
1	A	148	ILE	CB-CA-C	-13.22	94.78	111.70
1	A	160	THR	CB-CA-C	13.21	132.35	109.24
1	A	215	ALA	CA-C-O	-12.06	107.77	120.55
1	A	163	GLY	CA-C-N	-11.30	107.36	121.04
1	A	163	GLY	C-N-CA	-11.30	107.36	121.04
1	B	44	LEU	N-CA-C	-10.91	98.27	111.69
1	B	7	LEU	N-CA-C	10.38	122.35	111.14
1	B	135	ILE	CA-C-N	-10.32	108.87	119.92
1	B	135	ILE	C-N-CA	-10.32	108.87	119.92
1	B	202	VAL	CA-C-O	-10.10	110.54	121.05
1	A	165	VAL	N-CA-C	-9.83	100.01	110.23
1	A	30	ALA	N-CA-C	-9.68	101.40	113.01
1	A	135	ILE	N-CA-C	-9.62	97.31	107.60
1	A	17	PRO	CA-C-N	9.44	138.69	121.70
1	A	17	PRO	C-N-CA	9.44	138.69	121.70
1	B	219	ALA	N-CA-C	-9.36	99.44	112.45
1	B	12	GLN	N-CA-C	-9.06	96.36	109.96
1	B	60	GLY	N-CA-C	-8.94	101.82	112.64
1	B	202	VAL	O-C-N	8.85	130.57	121.89
1	B	144	ARG	N-CA-C	8.84	120.91	111.28
1	B	203	ASN	CA-C-N	-8.79	108.67	120.63
1	B	203	ASN	C-N-CA	-8.79	108.67	120.63
1	B	183	ALA	N-CA-C	-8.73	100.95	111.69
1	A	160	THR	N-CA-C	-8.54	102.99	113.41
1	B	244	VAL	N-CA-C	8.42	120.92	108.45
1	A	165	VAL	CB-CA-C	-8.34	101.03	111.70
1	B	28	THR	CB-CA-C	-8.29	99.62	112.31
1	B	206	ARG	N-CA-C	-8.19	102.04	110.97
1	A	16	ASP	CA-C-N	8.11	127.68	119.24
1	A	16	ASP	C-N-CA	8.11	127.68	119.24
1	A	135	ILE	CA-C-N	8.05	129.90	119.84
1	A	135	ILE	C-N-CA	8.05	129.90	119.84
1	B	54	ASP	CA-C-N	-7.96	108.76	120.38
1	B	54	ASP	C-N-CA	-7.96	108.76	120.38
1	B	206	ARG	N-CA-CB	7.88	121.41	109.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	GLU	N-CA-C	-7.86	102.66	111.07
1	A	3	GLN	N-CA-C	-7.85	102.03	111.69
1	A	8	LEU	N-CA-C	-7.85	102.68	111.71
1	B	38	GLU	N-CA-C	-7.85	103.50	113.23
1	B	218	LYS	N-CA-C	-7.83	103.73	113.20
1	A	166	VAL	CB-CA-C	-7.72	100.20	112.16
1	B	173	ILE	CB-CA-C	-7.70	101.75	112.14
1	B	237	ARG	N-CA-C	-7.68	103.70	113.23
1	B	30	ALA	N-CA-C	-7.68	94.44	110.80
1	B	229	GLU	CA-C-N	7.67	130.97	120.46
1	B	229	GLU	C-N-CA	7.67	130.97	120.46
1	B	217	GLN	N-CA-C	-7.63	102.90	111.14
1	B	220	ASN	CB-CG-ND2	7.60	127.80	116.40
1	A	247	GLU	N-CA-C	7.57	123.55	109.24
1	A	161	THR	N-CA-C	7.49	121.94	108.69
1	B	167	ASP	CA-C-O	7.49	128.59	120.20
1	A	166	VAL	CA-C-N	-7.48	110.25	120.28
1	A	166	VAL	C-N-CA	-7.48	110.25	120.28
1	A	200	ALA	CA-C-N	-7.46	108.27	120.72
1	A	200	ALA	C-N-CA	-7.46	108.27	120.72
1	B	198	LEU	CA-C-O	-7.40	113.28	120.90
1	A	17	PRO	N-CA-C	7.39	125.75	113.78
1	B	202	VAL	CA-C-N	-7.37	108.41	120.72
1	B	202	VAL	C-N-CA	-7.37	108.41	120.72
1	B	217	GLN	CA-C-O	7.34	128.26	120.70
1	A	213	GLU	N-CA-C	-7.33	103.28	111.71
1	A	193	GLU	N-CA-C	-7.24	103.42	111.82
1	B	203	ASN	N-CA-C	-7.11	103.86	112.54
1	A	215	ALA	O-C-N	7.06	129.60	122.12
1	A	148	ILE	N-CA-CB	6.97	117.94	110.62
1	B	172	GLU	N-CA-C	-6.95	104.93	113.41
1	B	43	VAL	N-CA-C	-6.94	103.54	110.62
1	B	198	LEU	CD1-CG-CD2	-6.92	95.58	110.80
1	B	137	ARG	N-CA-C	-6.91	103.83	111.36
1	A	76	GLU	N-CA-C	-6.89	104.75	113.02
1	A	132	LEU	CA-C-N	-6.88	112.96	122.93
1	A	132	LEU	C-N-CA	-6.88	112.96	122.93
1	A	27	GLN	N-CA-C	6.87	119.32	108.67
1	A	149	GLN	CA-C-O	-6.87	113.55	120.90
1	B	157	PHE	N-CA-C	6.85	118.84	109.11
1	A	35	TYR	N-CA-C	-6.84	104.93	113.28
1	B	48	ALA	N-CA-C	-6.79	104.01	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	ALA	N-CA-C	-6.76	103.91	111.28
1	B	81	PHE	CA-C-N	-6.71	110.62	120.28
1	B	81	PHE	C-N-CA	-6.71	110.62	120.28
1	B	205	ALA	CA-C-O	-6.70	110.93	120.51
1	A	132	LEU	N-CA-C	-6.64	96.65	110.80
1	B	35	TYR	N-CA-C	-6.53	104.00	112.68
1	A	256	VAL	N-CA-C	-6.52	106.62	111.90
1	B	32	ILE	O-C-N	6.49	128.63	121.94
1	B	183	ALA	CA-C-N	-6.41	114.38	123.10
1	B	183	ALA	C-N-CA	-6.41	114.38	123.10
1	A	55	LEU	N-CA-C	6.40	119.07	111.71
1	B	233	ILE	CB-CG1-CD1	-6.39	100.39	113.80
1	B	243	GLY	CA-C-N	-6.36	113.56	122.71
1	B	243	GLY	C-N-CA	-6.36	113.56	122.71
1	A	179	GLU	N-CA-C	-6.30	104.33	111.07
1	A	220	ASN	CA-C-N	-6.28	112.28	120.44
1	A	220	ASN	C-N-CA	-6.28	112.28	120.44
1	A	88	ILE	N-CA-C	-6.22	104.78	110.82
1	B	6	ARG	N-CA-C	-6.21	97.57	110.80
1	B	214	ILE	N-CA-C	6.16	122.15	109.34
1	A	204	LEU	N-CA-C	6.12	117.64	110.97
1	A	183	ALA	CA-C-N	-6.08	114.84	123.11
1	A	183	ALA	C-N-CA	-6.08	114.84	123.11
1	B	3	GLN	N-CA-C	-6.07	97.88	110.80
1	A	216	LEU	N-CA-C	-6.06	104.60	111.14
1	A	86	ALA	CA-C-N	-6.04	112.23	120.44
1	A	86	ALA	C-N-CA	-6.04	112.23	120.44
1	A	22	PRO	CB-CA-C	6.01	121.47	111.56
1	B	204	LEU	CB-CG-CD2	-6.00	92.71	110.70
1	A	82	ASN	CB-CA-C	5.98	120.22	110.95
1	B	28	THR	N-CA-C	-5.95	102.47	111.34
1	A	69	TYR	N-CA-C	-5.95	101.82	111.04
1	A	192	GLU	CB-CA-C	-5.94	101.47	110.92
1	A	227	PHE	N-CA-C	-5.91	104.53	110.97
1	A	45	ASP	N-CA-C	-5.88	104.56	110.97
1	B	169	VAL	N-CA-C	-5.88	104.12	110.23
1	A	183	ALA	N-CA-C	-5.86	104.08	111.11
1	A	210	THR	CB-CA-C	-5.84	101.28	112.43
1	A	224	GLU	N-CA-C	-5.83	104.85	111.14
1	B	250	GLU	CA-C-N	-5.83	111.66	122.09
1	B	250	GLU	C-N-CA	-5.83	111.66	122.09
1	A	84	ILE	N-CA-CB	5.80	116.94	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	172	GLU	CA-CB-CG	-5.79	102.51	114.10
1	A	19	ASN	N-CA-C	5.79	117.87	108.26
1	A	72	MET	CG-SD-CE	-5.77	88.20	100.90
1	B	234	VAL	CA-C-N	-5.75	111.40	120.60
1	B	234	VAL	C-N-CA	-5.75	111.40	120.60
1	A	42	GLU	N-CA-C	-5.75	104.98	112.23
1	A	49	ARG	N-CA-C	5.74	118.31	111.71
1	B	133	ASP	CB-CA-C	5.71	120.05	109.54
1	B	212	ALA	N-CA-C	-5.68	105.01	111.14
1	A	256	VAL	CB-CA-C	5.68	116.75	111.30
1	A	206	ARG	CA-C-N	-5.68	110.70	121.54
1	A	206	ARG	C-N-CA	-5.68	110.70	121.54
1	B	194	MET	CG-SD-CE	5.67	113.36	100.90
1	B	203	ASN	CA-C-O	5.66	126.34	119.38
1	B	50	GLU	CA-C-N	-5.63	113.06	122.17
1	B	50	GLU	C-N-CA	-5.63	113.06	122.17
1	A	90	ASP	CB-CA-C	-5.56	100.00	110.01
1	A	165	VAL	N-CA-CB	5.56	116.45	110.62
1	B	185	VAL	CB-CA-C	-5.55	102.19	111.29
1	B	198	LEU	CA-C-N	-5.55	112.27	120.38
1	B	198	LEU	C-N-CA	-5.55	112.27	120.38
1	B	41	TYR	N-CA-C	5.54	117.40	111.36
1	B	218	LYS	CA-C-O	-5.53	111.88	119.12
1	B	142	LEU	CA-C-N	5.51	127.94	120.44
1	B	142	LEU	C-N-CA	5.51	127.94	120.44
1	B	213	GLU	N-CA-CB	5.51	118.22	110.12
1	B	184	VAL	N-CA-C	5.48	115.44	106.72
1	A	149	GLN	N-CA-C	5.47	117.67	111.11
1	A	18	GLU	CB-CA-C	5.46	120.48	110.10
1	A	20	GLY	CA-C-N	5.42	131.45	121.70
1	A	20	GLY	C-N-CA	5.42	131.45	121.70
1	A	147	LYS	CA-C-N	-5.41	113.69	120.77
1	A	147	LYS	C-N-CA	-5.41	113.69	120.77
1	B	143	MET	N-CA-C	-5.40	105.31	111.14
1	B	32	ILE	N-CA-C	5.37	115.51	110.30
1	A	221	GLU	N-CA-C	5.37	116.81	111.07
1	A	219	ALA	N-CA-C	-5.37	104.85	111.40
1	B	172	GLU	CA-C-N	-5.35	113.14	120.46
1	B	172	GLU	C-N-CA	-5.35	113.14	120.46
1	B	252	VAL	N-CA-CB	-5.34	105.01	110.62
1	A	231	GLU	N-CA-C	-5.31	105.40	111.14
1	B	217	GLN	CB-CA-C	5.31	119.29	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	VAL	CB-CA-C	-5.30	102.60	111.29
1	A	213	GLU	CA-C-N	-5.29	111.62	120.30
1	A	213	GLU	C-N-CA	-5.29	111.62	120.30
1	B	149	GLN	CA-C-O	-5.28	114.38	120.24
1	B	202	VAL	N-CA-CB	-5.28	103.88	110.47
1	A	45	ASP	N-CA-CB	5.27	117.61	109.91
1	B	215	ALA	N-CA-CB	-5.24	101.64	110.49
1	B	167	ASP	CA-C-N	-5.22	111.91	121.52
1	B	167	ASP	C-N-CA	-5.22	111.91	121.52
1	A	83	ASP	N-CA-CB	5.22	119.31	110.49
1	B	171	GLU	CA-CB-CG	-5.19	103.72	114.10
1	B	162	LEU	N-CA-C	5.17	116.60	111.07
1	A	44	LEU	N-CA-C	-5.17	107.14	113.50
1	A	44	LEU	CA-C-N	-5.16	113.84	120.65
1	A	44	LEU	C-N-CA	-5.16	113.84	120.65
1	B	203	ASN	OD1-CG-ND2	5.16	127.76	122.60
1	B	240	GLU	N-CA-C	5.16	118.35	110.36
1	B	25	LYS	N-CA-C	5.14	125.39	111.00
1	A	144	ARG	CB-CG-CD	-5.14	99.48	111.30
1	A	139	LEU	N-CA-C	5.13	121.16	109.81
1	A	18	GLU	N-CA-C	5.09	125.26	111.00
1	A	34	PRO	N-CA-C	5.05	120.47	113.65
1	B	68	PHE	N-CA-C	5.04	119.63	111.37
1	A	15	ARG	N-CA-C	-5.03	106.83	113.17
1	B	229	GLU	N-CA-C	-5.02	104.90	111.02
1	A	87	ALA	N-CA-C	-5.01	105.72	111.14
1	B	213	GLU	CA-CB-CG	-5.00	104.10	114.10

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	18	GLU	CA
1	A	241	MET	CA
1	B	129	HIS	CA

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	ARG	Peptide
1	A	172	GLU	Peptide
1	A	21	CYS	Peptide
1	A	238	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	A	91	LYS	Peptide
1	A	94	ARG	Peptide
1	B	128	GLN	Peptide
1	B	129	HIS	Peptide
1	B	2	ASN	Peptide
1	B	204	LEU	Mainchain
1	B	216	LEU	Mainchain
1	B	244	VAL	Peptide
1	B	25	LYS	Peptide
1	B	27	GLN	Peptide
1	B	29	PHE	Peptide
1	B	3	GLN	Peptide
1	B	78	ARG	Peptide

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	1829	0	1785	371	6
1	B	1784	0	1750	392	6
2	B	1	0	0	0	0
3	B	31	0	12	12	0
4	A	5	0	0	5	0
4	B	8	0	0	1	0
All	All	3658	0	3547	715	6

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 99.

All (715) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:PRO:CG	1:A:140:PRO:CB	1.79	1.43
1:A:9:THR:O	1:A:12:GLN:N	1.66	1.26
1:A:240:GLU:HB3	1:A:242:THR:N	1.55	1.21
1:A:190:LEU:HD12	1:A:190:LEU:C	1.59	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ILE:O	1:A:14:LEU:HB2	1.40	1.20
1:A:161:THR:O	1:A:164:PRO:HD2	1.39	1.18
1:A:95:ARG:HA	1:A:95:ARG:CZ	1.71	1.18
1:A:240:GLU:HB3	1:A:242:THR:CA	1.73	1.18
1:A:240:GLU:HB3	1:A:242:THR:C	1.70	1.14
1:B:214:ILE:HG22	1:B:215:ALA:N	1.63	1.14
1:A:246:LEU:O	1:A:249:MET:HB2	1.52	1.10
1:B:231:GLU:HA	1:B:241:MET:HE3	1.17	1.10
1:B:39:GLU:HA	1:B:39:GLU:OE2	1.33	1.10
1:B:6:ARG:CG	1:B:10:ILE:HD11	1.81	1.09
1:B:6:ARG:HG2	1:B:10:ILE:HD11	1.20	1.09
1:B:139:LEU:HD23	1:B:140:PRO:HD2	1.35	1.08
1:B:29:PHE:H	1:B:32:ILE:HD13	1.15	1.07
1:A:206:ARG:O	1:A:207:HIS:CB	2.00	1.06
1:A:240:GLU:HA	1:A:242:THR:N	1.70	1.06
1:B:11:MET:CE	1:B:14:LEU:HD23	1.84	1.06
1:A:245:ASP:HB3	1:A:246:LEU:HA	1.34	1.06
1:B:197:LEU:O	1:B:201:THR:HG22	1.55	1.04
1:A:39:GLU:OE1	1:A:61:ASP:HB2	1.55	1.04
1:B:28:THR:N	1:B:32:ILE:HD11	1.71	1.04
1:B:157:PHE:CD2	1:B:157:PHE:O	2.10	1.03
1:A:132:LEU:HA	1:A:135:ILE:CD1	1.89	1.02
1:A:240:GLU:CB	1:A:242:THR:N	2.21	1.02
1:B:28:THR:H	1:B:32:ILE:HD11	1.21	1.01
1:A:161:THR:O	1:A:164:PRO:CD	2.08	1.01
1:A:3:GLN:H	1:B:82:ASN:ND2	1.58	1.01
1:B:28:THR:HB	1:B:30:ALA:O	1.61	1.00
1:B:217:GLN:OE1	1:B:217:GLN:HA	1.59	1.00
1:A:214:ILE:HD12	1:B:34:PRO:HB3	1.44	1.00
1:A:23:TRP:CZ2	1:A:27:GLN:NE2	2.31	0.99
1:A:146:GLN:HE22	1:A:212:ALA:H	1.10	0.97
1:B:32:ILE:HD12	1:B:32:ILE:N	1.80	0.97
1:A:245:ASP:HA	1:A:248:THR:OG1	1.63	0.96
1:B:6:ARG:C	1:B:10:ILE:HD12	1.91	0.96
1:B:177:MET:HE3	1:B:177:MET:HA	1.47	0.96
1:A:214:ILE:CD1	1:B:34:PRO:HB3	1.96	0.95
1:A:240:GLU:CA	1:A:242:THR:N	2.28	0.95
1:B:28:THR:H	1:B:32:ILE:CD1	1.79	0.95
1:A:143:MET:HE1	1:B:38:GLU:HB2	1.49	0.95
1:B:6:ARG:HG2	1:B:10:ILE:CD1	1.95	0.94
1:A:146:GLN:NE2	1:A:212:ALA:H	1.64	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ARG:HG2	1:A:237:ARG:HH11	1.32	0.94
1:A:240:GLU:CA	1:A:242:THR:H	1.80	0.94
1:A:3:GLN:N	1:B:82:ASN:HD21	1.65	0.94
1:A:233:ILE:HG21	1:A:252:VAL:HG11	1.49	0.94
1:A:253:TRP:HZ2	3:B:265:ATP:O3'	1.51	0.94
1:B:32:ILE:N	1:B:32:ILE:CD1	2.31	0.94
1:A:68:PHE:O	1:A:72:MET:HE2	1.68	0.94
1:B:146:GLN:HE22	1:B:212:ALA:H	1.00	0.93
1:A:10:ILE:O	1:A:14:LEU:CB	2.17	0.92
1:B:172:GLU:O	1:B:176:VAL:HG23	1.69	0.92
1:A:20:GLY:HA3	1:A:21:CYS:CB	1.98	0.92
1:A:204:LEU:CD2	1:A:208:LEU:HD13	1.98	0.92
1:B:11:MET:HE2	1:B:14:LEU:HD23	1.48	0.92
1:A:49:ARG:NH2	1:A:51:ASP:OD1	2.02	0.92
1:A:146:GLN:HE22	1:A:212:ALA:N	1.66	0.92
1:A:179:GLU:OE1	1:A:179:GLU:HA	1.67	0.92
1:A:240:GLU:HA	1:A:242:THR:H	1.24	0.92
1:B:157:PHE:O	1:B:157:PHE:HD2	1.49	0.91
1:B:10:ILE:HG23	1:B:14:LEU:HD11	1.51	0.91
1:A:245:ASP:HA	1:A:248:THR:HG1	1.36	0.90
1:B:32:ILE:HG21	1:B:69:TYR:HE2	1.36	0.90
1:B:187:GLN:OE1	1:B:187:GLN:HA	1.69	0.90
1:A:206:ARG:O	1:A:207:HIS:HB2	1.12	0.90
1:B:11:MET:HE3	1:B:14:LEU:CD2	2.01	0.90
1:A:78:ARG:HG2	1:A:78:ARG:HH11	1.38	0.89
1:B:214:ILE:HG22	1:B:215:ALA:H	1.27	0.89
1:B:23:TRP:HE3	1:B:23:TRP:O	1.55	0.89
1:B:220:ASN:OD1	1:B:220:ASN:N	2.03	0.89
1:B:80:ASP:O	1:B:83:ASP:HB2	1.72	0.89
1:B:29:PHE:N	1:B:32:ILE:HD13	1.88	0.88
1:A:93:GLU:O	1:A:96:HIS:HB3	1.73	0.88
1:B:5:ASP:O	1:B:6:ARG:C	2.17	0.88
1:B:23:TRP:CZ3	1:B:27:GLN:NE2	2.42	0.87
1:B:39:GLU:OE2	1:B:39:GLU:CA	2.18	0.87
1:B:139:LEU:HD23	1:B:140:PRO:CD	2.05	0.86
1:B:23:TRP:N	1:B:24:ASP:C	2.33	0.86
1:A:3:GLN:H	1:B:82:ASN:HD21	0.90	0.86
1:A:14:LEU:CD2	1:A:24:ASP:HB2	2.06	0.86
1:A:82:ASN:HD22	1:A:82:ASN:C	1.83	0.86
1:A:43:VAL:HA	4:A:266:HOH:O	1.76	0.86
1:A:144:ARG:O	1:A:148:ILE:HG13	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLN:OE1	1:A:203:ASN:ND2	2.09	0.85
1:A:240:GLU:OE1	1:A:242:THR:HB	1.75	0.85
1:B:230:VAL:HG12	1:B:241:MET:HE1	1.58	0.85
1:B:244:VAL:HG11	1:B:248:THR:HB	1.59	0.84
1:A:95:ARG:HA	1:A:95:ARG:NH1	1.92	0.84
1:A:162:LEU:O	1:A:162:LEU:HD12	1.76	0.84
1:A:240:GLU:CB	1:A:242:THR:C	2.48	0.84
1:A:245:ASP:CB	1:A:246:LEU:HA	1.97	0.84
1:A:14:LEU:HD21	1:A:24:ASP:HB2	1.59	0.84
1:A:11:MET:CE	1:A:11:MET:HA	2.07	0.83
1:B:13:ARG:HH21	1:B:14:LEU:CD1	1.91	0.83
1:A:148:ILE:O	1:A:151:ARG:HB2	1.78	0.83
1:A:190:LEU:C	1:A:190:LEU:CD1	2.44	0.83
1:A:11:MET:O	1:A:12:GLN:O	1.96	0.83
1:B:32:ILE:HG21	1:B:69:TYR:CE2	2.12	0.83
1:B:83:ASP:O	1:B:86:ALA:HB3	1.79	0.83
1:A:132:LEU:HA	1:A:135:ILE:HD11	1.61	0.83
1:B:136:PRO:HG2	1:B:139:LEU:HD12	1.60	0.83
1:A:204:LEU:HD21	1:A:208:LEU:HD13	1.60	0.82
1:B:139:LEU:HD22	1:B:143:MET:HG2	1.61	0.82
1:B:139:LEU:HD21	1:B:143:MET:SD	2.19	0.82
1:A:240:GLU:CB	1:A:242:THR:H	1.90	0.82
1:A:11:MET:O	1:A:12:GLN:C	2.23	0.82
1:A:190:LEU:HD12	1:A:190:LEU:O	1.80	0.82
1:B:32:ILE:CD1	1:B:32:ILE:H	1.90	0.82
1:B:245:ASP:OD2	1:B:248:THR:N	2.12	0.82
1:B:140:PRO:HG2	1:B:213:GLU:OE2	1.80	0.81
1:A:141:ALA:HB1	1:B:216:LEU:HD23	1.62	0.81
1:A:28:THR:HB	4:A:265:HOH:O	1.79	0.81
1:B:10:ILE:O	1:B:14:LEU:HD13	1.80	0.81
1:B:245:ASP:OD2	1:B:245:ASP:C	2.23	0.81
3:B:265:ATP:C8	3:B:265:ATP:O2'	2.33	0.81
1:A:246:LEU:C	1:A:247:GLU:HG3	2.04	0.80
1:A:246:LEU:O	1:A:249:MET:CB	2.28	0.80
1:A:78:ARG:HH11	1:A:78:ARG:CG	1.95	0.80
1:A:246:LEU:HB2	1:A:249:MET:HB2	1.62	0.80
1:A:247:GLU:HA	1:A:248:THR:C	2.07	0.79
1:B:88:ILE:C	1:B:88:ILE:HD12	2.08	0.79
1:B:214:ILE:CG2	1:B:215:ALA:N	2.44	0.79
1:A:146:GLN:OE1	1:A:211:LYS:HA	1.83	0.79
1:A:171:GLU:CG	1:A:171:GLU:O	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:ASN:HD22	1:A:83:ASP:N	1.78	0.79
1:A:78:ARG:HG2	1:A:78:ARG:NH1	1.96	0.79
1:A:149:GLN:CD	1:A:203:ASN:ND2	2.41	0.79
1:B:244:VAL:HG11	1:B:248:THR:CB	2.13	0.78
1:A:20:GLY:HA3	1:A:21:CYS:HB2	1.65	0.78
1:A:20:GLY:HA3	1:A:21:CYS:HB3	1.64	0.78
1:B:129:HIS:O	1:B:130:SER:CB	2.30	0.78
1:A:234:VAL:O	1:A:234:VAL:CG1	2.31	0.78
1:B:23:TRP:CE3	1:B:27:GLN:NE2	2.52	0.78
1:A:63:LEU:HD11	1:B:81:PHE:CZ	2.18	0.78
1:B:81:PHE:HA	1:B:84:ILE:CD1	2.14	0.78
1:B:11:MET:HE3	1:B:14:LEU:HD23	1.59	0.77
1:B:25:LYS:HB3	1:B:27:GLN:HG2	1.66	0.77
1:B:31:THR:O	1:B:34:PRO:HD2	1.84	0.77
1:B:129:HIS:O	1:B:130:SER:HB2	1.82	0.77
1:A:6:ARG:O	1:A:10:ILE:HD12	1.86	0.76
1:A:137:ARG:HH11	1:A:137:ARG:HG2	1.49	0.76
1:A:246:LEU:CD1	1:A:246:LEU:H	1.97	0.76
1:A:132:LEU:HA	1:A:135:ILE:HD13	1.67	0.76
1:B:255:GLN:HA	1:B:258:ARG:NH2	2.00	0.76
1:B:70:ALA:HA	1:B:84:ILE:HD11	1.67	0.76
1:B:11:MET:CE	1:B:14:LEU:CD2	2.58	0.76
1:A:204:LEU:O	1:A:205:ALA:C	2.27	0.75
1:B:61:ASP:O	1:B:62:LEU:C	2.25	0.75
1:A:80:ASP:N	1:A:83:ASP:OD2	2.18	0.75
1:A:240:GLU:OE1	1:A:242:THR:CB	2.34	0.75
1:A:169:VAL:O	1:A:170:TYR:C	2.30	0.75
1:A:246:LEU:C	1:A:249:MET:HB2	2.11	0.74
1:B:64:PHE:CD1	1:B:64:PHE:C	2.63	0.74
1:B:139:LEU:CD2	1:B:143:MET:SD	2.76	0.74
1:A:82:ASN:C	1:A:82:ASN:ND2	2.46	0.74
1:B:81:PHE:HA	1:B:84:ILE:HG13	1.67	0.74
1:B:23:TRP:O	1:B:23:TRP:CE3	2.41	0.73
1:B:85:CYS:O	1:B:89:SER:OG	2.04	0.73
1:A:9:THR:O	1:A:11:MET:C	2.31	0.73
1:B:33:ALA:O	1:B:35:TYR:N	2.21	0.73
1:B:195:GLY:O	1:B:198:LEU:N	2.21	0.72
1:A:39:GLU:O	1:A:40:THR:C	2.25	0.72
1:A:130:SER:HB2	1:B:231:GLU:OE1	1.89	0.72
1:A:204:LEU:HD23	1:A:208:LEU:HD13	1.71	0.72
1:A:88:ILE:O	1:A:89:SER:C	2.32	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:THR:CB	1:B:30:ALA:O	2.35	0.72
1:A:208:LEU:HD23	1:B:190:LEU:CD1	2.20	0.72
1:B:6:ARG:HG3	1:B:10:ILE:HD11	1.72	0.71
1:A:217:GLN:O	1:A:220:ASN:HB2	1.89	0.71
1:B:203:ASN:HD21	1:B:206:ARG:HH21	1.34	0.71
1:B:10:ILE:CG2	1:B:14:LEU:HD11	2.20	0.71
1:A:253:TRP:CZ2	3:B:265:ATP:O3'	2.33	0.71
1:B:214:ILE:O	1:B:217:GLN:N	2.24	0.71
1:A:240:GLU:CB	1:A:242:THR:O	2.39	0.71
1:B:245:ASP:OD2	1:B:247:GLU:N	2.22	0.71
1:B:147:LYS:O	1:B:150:LYS:HB2	1.90	0.70
1:A:245:ASP:HB3	1:A:246:LEU:CA	2.15	0.70
1:B:203:ASN:HD21	1:B:206:ARG:NH2	1.89	0.70
1:B:89:SER:O	1:B:93:GLU:OE1	2.09	0.70
1:B:54:ASP:O	1:B:55:LEU:C	2.28	0.70
1:B:65:GLN:O	1:B:68:PHE:N	2.25	0.70
1:B:81:PHE:HA	1:B:84:ILE:CG1	2.22	0.70
1:B:214:ILE:O	1:B:217:GLN:HB2	1.90	0.70
1:B:86:ALA:O	1:B:90:ASP:OD2	2.10	0.70
1:B:51:ASP:OD2	1:B:51:ASP:C	2.32	0.69
1:A:177:MET:O	1:A:181:ARG:HG3	1.91	0.69
1:B:146:GLN:NE2	1:B:212:ALA:H	1.84	0.69
3:B:265:ATP:H5'2	3:B:265:ATP:O1B	1.91	0.69
1:A:145:ALA:O	1:A:146:GLN:C	2.35	0.69
1:A:47:ILE:HG12	1:A:47:ILE:O	1.90	0.69
1:A:8:LEU:O	1:A:11:MET:HB2	1.92	0.69
1:A:158:ASP:OD1	1:A:159:TRP:N	2.26	0.69
1:B:216:LEU:O	1:B:220:ASN:OD1	2.11	0.69
1:B:6:ARG:O	1:B:10:ILE:HD12	1.92	0.68
1:B:135:ILE:O	1:B:136:PRO:C	2.35	0.68
1:A:15:ARG:NE	1:A:75:GLU:OE2	2.25	0.68
1:B:11:MET:HE3	1:B:14:LEU:HD21	1.74	0.68
1:A:82:ASN:OD1	1:B:2:ASN:N	2.27	0.68
1:B:39:GLU:OE2	1:B:42:GLU:HG3	1.93	0.68
1:A:14:LEU:O	1:A:14:LEU:HD23	1.94	0.68
1:A:208:LEU:HD23	1:B:190:LEU:HD11	1.76	0.68
1:B:146:GLN:HE22	1:B:212:ALA:N	1.83	0.68
1:B:149:GLN:OE1	1:B:203:ASN:HA	1.93	0.68
1:B:245:ASP:OD1	1:B:247:GLU:HB2	1.93	0.68
1:B:32:ILE:HD13	1:B:32:ILE:H	1.56	0.68
1:B:27:GLN:C	1:B:32:ILE:HD11	2.19	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:GLU:CA	1:B:241:MET:HE3	2.11	0.67
1:B:64:PHE:O	1:B:67:VAL:HG22	1.93	0.67
1:A:47:ILE:HG13	1:B:29:PHE:O	1.94	0.67
1:A:21:CYS:N	1:A:25:LYS:HD3	2.10	0.67
1:B:177:MET:HA	1:B:177:MET:CE	2.23	0.67
1:B:234:VAL:HG12	1:B:235:ALA:N	2.08	0.67
1:A:140:PRO:HD2	1:A:143:MET:HG3	1.77	0.67
1:B:24:ASP:N	1:B:25:LYS:O	2.27	0.67
1:B:233:ILE:O	1:B:237:ARG:HD2	1.93	0.66
1:B:258:ARG:HB2	1:B:258:ARG:CZ	2.24	0.66
1:A:14:LEU:HD21	1:A:24:ASP:CB	2.24	0.66
1:B:23:TRP:HZ3	1:B:27:GLN:HE22	1.41	0.66
1:A:232:ARG:NH1	1:A:233:ILE:HG13	2.10	0.66
1:A:234:VAL:O	1:A:234:VAL:HG12	1.93	0.66
1:A:236:ALA:O	1:A:238:GLY:N	2.29	0.66
1:A:253:TRP:HZ2	3:B:265:ATP:HO3'	0.72	0.66
1:A:94:ARG:HH12	1:A:95:ARG:NH2	1.92	0.66
1:B:189:LYS:O	1:B:193:GLU:HG2	1.95	0.66
1:A:10:ILE:CG2	1:A:14:LEU:HD12	2.25	0.66
1:A:14:LEU:O	1:A:25:LYS:HG3	1.96	0.66
1:A:47:ILE:O	1:A:47:ILE:CG1	2.44	0.66
1:B:58:GLU:OE2	1:B:58:GLU:HA	1.94	0.66
1:A:240:GLU:HB3	1:A:242:THR:O	1.92	0.65
1:B:69:TYR:O	1:B:73:ALA:HB3	1.96	0.65
1:A:76:GLU:HB2	1:A:78:ARG:HD2	1.79	0.65
1:B:88:ILE:HD12	1:B:88:ILE:O	1.96	0.65
1:A:85:CYS:O	1:A:89:SER:N	2.24	0.65
1:B:226:ARG:HA	1:B:229:GLU:HG3	1.78	0.65
1:A:10:ILE:HG22	1:A:14:LEU:HD12	1.78	0.65
1:A:146:GLN:O	1:A:150:LYS:N	2.28	0.65
1:A:237:ARG:HG2	1:A:237:ARG:NH1	2.01	0.65
1:B:23:TRP:C	1:B:25:LYS:HB2	2.22	0.65
1:A:167:ASP:O	1:A:170:TYR:HB2	1.96	0.65
1:B:81:PHE:CE2	1:B:85:CYS:SG	2.88	0.65
1:A:131:ALA:O	1:A:151:ARG:HD2	1.97	0.65
1:A:169:VAL:O	1:A:171:GLU:N	2.30	0.65
1:B:168:LYS:HG3	1:B:168:LYS:O	1.97	0.64
1:A:148:ILE:CD1	1:B:220:ASN:HB3	2.27	0.64
1:B:243:GLY:O	1:B:244:VAL:HG22	1.96	0.64
1:A:76:GLU:HB2	1:A:78:ARG:CD	2.27	0.64
1:A:76:GLU:OE1	1:A:78:ARG:NE	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:GLU:O	1:A:171:GLU:HG3	1.97	0.64
1:A:196:ASP:O	1:A:197:LEU:C	2.40	0.64
1:B:234:VAL:HG21	1:B:241:MET:HG2	1.80	0.64
1:A:62:LEU:O	1:A:63:LEU:C	2.40	0.64
1:A:246:LEU:HB2	1:A:249:MET:CB	2.27	0.64
1:A:92:LEU:HD13	1:B:10:ILE:HG21	1.78	0.64
1:A:229:GLU:O	1:A:230:VAL:C	2.41	0.64
1:B:74:GLN:HG3	1:B:80:ASP:HB2	1.79	0.64
1:A:228:ARG:NH2	1:B:133:ASP:OD1	2.31	0.64
1:A:14:LEU:CD2	1:A:24:ASP:CB	2.74	0.63
1:A:47:ILE:HD11	1:B:29:PHE:C	2.23	0.63
1:A:246:LEU:O	1:A:246:LEU:HD22	1.98	0.63
1:A:88:ILE:CG2	1:A:89:SER:N	2.61	0.63
1:A:214:ILE:HD11	1:B:34:PRO:HB3	1.78	0.63
1:A:246:LEU:CB	1:A:249:MET:HB2	2.28	0.63
1:B:7:LEU:HA	1:B:10:ILE:HD12	1.79	0.63
1:A:27:GLN:OE1	1:A:27:GLN:HA	1.98	0.63
1:A:216:LEU:O	1:A:217:GLN:C	2.40	0.63
1:B:13:ARG:HH21	1:B:14:LEU:HD12	1.62	0.63
1:B:70:ALA:HB1	1:B:81:PHE:HB2	1.80	0.63
1:B:234:VAL:HG13	1:B:239:LEU:O	1.99	0.63
1:A:246:LEU:H	1:A:246:LEU:HD13	1.63	0.63
1:B:10:ILE:O	1:B:14:LEU:CD1	2.45	0.63
1:A:169:VAL:HG12	1:A:170:TYR:N	2.14	0.62
1:B:25:LYS:HB3	1:B:27:GLN:CG	2.29	0.62
1:A:203:ASN:O	1:A:206:ARG:O	2.17	0.62
1:B:5:ASP:C	1:B:7:LEU:N	2.50	0.62
1:A:85:CYS:HB2	1:B:3:GLN:HB3	1.81	0.62
1:A:9:THR:O	1:A:11:MET:N	2.32	0.62
1:A:148:ILE:HD11	1:B:220:ASN:HB3	1.81	0.62
1:B:74:GLN:CG	1:B:80:ASP:HB2	2.29	0.62
1:B:67:VAL:O	1:B:70:ALA:HB3	1.99	0.62
1:B:88:ILE:C	1:B:88:ILE:CD1	2.73	0.62
1:A:218:LYS:HE3	1:B:191:GLU:OE1	1.98	0.62
1:B:142:LEU:HD12	1:B:213:GLU:HA	1.81	0.62
1:A:88:ILE:HG23	1:A:89:SER:N	2.15	0.62
1:A:162:LEU:HD12	1:A:162:LEU:C	2.23	0.62
1:B:69:TYR:O	1:B:73:ALA:CB	2.48	0.62
1:B:3:GLN:C	1:B:5:ASP:N	2.56	0.61
1:A:12:GLN:C	1:A:14:LEU:H	2.07	0.61
1:B:55:LEU:O	1:B:59:LEU:HG	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:PHE:HA	1:B:84:ILE:HD12	1.82	0.61
1:A:3:GLN:O	1:A:6:ARG:N	2.33	0.61
1:A:169:VAL:O	1:A:172:GLU:N	2.30	0.61
1:B:6:ARG:CG	1:B:10:ILE:CD1	2.66	0.61
1:A:11:MET:HA	1:A:11:MET:HE2	1.82	0.61
1:A:85:CYS:O	1:A:88:ILE:HG22	2.00	0.61
1:B:234:VAL:HG12	1:B:235:ALA:CA	2.31	0.61
1:A:42:GLU:C	4:A:266:HOH:O	2.43	0.61
1:A:67:VAL:HG12	1:A:68:PHE:N	2.15	0.61
1:B:142:LEU:O	1:B:145:ALA:HB3	2.00	0.61
1:A:92:LEU:CD1	1:B:10:ILE:HG21	2.30	0.61
1:B:186:ASP:OD1	1:B:186:ASP:C	2.43	0.61
1:B:157:PHE:CD2	1:B:157:PHE:C	2.78	0.61
1:A:4:ILE:O	1:A:8:LEU:HG	2.00	0.61
1:B:145:ALA:O	1:B:149:GLN:HG3	2.00	0.61
1:B:81:PHE:C	1:B:81:PHE:CD2	2.79	0.61
1:A:21:CYS:H	1:A:25:LYS:HD3	1.64	0.60
1:A:23:TRP:CE2	1:A:27:GLN:NE2	2.69	0.60
1:B:197:LEU:O	1:B:201:THR:CG2	2.42	0.60
1:A:39:GLU:HA	1:A:42:GLU:HG3	1.83	0.60
1:B:231:GLU:HA	1:B:241:MET:CE	2.12	0.60
1:B:227:PHE:O	1:B:230:VAL:HB	2.01	0.60
1:A:15:ARG:HA	1:A:25:LYS:HG2	1.84	0.60
1:A:11:MET:HA	1:A:11:MET:HE3	1.83	0.60
1:A:132:LEU:CA	1:A:135:ILE:CD1	2.75	0.60
1:A:171:GLU:O	1:A:171:GLU:HG2	2.02	0.60
1:B:32:ILE:CG2	1:B:69:TYR:HE2	2.13	0.60
1:B:164:PRO:HA	1:B:167:ASP:HB2	1.83	0.60
1:A:94:ARG:HH12	1:A:95:ARG:HH21	1.48	0.59
1:A:208:LEU:CD2	1:B:190:LEU:HD11	2.32	0.59
1:A:203:ASN:ND2	1:A:206:ARG:NH1	2.49	0.59
1:B:142:LEU:HB2	1:B:213:GLU:HB2	1.82	0.59
1:B:245:ASP:OD2	1:B:245:ASP:O	2.20	0.59
1:B:28:THR:N	1:B:32:ILE:CD1	2.47	0.59
1:B:29:PHE:N	1:B:32:ILE:CD1	2.64	0.59
1:A:233:ILE:CG2	1:A:252:VAL:HG11	2.30	0.59
1:A:95:ARG:CZ	1:A:95:ARG:CA	2.66	0.59
1:A:247:GLU:C	1:A:251:GLU:HB2	2.26	0.59
1:B:13:ARG:NH2	1:B:14:LEU:CD1	2.64	0.59
1:A:49:ARG:HG2	1:A:49:ARG:HH21	1.68	0.59
1:A:240:GLU:HB2	1:A:242:THR:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:THR:O	1:A:249:MET:C	2.46	0.59
1:B:31:THR:HG23	1:B:32:ILE:HD12	1.83	0.59
1:B:32:ILE:CG2	1:B:69:TYR:CE2	2.84	0.59
1:B:80:ASP:CG	1:B:81:PHE:N	2.60	0.59
1:A:229:GLU:HG3	1:A:233:ILE:HD12	1.85	0.58
1:B:30:ALA:H	1:B:32:ILE:H	1.51	0.58
1:B:83:ASP:O	1:B:86:ALA:CB	2.50	0.58
1:B:234:VAL:HG12	1:B:235:ALA:HA	1.85	0.58
1:B:255:GLN:HE21	1:B:259:GLN:HE21	1.51	0.58
1:B:83:ASP:O	1:B:84:ILE:C	2.46	0.58
1:B:203:ASN:ND2	1:B:206:ARG:HH21	2.01	0.58
1:B:171:GLU:O	1:B:175:GLU:HG3	2.03	0.58
1:B:25:LYS:CB	1:B:27:GLN:HG2	2.34	0.58
1:B:136:PRO:CG	1:B:139:LEU:HD12	2.33	0.58
1:A:226:ARG:NH1	1:A:253:TRP:CZ2	2.71	0.58
1:A:235:ALA:O	1:A:236:ALA:C	2.47	0.57
1:A:246:LEU:CA	1:A:249:MET:HB2	2.34	0.57
1:A:211:LYS:O	1:A:212:ALA:C	2.43	0.57
1:A:233:ILE:HG21	1:A:252:VAL:CG1	2.29	0.57
1:B:30:ALA:H	1:B:32:ILE:N	2.02	0.57
1:B:11:MET:HA	1:B:14:LEU:HD22	1.86	0.57
1:A:240:GLU:CA	1:A:241:MET:C	2.65	0.57
1:B:74:GLN:CB	1:B:80:ASP:HB2	2.35	0.57
1:A:142:LEU:HD21	1:B:142:LEU:HD21	1.85	0.57
1:B:228:ARG:HA	1:B:231:GLU:HG3	1.86	0.57
1:A:39:GLU:C	1:A:41:TYR:N	2.63	0.57
1:B:10:ILE:O	1:B:14:LEU:HD22	2.05	0.57
1:A:94:ARG:NH1	1:A:95:ARG:HH21	2.03	0.57
1:B:13:ARG:HH21	1:B:14:LEU:HD13	1.69	0.56
1:B:63:LEU:HG	1:B:63:LEU:O	2.05	0.56
1:A:240:GLU:OE1	1:A:242:THR:OG1	2.23	0.56
1:A:253:TRP:HE1	3:B:265:ATP:H4'	1.71	0.56
1:B:11:MET:HA	1:B:14:LEU:CD2	2.35	0.56
1:B:68:PHE:HA	1:B:71:GLN:HB2	1.87	0.56
1:B:84:ILE:C	1:B:86:ALA:H	2.11	0.56
1:A:221:GLU:OE1	1:A:221:GLU:HA	2.06	0.56
1:A:247:GLU:O	1:A:251:GLU:HB2	2.06	0.56
1:B:139:LEU:HD22	1:B:143:MET:CG	2.33	0.56
1:B:226:ARG:O	1:B:230:VAL:HG23	2.05	0.56
1:A:9:THR:C	1:A:11:MET:N	2.62	0.56
1:A:68:PHE:O	1:A:72:MET:CE	2.50	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:GLN:HG3	1:A:74:GLN:O	2.05	0.56
1:A:234:VAL:O	1:A:234:VAL:HG13	2.06	0.56
1:B:33:ALA:C	1:B:35:TYR:H	2.11	0.56
1:A:2:ASN:N	1:A:4:ILE:HG22	2.21	0.55
1:B:255:GLN:HA	1:B:258:ARG:HH22	1.69	0.55
1:A:59:LEU:HD21	1:B:69:TYR:HD1	1.71	0.55
1:B:166:VAL:O	1:B:167:ASP:C	2.49	0.55
1:B:198:LEU:O	1:B:199:PHE:C	2.48	0.55
1:B:202:VAL:C	1:B:204:LEU:N	2.58	0.55
1:B:244:VAL:HG12	1:B:245:ASP:N	2.22	0.55
1:B:8:LEU:C	1:B:10:ILE:H	2.15	0.55
1:A:29:PHE:C	1:A:31:THR:N	2.62	0.55
1:B:8:LEU:O	1:B:10:ILE:N	2.39	0.55
1:B:172:GLU:OE2	3:B:265:ATP:O2A	2.25	0.55
1:B:68:PHE:O	1:B:71:GLN:CB	2.55	0.55
1:B:151:ARG:HA	1:B:154:ASN:ND2	2.22	0.54
1:A:254:GLN:O	1:A:257:ALA:HB3	2.07	0.54
1:A:32:ILE:O	1:A:35:TYR:HD2	1.90	0.54
1:A:255:GLN:HA	1:A:258:ARG:CZ	2.38	0.54
1:B:166:VAL:C	1:B:168:LYS:N	2.61	0.54
1:A:46:ALA:O	1:A:48:ALA:N	2.40	0.54
1:A:233:ILE:O	1:A:237:ARG:NH1	2.41	0.54
1:A:31:THR:O	1:A:34:PRO:HD2	2.07	0.54
1:A:132:LEU:HD11	1:B:227:PHE:CD2	2.42	0.54
1:B:73:ALA:O	1:B:74:GLN:C	2.51	0.54
1:A:239:LEU:HD23	1:A:239:LEU:O	2.08	0.54
1:B:195:GLY:O	1:B:197:LEU:N	2.41	0.54
1:A:168:LYS:O	1:A:168:LYS:HG3	2.07	0.54
1:A:239:LEU:HD23	1:A:239:LEU:C	2.33	0.53
1:B:30:ALA:N	1:B:32:ILE:H	2.05	0.53
1:A:67:VAL:O	1:A:68:PHE:C	2.51	0.53
1:A:82:ASN:O	1:A:83:ASP:C	2.51	0.53
1:B:81:PHE:CA	1:B:84:ILE:HG13	2.38	0.53
1:A:64:PHE:CE1	1:B:92:LEU:HD11	2.44	0.53
1:A:81:PHE:CE2	1:A:85:CYS:SG	3.01	0.53
1:A:216:LEU:HD23	1:B:142:LEU:HD23	1.91	0.53
1:A:12:GLN:O	1:A:14:LEU:N	2.41	0.53
1:A:208:LEU:HD23	1:B:190:LEU:HD12	1.89	0.53
1:A:4:ILE:O	1:A:7:LEU:HB3	2.09	0.53
1:B:162:LEU:HD12	1:B:162:LEU:O	2.09	0.53
1:A:227:PHE:O	1:A:228:ARG:C	2.51	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:PRO:HD2	1:B:139:LEU:HD12	1.91	0.53
1:B:179:GLU:OE1	1:B:179:GLU:HA	2.09	0.52
1:A:47:ILE:CG1	1:B:29:PHE:O	2.58	0.52
1:A:55:LEU:O	1:A:59:LEU:HD12	2.09	0.52
1:A:74:GLN:HB2	1:A:79:PHE:O	2.10	0.52
1:A:168:LYS:O	1:A:168:LYS:CG	2.56	0.52
1:B:61:ASP:O	1:B:64:PHE:N	2.43	0.52
1:B:231:GLU:O	1:B:234:VAL:HB	2.09	0.52
1:A:3:GLN:CG	1:B:82:ASN:OD1	2.58	0.52
1:B:226:ARG:O	1:B:227:PHE:C	2.50	0.52
1:B:11:MET:HG2	1:B:71:GLN:CG	2.40	0.52
1:B:70:ALA:CA	1:B:84:ILE:HD11	2.37	0.52
1:B:81:PHE:O	1:B:85:CYS:SG	2.68	0.52
1:B:3:GLN:O	1:B:7:LEU:HB2	2.10	0.52
1:A:166:VAL:O	1:A:167:ASP:C	2.45	0.52
1:B:55:LEU:HD11	1:B:59:LEU:HD21	1.92	0.52
1:A:133:ASP:OD1	1:B:228:ARG:NH2	2.42	0.52
1:A:147:LYS:O	1:A:148:ILE:C	2.47	0.52
1:B:74:GLN:HB2	1:B:80:ASP:HB2	1.92	0.52
1:B:81:PHE:O	1:B:82:ASN:C	2.51	0.52
1:A:95:ARG:HA	1:A:95:ARG:NE	2.21	0.51
1:B:204:LEU:C	1:B:204:LEU:HD22	2.35	0.51
1:B:244:VAL:HG12	1:B:245:ASP:CB	2.39	0.51
1:A:53:ASP:O	1:A:56:ARG:HG3	2.10	0.51
1:A:137:ARG:HG2	1:A:137:ARG:NH1	2.23	0.51
1:B:255:GLN:HE21	1:B:259:GLN:NE2	2.09	0.51
1:B:203:ASN:C	1:B:203:ASN:HD22	2.18	0.51
1:A:74:GLN:O	1:A:74:GLN:CG	2.56	0.51
1:B:154:ASN:C	1:B:156:GLY:H	2.19	0.51
1:A:92:LEU:HD13	1:B:10:ILE:CG2	2.40	0.51
1:A:255:GLN:HG3	1:A:258:ARG:HH22	1.75	0.51
1:A:28:THR:OG1	1:A:31:THR:HG23	2.11	0.51
1:A:246:LEU:H	1:A:246:LEU:HD12	1.75	0.51
1:A:79:PHE:CE1	1:B:56:ARG:HB2	2.46	0.51
1:A:256:VAL:HG13	4:A:268:HOH:O	2.11	0.51
1:B:58:GLU:OE2	1:B:58:GLU:CA	2.59	0.51
1:B:204:LEU:CD2	1:B:208:LEU:HD22	2.40	0.51
1:A:47:ILE:CD1	1:B:29:PHE:C	2.83	0.51
1:A:173:ILE:O	1:A:177:MET:HG2	2.10	0.51
1:B:134:ASP:CG	1:B:134:ASP:O	2.54	0.51
1:A:74:GLN:HE21	1:A:80:ASP:HA	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:THR:O	1:A:10:ILE:C	2.54	0.50
1:B:64:PHE:C	1:B:64:PHE:HD1	2.19	0.50
1:B:244:VAL:CG1	1:B:248:THR:HB	2.38	0.50
1:A:204:LEU:O	1:A:206:ARG:N	2.43	0.50
1:B:204:LEU:O	1:B:205:ALA:C	2.54	0.50
1:A:46:ALA:C	1:A:48:ALA:H	2.19	0.50
1:A:74:GLN:HE22	1:A:80:ASP:HB2	1.76	0.50
1:A:142:LEU:HB2	1:A:213:GLU:HB2	1.92	0.50
1:A:193:GLU:OE2	1:A:193:GLU:HA	2.09	0.50
1:A:258:ARG:O	1:A:260:GLU:N	2.45	0.50
1:B:7:LEU:N	1:B:10:ILE:HD12	2.26	0.50
1:B:11:MET:HG2	1:B:71:GLN:HG2	1.93	0.50
1:B:32:ILE:HG22	1:B:69:TYR:OH	2.12	0.50
1:B:128:GLN:O	1:B:129:HIS:O	2.29	0.50
1:A:71:GLN:O	1:A:74:GLN:N	2.43	0.50
1:B:14:LEU:C	1:B:24:ASP:OD1	2.54	0.50
1:B:64:PHE:O	1:B:64:PHE:HD1	1.94	0.50
1:B:234:VAL:CG1	1:B:239:LEU:O	2.59	0.50
1:B:6:ARG:C	1:B:10:ILE:CD1	2.76	0.50
1:A:63:LEU:O	1:A:66:VAL:N	2.44	0.50
1:A:7:LEU:O	1:A:8:LEU:C	2.54	0.49
1:B:191:GLU:O	1:B:192:GLU:C	2.55	0.49
1:A:141:ALA:CB	1:B:216:LEU:HD23	2.38	0.49
1:A:203:ASN:ND2	1:A:206:ARG:HH12	2.10	0.49
1:B:13:ARG:NH2	1:B:14:LEU:HD13	2.26	0.49
1:A:29:PHE:C	1:A:31:THR:H	2.20	0.49
1:A:142:LEU:HD12	1:A:213:GLU:HA	1.94	0.49
1:B:64:PHE:O	1:B:65:GLN:C	2.55	0.49
1:A:230:VAL:O	1:A:234:VAL:N	2.41	0.49
1:B:23:TRP:N	1:B:25:LYS:N	2.61	0.49
1:A:237:ARG:NH1	1:A:237:ARG:CG	2.74	0.49
1:A:80:ASP:O	1:A:81:PHE:C	2.54	0.49
1:B:195:GLY:O	1:B:196:ASP:C	2.55	0.49
1:A:92:LEU:O	1:A:95:ARG:N	2.45	0.49
1:A:204:LEU:HD21	1:A:208:LEU:CD1	2.37	0.49
1:B:220:ASN:O	1:B:224:GLU:HB2	2.12	0.49
1:A:145:ALA:HB1	1:A:199:PHE:CE1	2.47	0.49
1:A:233:ILE:HG23	1:A:237:ARG:NH1	2.28	0.49
1:B:162:LEU:O	1:B:165:VAL:HB	2.13	0.49
1:B:170:TYR:C	1:B:172:GLU:H	2.21	0.49
1:A:2:ASN:N	1:B:82:ASN:ND2	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:GLU:O	1:B:43:VAL:C	2.56	0.48
1:A:95:ARG:NH1	1:A:95:ARG:CA	2.72	0.48
1:B:62:LEU:HD23	1:B:62:LEU:HA	1.66	0.48
1:A:199:PHE:O	1:A:200:ALA:C	2.55	0.48
1:B:7:LEU:O	1:B:7:LEU:HD22	2.13	0.48
1:B:54:ASP:O	1:B:56:ARG:N	2.46	0.48
1:A:161:THR:O	1:A:163:GLY:N	2.47	0.48
1:A:27:GLN:OE1	1:A:27:GLN:CA	2.60	0.48
1:B:64:PHE:CD1	1:B:64:PHE:O	2.66	0.48
1:B:259:GLN:HG3	4:B:269:HOH:O	2.13	0.48
1:A:245:ASP:CA	1:A:248:THR:HG1	2.15	0.48
1:B:128:GLN:C	1:B:129:HIS:O	2.57	0.48
1:B:170:TYR:O	1:B:172:GLU:N	2.47	0.48
1:B:178:TYR:C	1:B:178:TYR:CD2	2.92	0.48
3:B:265:ATP:PA	3:B:265:ATP:O1G	2.71	0.48
1:A:3:GLN:C	1:A:5:ASP:N	2.71	0.48
1:A:204:LEU:C	1:A:206:ARG:N	2.68	0.48
1:B:25:LYS:HB3	1:B:26:GLU:O	2.14	0.48
1:B:140:PRO:CG	1:B:213:GLU:OE2	2.58	0.48
1:A:162:LEU:HD21	1:A:208:LEU:HD12	1.95	0.47
1:A:194:MET:O	1:A:194:MET:HG3	2.10	0.47
1:B:71:GLN:NE2	1:B:75:GLU:OE2	2.47	0.47
1:A:88:ILE:O	1:A:90:ASP:N	2.47	0.47
1:A:213:GLU:CD	1:B:141:ALA:HB2	2.39	0.47
1:A:14:LEU:HD23	1:A:14:LEU:C	2.38	0.47
1:A:216:LEU:C	1:A:216:LEU:HD12	2.36	0.47
1:B:136:PRO:CD	1:B:139:LEU:HD12	2.44	0.47
1:A:94:ARG:HH22	1:A:95:ARG:HH21	1.60	0.47
1:A:12:GLN:O	1:A:16:ASP:N	2.46	0.47
1:B:180:ALA:HA	1:B:190:LEU:HD21	1.97	0.47
1:A:3:GLN:O	1:A:5:ASP:N	2.47	0.47
1:B:28:THR:O	1:B:29:PHE:CD2	2.67	0.47
1:B:81:PHE:CD2	1:B:85:CYS:SG	3.08	0.47
1:B:82:ASN:HA	1:B:85:CYS:SG	2.54	0.47
1:B:204:LEU:HD23	1:B:204:LEU:HA	1.38	0.47
1:A:143:MET:HE1	1:B:38:GLU:CB	2.33	0.47
1:A:21:CYS:O	1:A:25:LYS:HB2	2.14	0.47
1:A:94:ARG:NH2	1:A:95:ARG:HH21	2.12	0.47
1:B:144:ARG:O	1:B:148:ILE:HG13	2.14	0.47
1:A:246:LEU:O	1:A:249:MET:CA	2.63	0.47
1:B:10:ILE:O	1:B:14:LEU:CD2	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:ASP:O	1:B:187:GLN:C	2.57	0.46
1:A:44:LEU:O	1:A:45:ASP:C	2.52	0.46
1:A:130:SER:CB	1:B:231:GLU:OE1	2.59	0.46
1:B:202:VAL:O	1:B:203:ASN:C	2.53	0.46
1:B:157:PHE:CE2	3:B:265:ATP:N6	2.84	0.46
1:B:217:GLN:OE1	1:B:217:GLN:CA	2.45	0.46
1:A:16:ASP:HA	1:A:17:PRO:HD3	1.63	0.46
1:A:240:GLU:CD	1:A:242:THR:OG1	2.58	0.46
1:B:139:LEU:CD2	1:B:143:MET:HG2	2.41	0.46
1:A:3:GLN:O	1:A:4:ILE:C	2.59	0.46
1:A:69:TYR:O	1:A:70:ALA:C	2.59	0.46
1:A:150:LYS:O	1:A:153:ALA:HB3	2.15	0.46
1:B:28:THR:O	1:B:29:PHE:CB	2.62	0.46
1:B:139:LEU:CD2	1:B:143:MET:CG	2.93	0.46
1:B:194:MET:O	1:B:195:GLY:C	2.58	0.46
1:A:21:CYS:O	1:A:21:CYS:SG	2.74	0.46
1:B:11:MET:SD	1:B:64:PHE:HE1	2.39	0.46
1:A:74:GLN:NE2	1:A:80:ASP:CB	2.79	0.46
1:A:228:ARG:O	1:A:231:GLU:HB2	2.16	0.46
1:B:76:GLU:C	1:B:78:ARG:H	2.23	0.46
1:B:146:GLN:OE1	1:B:211:LYS:HA	2.15	0.46
1:B:214:ILE:O	1:B:218:LYS:N	2.44	0.46
1:A:68:PHE:HD2	1:A:72:MET:HE2	1.81	0.46
1:A:255:GLN:HA	1:A:258:ARG:NH1	2.31	0.45
1:A:38:GLU:O	1:A:42:GLU:HG2	2.16	0.45
1:A:63:LEU:HD21	1:B:63:LEU:CD1	2.46	0.45
1:A:161:THR:O	1:A:164:PRO:HD3	2.06	0.45
1:B:26:GLU:OE1	1:B:72:MET:HE3	2.17	0.45
1:B:166:VAL:C	1:B:168:LYS:H	2.23	0.45
1:B:206:ARG:O	1:B:207:HIS:C	2.56	0.45
1:B:150:LYS:O	1:B:151:ARG:C	2.59	0.45
1:A:55:LEU:O	1:A:55:LEU:HG	2.16	0.45
1:A:88:ILE:C	1:A:90:ASP:N	2.74	0.45
1:A:256:VAL:O	1:A:260:GLU:HG3	2.17	0.45
1:A:258:ARG:O	1:A:259:GLN:C	2.60	0.45
1:B:6:ARG:O	1:B:10:ILE:CD1	2.61	0.45
1:A:88:ILE:CG2	1:A:89:SER:H	2.29	0.45
1:A:92:LEU:HD11	1:B:7:LEU:HD21	1.99	0.45
1:B:203:ASN:HD21	1:B:207:HIS:HE1	1.65	0.45
1:A:177:MET:HE3	1:A:177:MET:HB3	1.83	0.45
1:B:79:PHE:O	1:B:80:ASP:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:ARG:NH2	3:B:265:ATP:O2B	2.50	0.45
1:A:40:THR:OG1	1:B:40:THR:OG1	2.15	0.44
1:A:142:LEU:CB	1:A:213:GLU:HB2	2.47	0.44
1:B:3:GLN:N	1:B:5:ASP:H	2.15	0.44
1:B:11:MET:CG	1:B:71:GLN:CG	2.94	0.44
1:A:204:LEU:CD2	1:A:204:LEU:C	2.90	0.44
1:B:86:ALA:O	1:B:89:SER:HB2	2.17	0.44
1:A:35:TYR:CD2	1:A:35:TYR:N	2.85	0.44
1:A:234:VAL:O	1:A:237:ARG:HB2	2.17	0.44
1:B:195:GLY:C	1:B:197:LEU:N	2.74	0.44
1:B:228:ARG:O	1:B:229:GLU:C	2.60	0.44
1:A:80:ASP:C	1:A:82:ASN:N	2.70	0.44
1:A:216:LEU:O	1:A:216:LEU:HD12	2.17	0.44
1:B:88:ILE:O	1:B:88:ILE:CD1	2.62	0.44
1:A:15:ARG:HA	1:A:25:LYS:CG	2.46	0.44
1:B:31:THR:HG23	1:B:32:ILE:CD1	2.46	0.44
1:B:83:ASP:HA	1:B:86:ALA:HB2	1.99	0.44
1:A:14:LEU:HD22	1:A:24:ASP:CB	2.48	0.44
1:A:20:GLY:CA	1:A:21:CYS:HB3	2.39	0.44
1:A:191:GLU:O	1:A:192:GLU:C	2.58	0.44
1:B:170:TYR:C	1:B:172:GLU:N	2.72	0.44
1:A:9:THR:O	1:A:11:MET:CA	2.65	0.44
1:A:139:LEU:HA	1:A:139:LEU:HD23	1.59	0.44
1:A:203:ASN:HD22	1:A:203:ASN:HA	1.52	0.44
1:B:11:MET:HE1	1:B:64:PHE:CZ	2.52	0.44
1:B:60:GLY:O	1:B:64:PHE:N	2.49	0.44
1:B:234:VAL:O	1:B:235:ALA:C	2.58	0.43
1:A:61:ASP:O	1:A:64:PHE:HB3	2.19	0.43
1:B:158:ASP:OD1	1:B:159:TRP:N	2.51	0.43
1:A:226:ARG:NH1	3:B:265:ATP:O3'	2.51	0.43
1:A:246:LEU:HB2	1:A:249:MET:HG3	2.01	0.43
1:A:247:GLU:CA	1:A:248:THR:C	2.86	0.43
1:B:54:ASP:C	1:B:56:ARG:N	2.75	0.43
1:B:167:ASP:O	1:B:170:TYR:HB2	2.18	0.43
1:A:66:VAL:O	1:A:66:VAL:HG13	2.19	0.43
1:A:208:LEU:HD11	1:B:177:MET:HE1	2.00	0.43
1:B:194:MET:O	1:B:195:GLY:O	2.36	0.43
1:B:233:ILE:HD13	1:B:233:ILE:HG21	1.39	0.43
1:B:222:LYS:HD2	1:B:226:ARG:NH2	2.33	0.43
1:A:28:THR:HG22	4:A:267:HOH:O	2.18	0.43
1:A:32:ILE:HG13	1:A:68:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLN:O	1:A:150:LYS:C	2.56	0.43
1:A:216:LEU:CD2	1:B:142:LEU:HD23	2.48	0.43
1:A:148:ILE:HD12	1:B:220:ASN:HB3	1.99	0.43
1:A:246:LEU:O	1:A:250:GLU:N	2.49	0.43
1:B:173:ILE:O	1:B:174:ASP:C	2.62	0.43
1:A:208:LEU:HD21	1:B:176:VAL:HG12	2.00	0.43
1:B:84:ILE:C	1:B:86:ALA:N	2.75	0.43
1:B:179:GLU:HB3	1:B:190:LEU:HD22	2.00	0.43
1:B:214:ILE:O	1:B:217:GLN:CB	2.62	0.43
1:B:228:ARG:HH11	1:B:228:ARG:HD2	1.67	0.43
1:B:244:VAL:HG12	1:B:245:ASP:HB3	2.01	0.43
1:A:141:ALA:O	1:A:142:LEU:C	2.62	0.43
1:B:94:ARG:C	1:B:94:ARG:CD	2.92	0.43
1:B:160:THR:O	1:B:160:THR:OG1	2.30	0.43
1:A:21:CYS:SG	1:A:22:PRO:O	2.70	0.42
1:B:197:LEU:O	1:B:200:ALA:HB3	2.19	0.42
1:B:245:ASP:CG	1:B:247:GLU:H	2.27	0.42
1:A:170:TYR:C	1:A:172:GLU:H	2.27	0.42
1:B:3:GLN:O	1:B:7:LEU:N	2.37	0.42
1:B:84:ILE:O	1:B:86:ALA:N	2.52	0.42
1:B:90:ASP:N	1:B:93:GLU:OE2	2.52	0.42
1:A:3:GLN:HG3	1:B:82:ASN:OD1	2.19	0.42
1:B:216:LEU:HA	1:B:216:LEU:HD12	1.88	0.42
1:B:204:LEU:HD22	1:B:204:LEU:O	2.20	0.42
1:A:46:ALA:C	1:A:48:ALA:N	2.77	0.42
1:B:26:GLU:OE1	1:B:26:GLU:HA	2.19	0.42
1:B:30:ALA:N	1:B:32:ILE:N	2.66	0.42
1:A:14:LEU:CD2	1:A:14:LEU:C	2.93	0.42
1:B:83:ASP:O	1:B:84:ILE:O	2.38	0.42
1:B:237:ARG:HB2	1:B:239:LEU:HD12	2.01	0.42
1:B:166:VAL:O	1:B:168:LYS:N	2.53	0.42
1:B:64:PHE:O	1:B:67:VAL:CG2	2.63	0.42
1:B:152:CYS:O	1:B:155:VAL:HG12	2.19	0.42
1:B:64:PHE:CZ	1:B:68:PHE:HE1	2.38	0.42
1:A:7:LEU:C	1:A:9:THR:N	2.73	0.42
1:A:229:GLU:C	1:A:231:GLU:N	2.71	0.42
1:A:23:TRP:CH2	1:A:27:GLN:NE2	2.76	0.41
1:A:62:LEU:O	1:A:65:GLN:N	2.53	0.41
1:A:88:ILE:HG13	1:A:92:LEU:HG	2.01	0.41
1:A:189:LYS:HD2	1:A:189:LYS:HA	1.83	0.41
1:A:227:PHE:O	1:A:230:VAL:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:GLU:H	1:B:42:GLU:HG2	1.58	0.41
1:B:89:SER:C	1:B:93:GLU:OE1	2.63	0.41
1:A:161:THR:O	1:A:162:LEU:C	2.64	0.41
1:A:246:LEU:HD13	1:A:247:GLU:HG3	2.02	0.41
1:B:11:MET:CG	1:B:71:GLN:HG2	2.49	0.41
1:B:11:MET:HE1	1:B:64:PHE:CE1	2.55	0.41
1:B:64:PHE:CZ	1:B:68:PHE:CE1	3.08	0.41
1:A:146:GLN:NE2	1:A:212:ALA:N	2.39	0.41
1:A:246:LEU:HD13	1:A:246:LEU:N	2.30	0.41
1:A:162:LEU:O	1:A:166:VAL:HG23	2.20	0.41
1:A:235:ALA:C	1:A:237:ARG:N	2.79	0.41
1:B:7:LEU:HA	1:B:7:LEU:HD23	1.77	0.41
1:B:206:ARG:O	1:B:208:LEU:N	2.54	0.41
3:B:265:ATP:O2'	3:B:265:ATP:H8	1.98	0.41
1:A:194:MET:HE2	1:A:194:MET:HB2	1.48	0.41
1:A:224:GLU:OE2	1:B:132:LEU:HB3	2.20	0.41
1:B:71:GLN:O	1:B:75:GLU:HG3	2.21	0.41
1:B:214:ILE:HA	1:B:217:GLN:HB2	2.03	0.41
1:A:137:ARG:O	1:A:138:SER:C	2.63	0.41
1:A:230:VAL:O	1:A:233:ILE:HB	2.21	0.41
1:B:68:PHE:O	1:B:71:GLN:HB3	2.21	0.41
1:B:223:PHE:O	1:B:224:GLU:C	2.62	0.41
1:A:9:THR:HB	1:A:10:ILE:H	1.57	0.41
1:A:139:LEU:HA	1:A:140:PRO:HD3	1.79	0.41
1:B:7:LEU:CA	1:B:10:ILE:HD12	2.48	0.41
1:A:20:GLY:CA	1:A:21:CYS:CB	2.78	0.41
1:A:39:GLU:O	1:A:41:TYR:N	2.52	0.41
1:A:86:ALA:O	1:A:90:ASP:HB2	2.21	0.41
1:A:159:TRP:N	1:A:159:TRP:CD1	2.88	0.41
1:A:173:ILE:HD12	1:A:173:ILE:HG21	1.83	0.41
1:A:187:GLN:HA	1:A:187:GLN:NE2	2.34	0.41
1:B:7:LEU:HA	1:B:10:ILE:CD1	2.50	0.41
1:B:204:LEU:C	1:B:204:LEU:CD2	2.84	0.41
1:B:235:ALA:O	1:B:236:ALA:C	2.63	0.41
1:B:253:TRP:CD1	1:B:253:TRP:C	2.98	0.41
1:B:8:LEU:O	1:B:11:MET:N	2.49	0.41
1:B:136:PRO:HD2	1:B:139:LEU:CD1	2.51	0.41
1:B:154:ASN:O	1:B:156:GLY:N	2.54	0.41
1:B:201:THR:O	1:B:204:LEU:CB	2.69	0.41
1:B:255:GLN:CA	1:B:258:ARG:NH2	2.80	0.41
1:A:59:LEU:HD21	1:B:69:TYR:CD1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:ARG:HH11	1:A:233:ILE:HG13	1.82	0.40
1:B:63:LEU:O	1:B:64:PHE:C	2.61	0.40
1:B:146:GLN:HE21	1:B:146:GLN:HB2	1.72	0.40
1:B:185:VAL:HG12	1:B:186:ASP:N	2.36	0.40
1:A:216:LEU:HB3	1:B:141:ALA:HB1	2.02	0.40
1:B:193:GLU:OE2	1:B:193:GLU:HA	2.19	0.40
1:B:203:ASN:ND2	1:B:206:ARG:NH2	2.63	0.40
1:B:204:LEU:HD21	1:B:208:LEU:HD22	2.03	0.40
1:B:201:THR:O	1:B:204:LEU:N	2.54	0.40
1:B:214:ILE:O	1:B:215:ALA:C	2.63	0.40
1:B:234:VAL:O	1:B:237:ARG:N	2.35	0.40
1:A:60:GLY:HA3	1:B:88:ILE:CG2	2.51	0.40
1:A:74:GLN:NE2	1:A:80:ASP:HA	2.36	0.40
1:B:240:GLU:OE1	1:B:240:GLU:HA	2.22	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:LEU:CD2	1:B:250:GLU:OE2[4_456]	1.26	0.94
1:A:241:MET:CA	1:B:250:GLU:OE1[4_456]	1.61	0.59
1:A:239:LEU:CG	1:B:254:GLN:NE2[4_456]	2.06	0.14
1:A:241:MET:C	1:B:250:GLU:OE1[4_456]	2.11	0.09
1:A:239:LEU:CD1	1:B:254:GLN:NE2[4_456]	2.13	0.07
1:A:241:MET:CB	1:B:250:GLU:OE1[4_456]	2.19	0.01

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	219/265 (83%)	133 (61%)	57 (26%)	29 (13%)	0 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	214/265 (81%)	148 (69%)	33 (15%)	33 (15%)	0	0
All	All	433/530 (82%)	281 (65%)	90 (21%)	62 (14%)	0	1

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	THR
1	A	21	CYS
1	A	22	PRO
1	A	47	ILE
1	A	96	HIS
1	A	136	PRO
1	A	138	SER
1	A	170	TYR
1	A	207	HIS
1	A	236	ALA
1	A	237	ARG
1	A	259	GLN
1	B	4	ILE
1	B	9	THR
1	B	25	LYS
1	B	27	GLN
1	B	29	PHE
1	B	33	ALA
1	B	65	GLN
1	B	66	VAL
1	B	77	GLY
1	B	84	ILE
1	B	89	SER
1	B	90	ASP
1	B	129	HIS
1	B	130	SER
1	B	245	ASP
1	A	4	ILE
1	A	10	ILE
1	A	12	GLN
1	A	18	GLU
1	A	64	PHE
1	A	169	VAL
1	A	238	GLY
1	A	249	MET
1	B	13	ARG

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Mol	Chain	Res	Type
1	B	75	GLU
1	B	195	GLY
1	B	215	ALA
1	A	24	ASP
1	A	162	LEU
1	A	228	ARG
1	A	239	LEU
1	A	248	THR
1	B	79	PHE
1	B	85	CYS
1	B	155	VAL
1	B	182	GLN
1	B	188	ALA
1	B	239	LEU
1	B	256	VAL
1	A	57	GLY
1	A	70	ALA
1	A	240	GLU
1	B	61	ASP
1	B	8	LEU
1	B	30	ALA
1	A	173	ILE
1	B	87	ALA
1	B	214	ILE
1	B	148	ILE
1	B	234	VAL

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	193/226 (85%)	133 (69%)	60 (31%)	0	1
1	B	187/226 (83%)	124 (66%)	63 (34%)	0	1
All	All	380/452 (84%)	257 (68%)	123 (32%)	0	1

All (123) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	11	MET
1	A	12	GLN
1	A	18	GLU
1	A	22	PRO
1	A	23	TRP
1	A	31	THR
1	A	39	GLU
1	A	42	GLU
1	A	47	ILE
1	A	49	ARG
1	A	50	GLU
1	A	54	ASP
1	A	56	ARG
1	A	63	LEU
1	A	65	GLN
1	A	66	VAL
1	A	67	VAL
1	A	74	GLN
1	A	78	ARG
1	A	82	ASN
1	A	90	ASP
1	A	94	ARG
1	A	95	ARG
1	A	136	PRO
1	A	137	ARG
1	A	138	SER
1	A	139	LEU
1	A	143	MET
1	A	146	GLN
1	A	155	VAL
1	A	162	LEU
1	A	173	ILE
1	A	175	GLU
1	A	179	GLU
1	A	190	LEU
1	A	194	MET
1	A	201	THR
1	A	203	ASN
1	A	204	LEU
1	A	206	ARG
1	A	207	HIS
1	A	216	LEU

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Mol	Chain	Res	Type
1	A	217	GLN
1	A	218	LYS
1	A	221	GLU
1	A	222	LYS
1	A	224	GLU
1	A	226	ARG
1	A	231	GLU
1	A	232	ARG
1	A	233	ILE
1	A	237	ARG
1	A	240	GLU
1	A	242	THR
1	A	246	LEU
1	A	247	GLU
1	A	251	GLU
1	A	259	GLN
1	A	260	GLU
1	B	3	GLN
1	B	4	ILE
1	B	7	LEU
1	B	11	MET
1	B	12	GLN
1	B	13	ARG
1	B	14	LEU
1	B	23	TRP
1	B	26	GLU
1	B	27	GLN
1	B	29	PHE
1	B	31	THR
1	B	32	ILE
1	B	38	GLU
1	B	39	GLU
1	B	42	GLU
1	B	49	ARG
1	B	53	ASP
1	B	55	LEU
1	B	56	ARG
1	B	62	LEU
1	B	71	GLN
1	B	85	CYS
1	B	88	ILE
1	B	90	ASP

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Mol	Chain	Res	Type
1	B	91	LYS
1	B	94	ARG
1	B	128	GLN
1	B	129	HIS
1	B	135	ILE
1	B	139	LEU
1	B	146	GLN
1	B	150	LYS
1	B	160	THR
1	B	161	THR
1	B	165	VAL
1	B	166	VAL
1	B	168	LYS
1	B	175	GLU
1	B	184	VAL
1	B	189	LYS
1	B	190	LEU
1	B	197	LEU
1	B	201	THR
1	B	204	LEU
1	B	208	LEU
1	B	210	THR
1	B	214	ILE
1	B	217	GLN
1	B	220	ASN
1	B	221	GLU
1	B	228	ARG
1	B	232	ARG
1	B	233	ILE
1	B	234	VAL
1	B	239	LEU
1	B	241	MET
1	B	242	THR
1	B	244	VAL
1	B	245	ASP
1	B	251	GLU
1	B	259	GLN
1	B	261	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	82	ASN
1	A	96	HIS
1	A	146	GLN
1	A	182	GLN
1	A	187	GLN
1	A	203	ASN
1	A	217	GLN
1	B	65	GLN
1	B	71	GLN
1	B	82	ASN
1	B	146	GLN
1	B	154	ASN
1	B	203	ASN
1	B	255	GLN
1	B	259	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is 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
3	ATP	B	265	2	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)

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
3	ATP	B	265	2	1/1/7/7	2/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	265	ATP	C5-C4	4.70	1.47	1.39
3	B	265	ATP	C5-C6	2.79	1.48	1.41
3	B	265	ATP	C8-N7	2.35	1.36	1.31
3	B	265	ATP	C5-N7	-2.24	1.35	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	265	ATP	C5-C4-N3	-5.84	118.67	126.72
3	B	265	ATP	N3-C4-N9	4.60	134.99	127.17
3	B	265	ATP	C2-N3-C4	3.72	120.92	111.83
3	B	265	ATP	C4-C5-N7	-3.48	106.61	110.58
3	B	265	ATP	N3-C2-N1	-3.25	123.66	128.58
3	B	265	ATP	C4-N9-C8	2.55	108.42	105.74
3	B	265	ATP	C3'-C2'-C1'	2.54	106.28	101.46
3	B	265	ATP	C5-N7-C8	2.54	107.44	103.45
3	B	265	ATP	C6-C5-N7	2.07	136.09	132.09

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	265	ATP	C1'

All (2) torsion outliers are listed below:

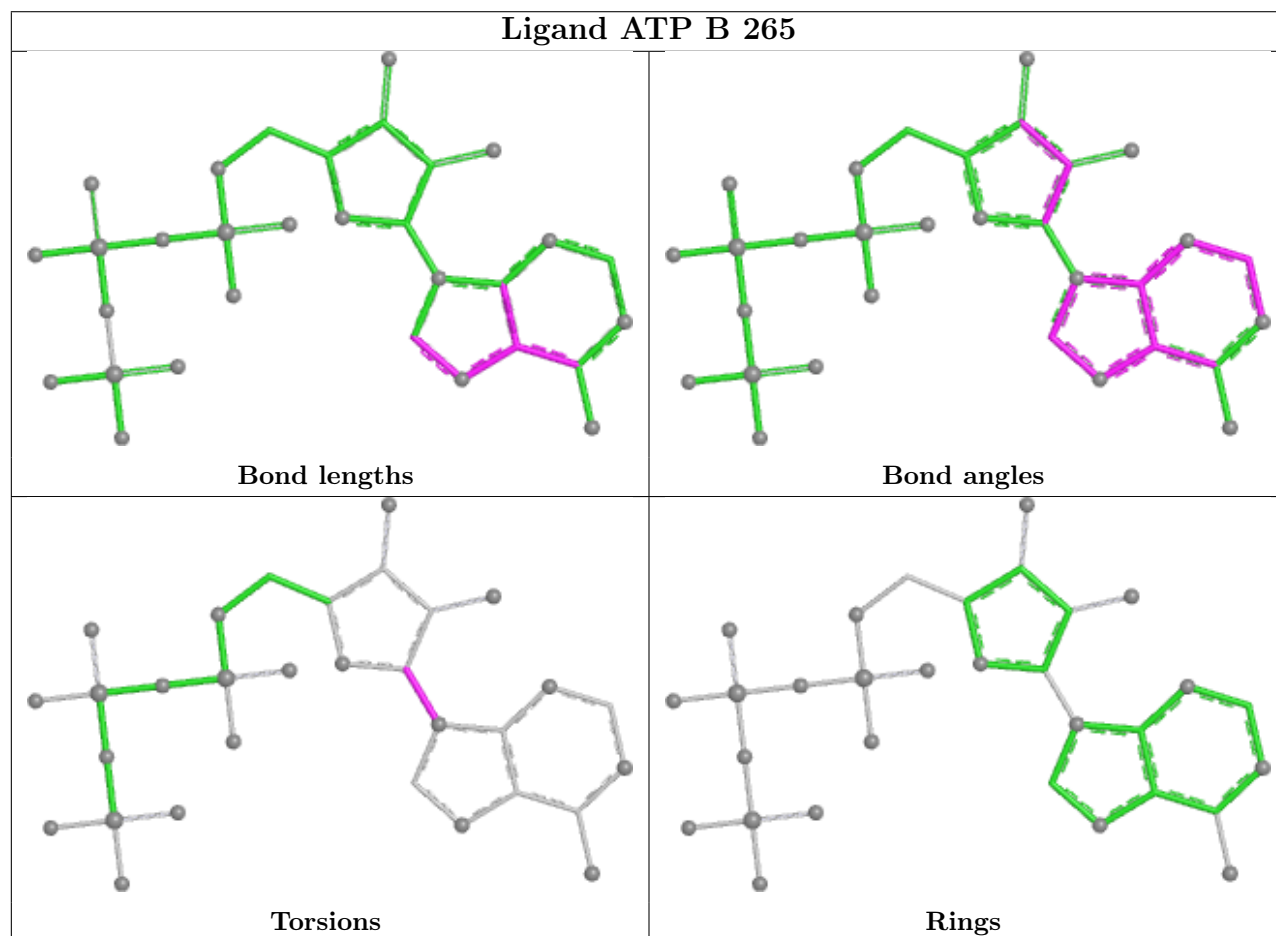
Mol	Chain	Res	Type	Atoms
3	B	265	ATP	O4'-C1'-N9-C4
3	B	265	ATP	O4'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	265	ATP	12	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, 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	225/265 (84%)	0.71	15 (6%) 24 12	14, 40, 77, 83	0
1	B	220/265 (83%)	0.60	14 (6%) 25 13	15, 38, 74, 79	0
All	All	445/530 (83%)	0.65	29 (6%) 25 13	14, 39, 76, 83	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	THR	6.3
1	A	241	MET	4.9
1	A	6	ARG	3.6
1	B	77	GLY	3.6
1	B	74	GLN	3.6
1	B	4	ILE	3.2
1	B	250	GLU	3.1
1	A	245	ASP	3.1
1	B	80	ASP	3.0
1	B	2	ASN	2.8
1	A	10	ILE	2.8
1	A	240	GLU	2.8
1	B	79	PHE	2.7
1	B	67	VAL	2.7
1	A	55	LEU	2.6
1	B	8	LEU	2.6
1	A	5	ASP	2.5
1	A	81	PHE	2.5
1	A	3	GLN	2.5
1	A	89	SER	2.5
1	B	261	ILE	2.4
1	B	92	LEU	2.4
1	A	7	LEU	2.3
1	B	83	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	97	PRO	2.2
1	A	2	ASN	2.1
1	A	238	GLY	2.1
1	B	85	CYS	2.1
1	B	5	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

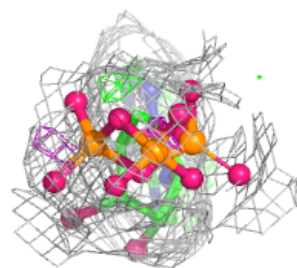
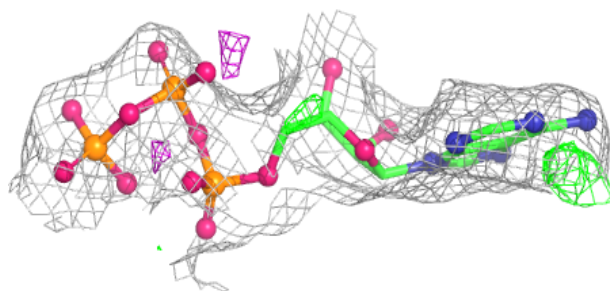
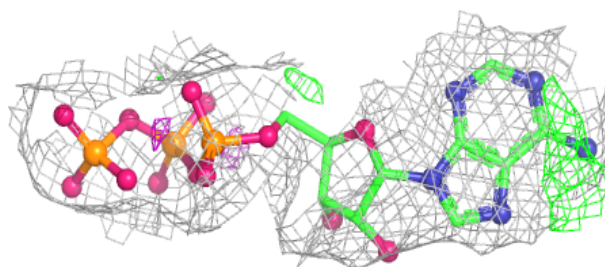
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ATP	B	265	31/31	0.71	0.18	73,80,106,108	0
2	MG	B	264	1/1	0.88	0.09	32,32,32,32	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.

Electron density around ATP B 265:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.