



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:38 PM UTC

PDB ID : 4UBF / pdb_00004ubf
Title : HsMCAK motor domain complex
Authors : Welburn, J.P.I.; Talapatra, S.K.
Deposited on : 2014-08-12
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

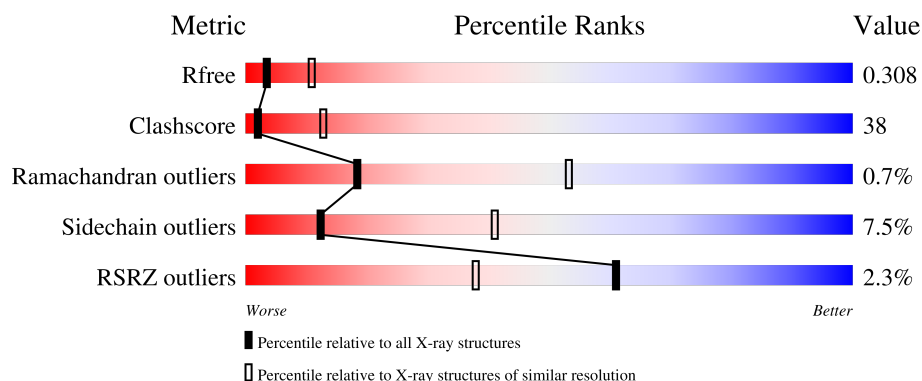
1 Overall quality at a glance

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	387	8% 43% 32% 20%
1	B	387	2% 40% 37% 5% 18%
1	C	387	2% 47% 34% 17%
1	D	387	3% 35% 40% 7% 17%
2	P	12	8% 25% 25% 42%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9707 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 Kinesin-like protein KIF2C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	3	0
			2322	1490	392	419	21			
1	B	319	Total	C	N	O	S	0	1	0
			2404	1537	412	434	21			
1	C	322	Total	C	N	O	S	0	1	0
			2412	1546	401	444	21			
1	D	322	Total	C	N	O	S	0	0	0
			2337	1501	389	428	19			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	MET	-	expression tag	UNP Q99661
A	208	GLY	-	expression tag	UNP Q99661
A	209	SER	-	expression tag	UNP Q99661
A	210	SER	-	expression tag	UNP Q99661
A	211	HIS	-	expression tag	UNP Q99661
A	212	HIS	-	expression tag	UNP Q99661
A	213	HIS	-	expression tag	UNP Q99661
A	214	HIS	-	expression tag	UNP Q99661
A	215	HIS	-	expression tag	UNP Q99661
A	216	HIS	-	expression tag	UNP Q99661
A	217	SER	-	expression tag	UNP Q99661
A	218	SER	-	expression tag	UNP Q99661
A	219	GLY	-	expression tag	UNP Q99661
A	220	LEU	-	expression tag	UNP Q99661
A	221	VAL	-	expression tag	UNP Q99661
A	222	PRO	-	expression tag	UNP Q99661
A	223	ARG	-	expression tag	UNP Q99661
A	224	GLY	-	expression tag	UNP Q99661
B	207	MET	-	expression tag	UNP Q99661
B	208	GLY	-	expression tag	UNP Q99661
B	209	SER	-	expression tag	UNP Q99661

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Chain	Residue	Modelled	Actual	Comment	Reference
B	210	SER	-	expression tag	UNP Q99661
B	211	HIS	-	expression tag	UNP Q99661
B	212	HIS	-	expression tag	UNP Q99661
B	213	HIS	-	expression tag	UNP Q99661
B	214	HIS	-	expression tag	UNP Q99661
B	215	HIS	-	expression tag	UNP Q99661
B	216	HIS	-	expression tag	UNP Q99661
B	217	SER	-	expression tag	UNP Q99661
B	218	SER	-	expression tag	UNP Q99661
B	219	GLY	-	expression tag	UNP Q99661
B	220	LEU	-	expression tag	UNP Q99661
B	221	VAL	-	expression tag	UNP Q99661
B	222	PRO	-	expression tag	UNP Q99661
B	223	ARG	-	expression tag	UNP Q99661
B	224	GLY	-	expression tag	UNP Q99661
C	207	MET	-	expression tag	UNP Q99661
C	208	GLY	-	expression tag	UNP Q99661
C	209	SER	-	expression tag	UNP Q99661
C	210	SER	-	expression tag	UNP Q99661
C	211	HIS	-	expression tag	UNP Q99661
C	212	HIS	-	expression tag	UNP Q99661
C	213	HIS	-	expression tag	UNP Q99661
C	214	HIS	-	expression tag	UNP Q99661
C	215	HIS	-	expression tag	UNP Q99661
C	216	HIS	-	expression tag	UNP Q99661
C	217	SER	-	expression tag	UNP Q99661
C	218	SER	-	expression tag	UNP Q99661
C	219	GLY	-	expression tag	UNP Q99661
C	220	LEU	-	expression tag	UNP Q99661
C	221	VAL	-	expression tag	UNP Q99661
C	222	PRO	-	expression tag	UNP Q99661
C	223	ARG	-	expression tag	UNP Q99661
C	224	GLY	-	expression tag	UNP Q99661
D	207	MET	-	expression tag	UNP Q99661
D	208	GLY	-	expression tag	UNP Q99661
D	209	SER	-	expression tag	UNP Q99661
D	210	SER	-	expression tag	UNP Q99661
D	211	HIS	-	expression tag	UNP Q99661
D	212	HIS	-	expression tag	UNP Q99661
D	213	HIS	-	expression tag	UNP Q99661
D	214	HIS	-	expression tag	UNP Q99661
D	215	HIS	-	expression tag	UNP Q99661

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Chain	Residue	Modelled	Actual	Comment	Reference
D	216	HIS	-	expression tag	UNP Q99661
D	217	SER	-	expression tag	UNP Q99661
D	218	SER	-	expression tag	UNP Q99661
D	219	GLY	-	expression tag	UNP Q99661
D	220	LEU	-	expression tag	UNP Q99661
D	221	VAL	-	expression tag	UNP Q99661
D	222	PRO	-	expression tag	UNP Q99661
D	223	ARG	-	expression tag	UNP Q99661
D	224	GLY	-	expression tag	UNP Q99661

- Molecule 2 is a protein called Kinesin-like protein KIF2C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	0	0	0
			48	27	8	13			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
4	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
4	C	1	Total 27	C 10	N 5	O 10	P 2	0	0
4	D	1	Total 27	C 10	N 5	O 10	P 2	0	0

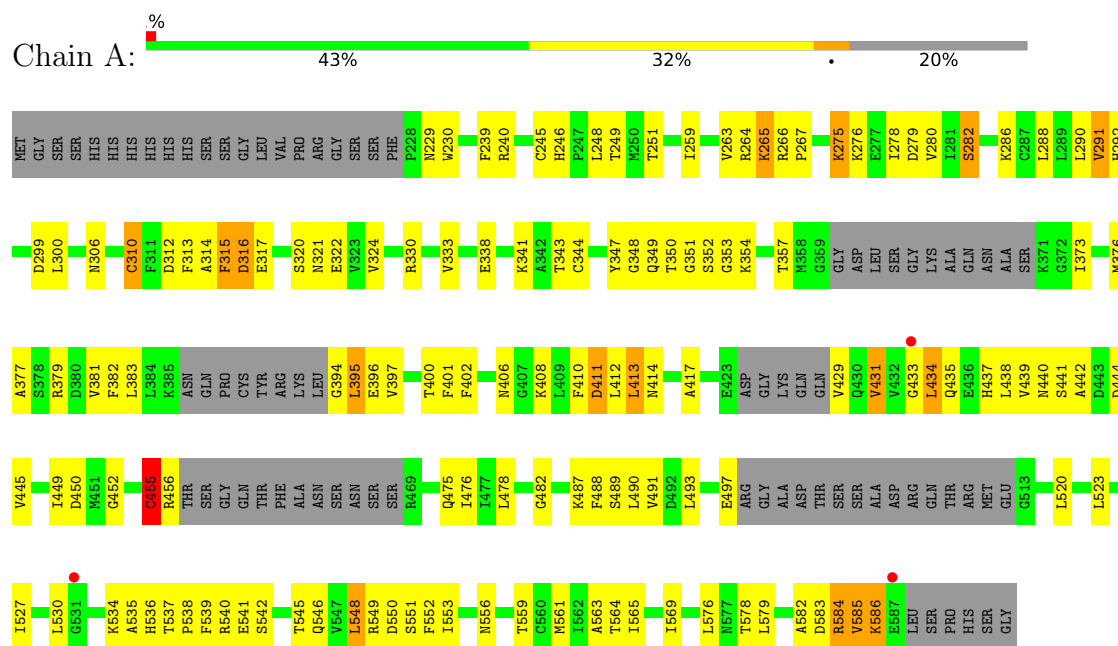
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	14	Total O 14 14	0	0
5	B	20	Total O 20 20	0	0
5	C	17	Total O 17 17	0	0
5	D	16	Total O 16 16	0	0
5	P	2	Total O 2 2	0	0

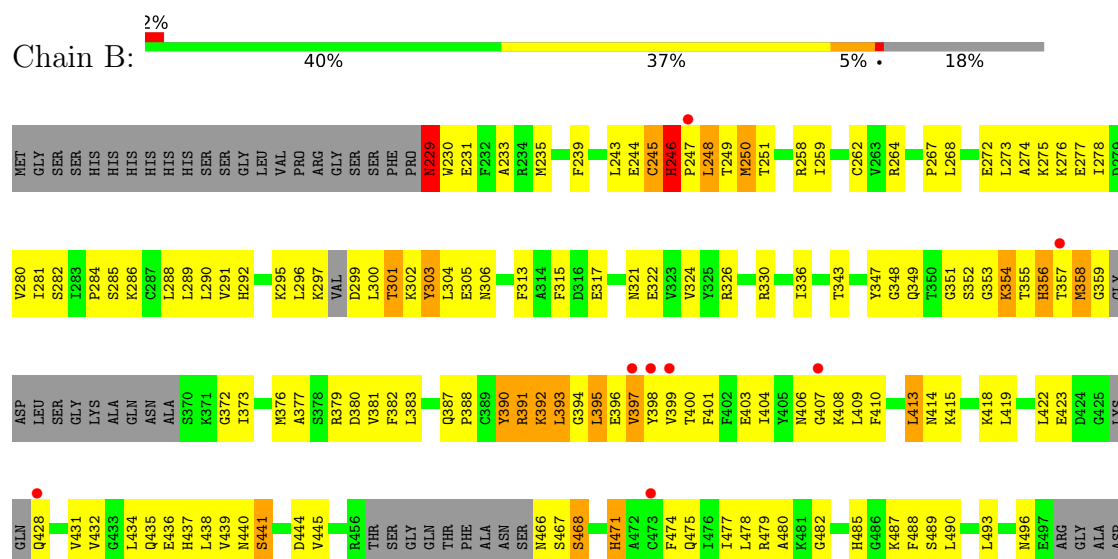
3 Residue-property plots

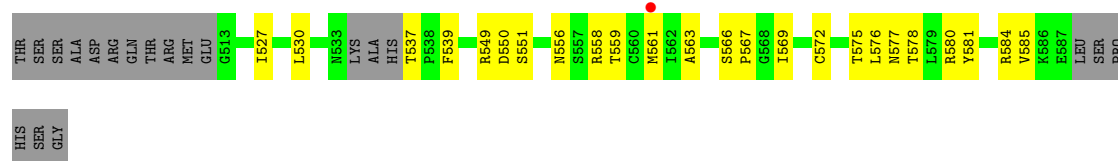
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Kinesin-like protein KIF2C

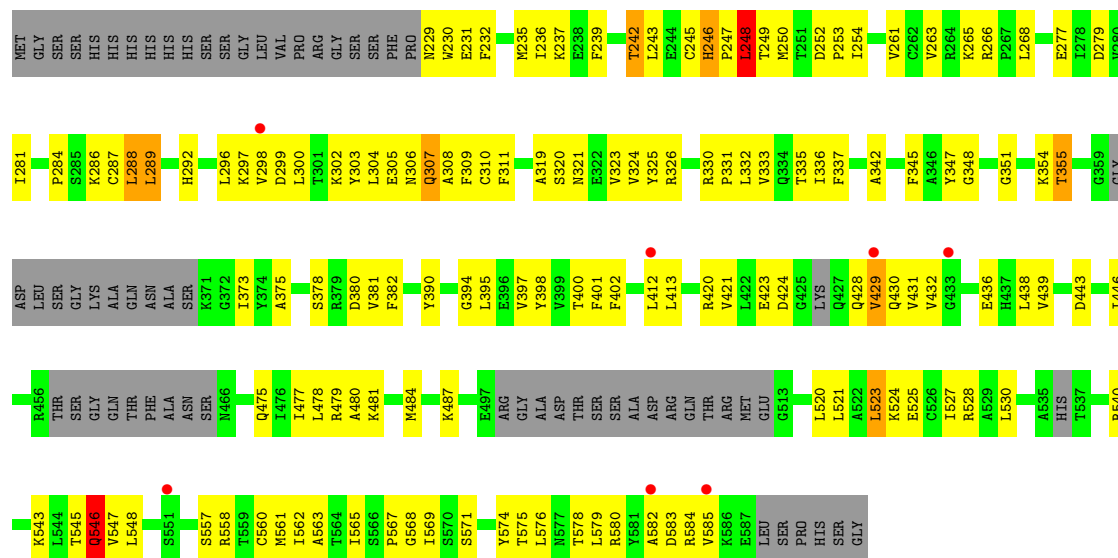


• Molecule 1: Kinesin-like protein KIF2C

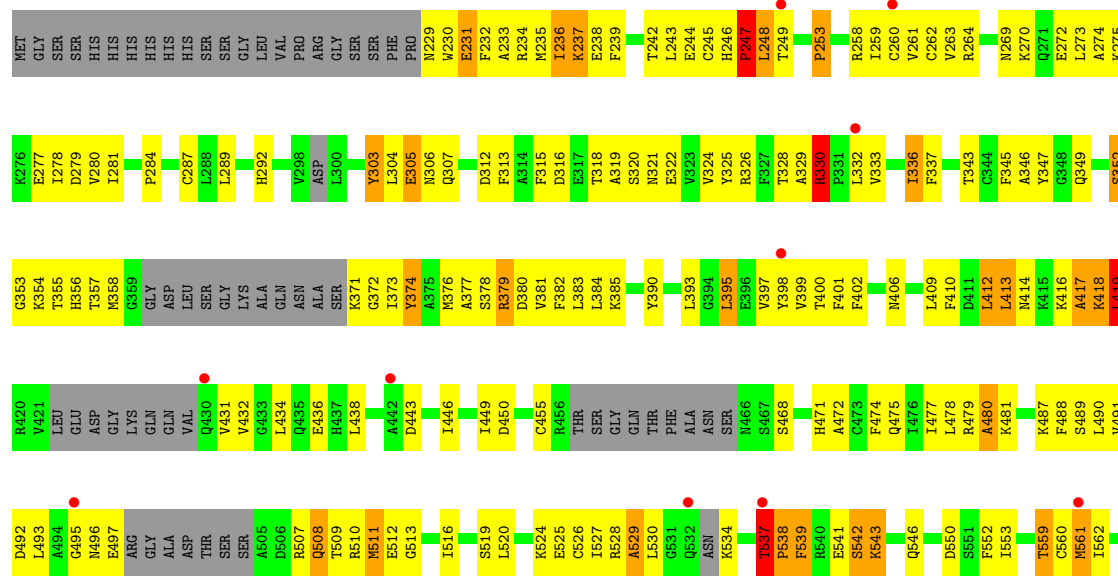




• Molecule 1: Kinesin-like protein KIF2C

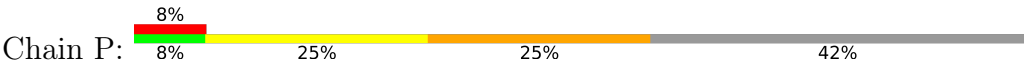


• Molecule 1: Kinesin-like protein KIF2C





● Molecule 2: Kinesin-like protein KIF2C



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.31Å 245.64Å 79.40Å 90.00° 95.84° 90.00°	Depositor
Resolution (Å)	29.49 – 3.00 29.49 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.49-3.00) 99.1 (29.49-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.264 , 0.286 (Not available) , 0.308	Depositor DCC
R_{free} test set	1761 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	77.5	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	9707	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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: MG, ADP

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	0.56	2/2368 (0.1%)	1.06	14/3198 (0.4%)
1	B	0.66	3/2443 (0.1%)	1.25	18/3295 (0.5%)
1	C	0.39	3/2451 (0.1%)	1.01	17/3307 (0.5%)
1	D	0.47	2/2372 (0.1%)	1.20	30/3208 (0.9%)
2	P	0.47	0/47	1.91	4/62 (6.5%)
All	All	0.53	10/9681 (0.1%)	1.14	83/13070 (0.6%)

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	B	0	2
1	C	0	1
1	D	0	2
All	All	0	5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	229	ASN	C-N	-24.10	0.99	1.33
1	A	455[A]	CYS	CA-C	9.62	1.65	1.52
1	A	455[B]	CYS	CA-C	9.62	1.65	1.52
1	B	356	HIS	CA-C	-7.16	1.44	1.52
1	C	246	HIS	C-N	5.42	1.40	1.33
1	D	247	PRO	N-CD	5.21	1.55	1.47
1	D	538	PRO	N-CD	5.10	1.54	1.47
1	C	253	PRO	N-CD	5.08	1.54	1.47
1	B	247	PRO	N-CD	5.07	1.54	1.47
1	C	247	PRO	N-CD	5.03	1.54	1.47

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	ASN	CA-C-N	24.46	168.25	121.54
1	B	229	ASN	C-N-CA	24.46	168.25	121.54
1	A	585	VAL	N-CA-C	-20.26	92.92	112.17
1	B	229	ASN	O-C-N	-19.85	91.24	123.00
1	D	491	VAL	N-CA-C	16.64	131.47	108.17
1	B	356	HIS	N-CA-C	-15.35	86.33	109.81
1	D	480	ALA	N-CA-C	13.11	125.58	111.03
1	C	546	GLN	N-CA-C	12.95	131.12	111.04
1	B	230	TRP	N-CA-C	12.04	136.45	110.80
1	D	561	MET	N-CA-C	10.70	127.65	107.75
1	D	508	GLN	N-CA-C	-10.52	92.33	108.31
1	B	230	TRP	N-CA-CB	-9.97	93.64	110.49
1	D	543	LYS	N-CA-C	-8.82	102.65	113.50
1	C	395	LEU	N-CA-C	8.71	123.38	110.48
1	A	411	ASP	N-CA-C	-8.59	94.90	108.90
1	D	542	SER	CB-CA-C	8.49	126.23	110.95
1	D	537	THR	C-N-CD	8.42	139.11	120.60
1	B	468	SER	N-CA-C	8.24	123.38	113.16
1	C	481	LYS	N-CA-C	-8.23	103.02	113.23
1	B	468	SER	N-CA-CB	-8.22	97.86	110.44
1	C	429	VAL	N-CA-C	8.10	126.18	109.34
1	D	419	LEU	N-CA-CB	8.06	124.15	110.77
1	B	392	LYS	N-CA-C	-8.03	99.93	110.53
1	D	559	THR	N-CA-C	8.02	120.92	108.96
1	A	585	VAL	N-CA-CB	7.99	122.90	112.28
1	C	289	LEU	N-CA-C	7.88	122.27	109.59
1	D	481	LYS	N-CA-C	-7.78	100.46	112.99
1	A	455[A]	CYS	CA-C-O	7.70	131.52	120.51
1	A	455[B]	CYS	CA-C-O	7.70	131.52	120.51
1	D	412	LEU	N-CA-C	-7.68	101.86	112.30
1	C	480	ALA	N-CA-C	7.14	122.49	111.56
1	C	246	HIS	CA-C-N	-7.13	113.36	120.98
1	C	246	HIS	C-N-CA	-7.13	113.36	120.98
1	A	433	GLY	N-CA-C	-7.01	105.41	115.64
1	D	480	ALA	CB-CA-C	-7.01	100.09	110.95
1	A	549	ARG	N-CA-C	6.87	121.79	113.41
1	D	330	ARG	CA-C-N	-6.86	111.27	119.84
1	D	330	ARG	C-N-CA	-6.86	111.27	119.84
1	C	547	VAL	N-CA-C	-6.82	102.07	111.89
1	A	482	GLY	N-CA-C	-6.63	105.75	115.63
1	C	546	GLN	N-CA-CB	-6.46	100.92	110.10
1	C	247	PRO	CB-CA-C	-6.44	100.27	110.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	354	LYS	N-CA-C	6.40	124.43	110.80
1	B	301	THR	N-CA-C	-6.38	98.84	109.24
1	C	248	LEU	N-CA-C	6.14	119.25	110.10
2	P	713	GLN	N-CA-C	6.14	118.95	109.07
1	D	529	ALA	N-CA-C	6.10	117.93	111.28
2	P	715	SER	N-CA-C	6.04	123.67	110.80
1	A	584	ARG	CB-CA-C	-6.01	101.92	111.48
1	A	584	ARG	CA-C-N	-5.99	113.35	122.76
1	A	584	ARG	C-N-CA	-5.99	113.35	122.76
1	B	390	TYR	N-CA-C	-5.78	104.41	113.02
1	D	585	VAL	N-CA-C	-5.72	107.41	112.90
1	D	431	VAL	N-CA-C	5.67	118.10	108.86
1	D	511	MET	N-CA-C	-5.63	98.80	110.80
1	D	418	LYS	N-CA-C	-5.60	98.87	110.80
1	D	374	TYR	N-CA-C	-5.56	105.14	111.14
1	D	491	VAL	N-CA-CB	-5.49	103.79	111.25
1	B	467	SER	CB-CA-C	5.45	122.16	110.21
1	D	418	LYS	CB-CA-C	5.43	121.23	110.42
1	C	430	GLN	N-CA-C	5.33	122.16	110.80
1	D	481	LYS	N-CA-CB	5.30	122.61	111.10
1	D	246	HIS	CA-C-N	-5.26	113.26	119.84
1	D	246	HIS	C-N-CA	-5.26	113.26	119.84
1	D	253	PRO	CB-CA-C	-5.26	102.88	111.56
2	P	710	LEU	CA-C-N	5.25	131.15	121.70
2	P	710	LEU	C-N-CA	5.25	131.15	121.70
1	A	565	ILE	N-CA-C	5.22	117.57	108.95
1	D	416	LYS	CB-CA-C	-5.21	101.53	111.48
1	B	415	LYS	N-CA-C	-5.19	102.65	110.70
1	C	252	ASP	CA-C-N	-5.19	113.35	119.84
1	C	252	ASP	C-N-CA	-5.19	113.35	119.84
1	D	566	SER	CA-C-N	5.19	125.27	119.87
1	D	566	SER	C-N-CA	5.19	125.27	119.87
1	B	246	HIS	CA-C-N	-5.16	113.39	119.84
1	B	246	HIS	C-N-CA	-5.16	113.39	119.84
1	B	585	VAL	CB-CA-C	5.11	116.55	110.93
1	C	394	GLY	N-CA-C	5.07	125.21	113.18
1	C	288	LEU	N-CA-C	5.04	116.74	108.52
1	A	316	ASP	N-CA-C	5.03	118.34	109.80
1	B	441	SER	N-CA-C	5.02	117.59	109.40
1	D	417	ALA	N-CA-CB	-5.00	102.63	110.79
1	A	586	LYS	N-CA-C	-5.00	106.02	111.82

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	229	ASN	Mainchain,Peptide
1	C	560[A]	CYS	Mainchain
1	D	330	ARG	Peptide
1	D	510	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	2322	0	2270	122	0
1	B	2404	0	2346	228	0
1	C	2412	0	2331	139	0
1	D	2337	0	2214	235	0
2	P	48	0	33	5	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	27	0	12	5	0
4	B	27	0	12	1	0
4	C	27	0	12	3	0
4	D	27	0	12	7	0
5	A	14	0	0	1	0
5	B	20	0	0	3	0
5	C	17	0	0	6	0
5	D	16	0	0	7	0
5	P	2	0	0	1	0
All	All	9707	0	9242	719	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 38.

All (719) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:413:LEU:HD12	1:B:437:HIS:CD2	1.14	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:413:LEU:CD1	1:B:437:HIS:HD2	1.02	1.59
1:D:395:LEU:HD12	1:D:480:ALA:CA	1.25	1.55
1:D:395:LEU:CD1	1:D:480:ALA:HA	1.36	1.51
1:D:384:LEU:HD21	1:D:390:TYR:CE2	1.48	1.47
1:C:250:MET:HG2	1:C:326:ARG:NH1	1.31	1.45
1:B:409:LEU:CD1	1:B:419:LEU:HB2	1.43	1.44
1:D:235:MET:CE	1:D:304:LEU:HD13	1.47	1.43
1:B:413:LEU:CD1	1:B:437:HIS:CD2	1.80	1.39
1:B:245:CYS:CB	1:B:284:PRO:HA	1.54	1.37
1:C:250:MET:CG	1:C:326:ARG:HH11	1.42	1.31
1:B:397:VAL:HG23	1:B:439:VAL:O	1.29	1.26
1:B:245:CYS:HB3	1:B:284:PRO:CA	1.66	1.23
1:C:524:LYS:HG3	1:C:585:VAL:CG2	1.68	1.23
1:C:250:MET:CG	1:C:326:ARG:NH1	2.00	1.21
1:D:345:PHE:HB2	1:D:561:MET:SD	1.82	1.18
1:B:397:VAL:O	1:B:438:LEU:HD12	1.02	1.18
1:B:245:CYS:CB	1:B:284:PRO:CA	2.19	1.17
1:C:524:LYS:CG	1:C:585:VAL:HG22	1.74	1.17
1:B:397:VAL:O	1:B:438:LEU:CD1	1.93	1.16
1:D:393:LEU:HB3	1:D:395:LEU:HD21	1.14	1.14
1:B:245:CYS:HB3	1:B:284:PRO:CB	1.78	1.12
1:B:388:PRO:HA	1:B:391:ARG:HD3	1.30	1.10
1:D:235:MET:HE3	1:D:304:LEU:CD1	1.80	1.10
1:D:349:GLN:HA	1:D:496:ASN:OD1	1.52	1.10
1:B:388:PRO:HA	1:B:391:ARG:CD	1.81	1.10
1:C:429:VAL:O	1:C:429:VAL:HG22	1.50	1.10
1:B:245:CYS:HB2	1:B:284:PRO:HA	1.32	1.09
1:B:409:LEU:HD11	1:B:419:LEU:CB	1.82	1.09
4:D:602:ADP:O1B	5:D:701:HOH:O	1.68	1.08
1:C:524:LYS:HG3	1:C:585:VAL:HG22	1.12	1.08
1:D:395:LEU:CD1	1:D:480:ALA:CA	2.07	1.08
1:D:384:LEU:CD2	1:D:390:TYR:CE2	2.37	1.06
1:C:250:MET:HG3	1:C:326:ARG:HH11	1.21	1.06
1:D:235:MET:CE	1:D:304:LEU:CD1	2.34	1.06
1:D:400:THR:HG22	1:D:436:GLU:HA	1.33	1.05
2:P:712:GLU:OE2	5:P:801:HOH:O	1.76	1.04
1:D:280:VAL:HG13	1:D:569:ILE:CD1	1.88	1.04
1:B:413:LEU:HD11	1:B:437:HIS:HD2	1.20	1.03
1:B:409:LEU:HD11	1:B:419:LEU:HB2	1.06	1.02
1:C:528:ARG:NH1	1:C:584:ARG:O	1.90	1.02
1:C:250:MET:HG2	1:C:326:ARG:HH12	1.20	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:ILE:HD13	1:B:559:THR:HG22	1.42	1.00
1:B:539:PHE:CD2	1:B:549:ARG:HD2	1.96	1.00
1:D:418:LYS:O	1:D:419:LEU:HD22	1.62	1.00
1:C:325:TYR:HB2	1:C:373:ILE:HD12	1.39	1.00
1:C:429:VAL:HG11	1:C:546:GLN:HG3	1.38	0.99
1:C:331:PRO:O	5:C:701:HOH:O	1.79	0.99
1:B:353:GLY:O	1:B:356:HIS:O	1.81	0.99
1:A:379:ARG:HG2	1:A:442:ALA:HB2	1.44	0.99
1:B:233:ALA:HA	1:B:278:ILE:HD11	1.42	0.99
1:B:409:LEU:CD1	1:B:419:LEU:CB	2.39	0.99
1:B:431:VAL:HG22	1:B:432:VAL:H	1.29	0.98
1:C:330:ARG:O	5:C:702:HOH:O	1.81	0.98
1:D:322:GLU:HA	1:D:376:MET:HE1	1.42	0.98
1:B:264:ARG:HH11	1:B:357:THR:HG23	1.30	0.96
1:D:384:LEU:HD21	1:D:390:TYR:CD2	1.99	0.96
1:D:542:SER:O	1:D:546:GLN:NE2	1.97	0.96
1:D:384:LEU:CD2	1:D:390:TYR:CD2	2.49	0.95
1:C:250:MET:O	1:C:326:ARG:NH1	1.98	0.95
1:B:397:VAL:CG2	1:B:439:VAL:O	2.12	0.95
1:D:395:LEU:HD12	1:D:480:ALA:CB	1.98	0.94
1:B:413:LEU:HD12	1:B:437:HIS:NE2	1.83	0.93
1:A:341:LYS:HG3	1:A:487:LYS:HB3	1.51	0.92
1:D:393:LEU:HB3	1:D:395:LEU:CD2	1.99	0.92
1:C:561:MET:O	1:C:562:ILE:N	2.02	0.92
1:B:413:LEU:HD13	1:B:437:HIS:CD2	2.02	0.91
1:D:235:MET:HE3	1:D:304:LEU:HD13	0.91	0.91
1:B:233:ALA:HA	1:B:278:ILE:CD1	2.01	0.91
1:D:542:SER:O	1:D:546:GLN:CD	2.15	0.90
1:D:395:LEU:H	1:D:395:LEU:HD22	1.35	0.89
1:C:420:ARG:O	1:C:432:VAL:HG22	1.72	0.89
1:D:384:LEU:CD2	1:D:390:TYR:HE2	1.80	0.88
1:D:493:LEU:HD22	1:D:520:LEU:HD21	1.54	0.88
1:B:398:TYR:CE2	1:B:438:LEU:HB2	2.08	0.88
1:D:235:MET:HE1	1:D:304:LEU:HD13	1.56	0.88
1:D:280:VAL:HG13	1:D:569:ILE:HD12	1.53	0.88
1:B:377:ALA:O	1:B:381:VAL:HG23	1.74	0.87
1:B:550:ASP:OD1	1:B:551:SER:N	2.07	0.87
1:D:345:PHE:CB	1:D:561:MET:SD	2.61	0.87
1:D:400:THR:OG1	1:D:475:GLN:NE2	2.05	0.87
1:B:409:LEU:HD13	1:B:419:LEU:HB2	1.54	0.86
1:D:400:THR:HG22	1:D:436:GLU:CA	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:VAL:HG13	1:D:569:ILE:HD13	1.56	0.86
1:D:347:TYR:HB2	1:D:493:LEU:HD13	1.56	0.86
1:D:377:ALA:O	1:D:381:VAL:HG23	1.75	0.85
1:A:248:LEU:HD21	1:A:315:PHE:HB3	1.58	0.85
1:A:379:ARG:CG	1:A:442:ALA:HB2	2.07	0.84
1:B:248:LEU:HB2	1:B:286:LYS:HB2	1.59	0.84
1:B:398:TYR:HA	1:B:438:LEU:HA	1.57	0.84
1:B:248:LEU:HD12	1:B:286:LYS:HG3	1.59	0.83
1:B:395:LEU:HD12	1:B:395:LEU:H	1.43	0.83
1:A:542:SER:OG	1:A:545:THR:HG23	1.77	0.83
1:C:429:VAL:O	1:C:429:VAL:CG2	2.25	0.83
1:C:248:LEU:CD1	1:C:286:LYS:HA	2.09	0.82
1:A:429:VAL:HG11	1:A:546:GLN:O	1.79	0.81
1:B:423:GLU:HB2	1:B:428:GLN:O	1.78	0.81
1:D:400:THR:CG2	1:D:436:GLU:HG2	2.10	0.81
1:D:395:LEU:HD22	1:D:395:LEU:N	1.93	0.81
1:B:248:LEU:HD12	1:B:286:LYS:CD	2.10	0.81
1:D:245:CYS:SG	1:D:247:PRO:HD3	2.20	0.81
1:D:395:LEU:HB3	1:D:479:ARG:O	1.79	0.81
1:A:412:LEU:HD13	1:A:452:GLY:O	1.81	0.80
1:B:358:MET:O	1:B:373:ILE:N	2.13	0.80
1:D:534:LYS:NZ	5:D:702:HOH:O	2.14	0.80
1:C:248:LEU:HD13	1:C:286:LYS:HA	1.62	0.80
1:D:395:LEU:CD1	1:D:480:ALA:CB	2.58	0.80
1:D:537:THR:OG1	1:D:539:PHE:N	2.14	0.80
1:D:393:LEU:CB	1:D:395:LEU:HD21	2.06	0.79
1:C:245:CYS:HB2	1:C:284:PRO:HA	1.64	0.79
1:C:325:TYR:HB2	1:C:373:ILE:CD1	2.12	0.79
1:C:400:THR:OG1	1:C:475:GLN:HB2	1.83	0.79
1:B:539:PHE:HB3	5:B:706:HOH:O	1.82	0.79
1:D:355:THR:HG22	1:D:492:ASP:OD2	1.83	0.79
1:B:408:LYS:O	1:B:410:PHE:CE2	2.35	0.79
1:A:402:PHE:HB2	1:A:410:PHE:O	1.83	0.78
1:D:379:ARG:HG2	1:D:379:ARG:HH11	1.47	0.78
1:B:233:ALA:HB2	1:B:278:ILE:HD12	1.66	0.78
1:A:266:ARG:HD2	1:A:352:SER:O	1.83	0.78
1:D:395:LEU:HD13	1:D:480:ALA:HA	1.57	0.78
1:A:382:PHE:HZ	1:A:439:VAL:HG23	1.49	0.77
1:B:399:VAL:N	1:B:437:HIS:O	2.16	0.77
1:D:322:GLU:CA	1:D:376:MET:HE1	2.14	0.77
1:B:245:CYS:CB	1:B:284:PRO:O	2.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:CYS:HB2	1:B:284:PRO:CA	2.02	0.76
2:P:711:GLU:HB2	2:P:712:GLU:HG3	1.67	0.76
1:C:250:MET:HE3	1:C:323:VAL:HG12	1.66	0.76
1:D:322:GLU:HA	1:D:376:MET:CE	2.15	0.76
1:B:248:LEU:HD12	1:B:286:LYS:CG	2.15	0.76
1:B:245:CYS:SG	1:B:284:PRO:HA	2.26	0.75
1:C:307:GLN:OE1	1:C:580:ARG:NH2	2.19	0.75
1:B:431:VAL:HG22	1:B:432:VAL:N	2.02	0.74
1:B:248:LEU:O	1:B:248:LEU:HD23	1.87	0.74
1:A:343:THR:HG22	1:A:489:SER:HB2	1.70	0.74
1:B:410:PHE:CE1	1:B:418:LYS:CG	2.70	0.74
1:B:295:LYS:NZ	1:B:305:GLU:OE1	2.18	0.74
1:B:245:CYS:HB2	1:B:284:PRO:O	1.88	0.74
1:A:412:LEU:HD22	1:A:455[B]:CYS:SG	2.28	0.73
1:B:391:ARG:HB3	1:B:391:ARG:NH1	2.03	0.73
1:B:259:ILE:HD11	1:B:530:LEU:HD23	1.71	0.73
1:B:245:CYS:CB	1:B:284:PRO:C	2.62	0.73
1:C:524:LYS:HG2	1:C:585:VAL:HG22	1.69	0.72
1:B:379:ARG:HG3	1:B:380:ASP:N	2.05	0.72
1:B:400:THR:CG2	1:B:475:GLN:HB2	2.19	0.72
1:B:282:SER:HB2	1:B:290:LEU:HB2	1.72	0.72
1:C:232:PHE:HE1	1:C:302:LYS:HB3	1.53	0.72
1:C:250:MET:O	1:C:326:ARG:CZ	2.38	0.72
1:D:231:GLU:O	1:D:234:ARG:HG2	1.90	0.72
1:B:243:LEU:HG	1:B:245:CYS:SG	2.30	0.71
1:B:259:ILE:CD1	1:B:559:THR:HG22	2.18	0.71
1:D:333:VAL:HG11	1:D:380:ASP:OD1	1.91	0.71
1:D:354:LYS:NZ	1:D:495:GLY:HA2	2.06	0.71
1:A:352:SER:N	4:A:602:ADP:O3B	2.23	0.71
1:A:379:ARG:HG2	1:A:442:ALA:CB	2.19	0.71
1:D:384:LEU:HD21	1:D:390:TYR:HE2	0.88	0.71
1:D:474:PHE:O	1:D:490:LEU:N	2.21	0.71
1:B:248:LEU:CD1	1:B:286:LYS:HG3	2.22	0.70
1:B:348:GLY:H	1:B:354:LYS:HD3	1.56	0.70
1:B:264:ARG:NH1	1:B:357:THR:HG23	2.05	0.70
1:B:296:LEU:HD11	1:B:302:LYS:HA	1.74	0.70
1:B:233:ALA:CB	1:B:278:ILE:HD12	2.21	0.70
1:B:387:GLN:O	1:B:391:ARG:CG	2.40	0.70
1:D:278:ILE:HG12	1:D:279:ASP:H	1.56	0.70
1:D:322:GLU:O	1:D:326:ARG:HG3	1.92	0.70
1:D:236:ILE:N	1:D:236:ILE:HD12	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:CYS:HB2	1:B:284:PRO:C	2.17	0.69
1:B:280:VAL:HG21	1:B:572:CYS:SG	2.31	0.69
1:C:288:LEU:HD12	1:C:309:PHE:O	1.93	0.69
1:D:384:LEU:CD2	1:D:390:TYR:HD2	2.03	0.69
1:D:543:LYS:HD2	1:D:546:GLN:HE22	1.56	0.69
1:C:310:CYS:SG	1:D:243:LEU:HB2	2.33	0.69
1:D:259:ILE:HG22	1:D:261:VAL:HG23	1.75	0.69
1:D:262:CYS:HB2	1:D:313:PHE:O	1.92	0.69
1:B:321:ASN:O	1:B:324:VAL:HG12	1.93	0.69
1:A:347:TYR:HB2	1:A:493:LEU:HD12	1.73	0.69
1:B:359:GLY:HA2	1:B:372:GLY:HA3	1.75	0.69
1:D:382:PHE:HE1	1:D:397:VAL:HG21	1.58	0.68
1:B:392:LYS:O	1:B:393:LEU:HD12	1.94	0.68
1:D:395:LEU:HD12	1:D:480:ALA:HA	0.69	0.68
1:D:529:ALA:HB3	1:D:537:THR:O	1.93	0.68
1:B:315:PHE:CE1	1:B:324:VAL:HA	2.28	0.68
1:D:418:LYS:O	1:D:419:LEU:CD2	2.41	0.68
1:B:292:HIS:CB	1:B:304:LEU:HD11	2.23	0.68
1:B:330:ARG:NH2	1:B:380:ASP:OD2	2.27	0.68
1:C:436:GLU:N	1:C:436:GLU:OE1	2.25	0.67
1:B:376:MET:HA	1:B:379:ARG:HG2	1.76	0.67
1:C:429:VAL:CG1	1:C:546:GLN:HG3	2.21	0.67
1:A:344:CYS:HB3	1:A:490:LEU:HD23	1.75	0.67
1:D:325:TYR:OH	1:D:377:ALA:HA	1.95	0.67
1:B:245:CYS:HB3	1:B:284:PRO:HB2	1.71	0.67
2:P:710:LEU:N	2:P:711:GLU:HB3	2.10	0.67
1:A:349:GLN:O	1:A:354:LYS:NZ	2.28	0.66
1:C:229:ASN:ND2	5:C:703:HOH:O	2.15	0.66
1:C:443:ASP:HA	1:C:446:ILE:HG22	1.77	0.66
1:D:543:LYS:HA	1:D:546:GLN:NE2	2.11	0.66
1:D:529:ALA:CB	1:D:537:THR:O	2.43	0.66
1:B:292:HIS:HB3	1:B:304:LEU:HD21	1.77	0.66
1:D:400:THR:HG21	1:D:436:GLU:HG2	1.76	0.66
1:A:229:ASN:OD1	1:A:230:TRP:N	2.29	0.66
1:B:244:GLU:O	1:B:244:GLU:HG3	1.94	0.66
1:B:391:ARG:CG	1:B:391:ARG:HH11	2.09	0.66
1:D:280:VAL:CG1	1:D:569:ILE:HD12	2.23	0.66
1:D:349:GLN:OE1	1:D:571:SER:OG	2.13	0.66
1:D:395:LEU:HD12	1:D:480:ALA:N	2.07	0.66
1:D:398:TYR:HB3	1:D:477:ILE:HD12	1.77	0.65
1:D:513:GLY:H	1:D:516:ILE:HG13	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:245:CYS:HB2	1:D:284:PRO:HA	1.76	0.65
1:D:354:LYS:HB3	1:D:492:ASP:OD1	1.96	0.65
1:B:391:ARG:HH11	1:B:391:ARG:HG2	1.61	0.65
1:A:411:ASP:OD2	1:A:435:GLN:HB2	1.97	0.65
1:D:537:THR:OG1	1:D:538:PRO:HA	1.97	0.65
1:A:266:ARG:CD	1:A:352:SER:O	2.45	0.65
1:B:303:TYR:O	5:B:702:HOH:O	2.14	0.65
1:C:527:ILE:HG21	1:C:585:VAL:HG11	1.79	0.65
1:B:354:LYS:C	1:B:356:HIS:O	2.40	0.64
1:A:379:ARG:CG	1:A:442:ALA:CB	2.75	0.64
1:B:398:TYR:CD2	1:B:438:LEU:HB2	2.31	0.64
1:B:561:MET:HE1	1:B:581:TYR:CE1	2.32	0.64
1:B:487:LYS:NZ	1:B:489:SER:OG	2.28	0.64
1:D:320:SER:OG	1:D:321:ASN:N	2.29	0.64
1:D:395:LEU:CD2	1:D:395:LEU:H	2.09	0.64
1:B:399:VAL:HG21	1:B:439:VAL:HG11	1.79	0.64
1:A:411:ASP:OD1	1:A:413:LEU:HB2	1.97	0.64
1:C:355:THR:OG1	4:C:602:ADP:O2B	2.14	0.64
1:B:382:PHE:HE2	1:B:440:ASN:C	2.05	0.64
1:C:527:ILE:CG2	1:C:585:VAL:HG11	2.28	0.63
1:B:292:HIS:HB3	1:B:304:LEU:HD11	1.79	0.63
1:D:380:ASP:OD1	1:D:381:VAL:N	2.32	0.63
1:A:394:GLY:O	1:A:395:LEU:HD12	1.98	0.63
1:A:400:THR:HB	1:A:475:GLN:HB2	1.80	0.63
1:A:583:ASP:OD1	1:A:586:LYS:NZ	2.31	0.63
1:D:277:GLU:HG2	1:D:569:ILE:HG12	1.80	0.63
1:A:320:SER:OG	1:A:321:ASN:N	2.29	0.63
1:A:379:ARG:O	1:A:383:LEU:N	2.32	0.63
1:B:259:ILE:HD11	1:B:530:LEU:CD2	2.29	0.63
1:A:240:ARG:NH2	1:A:279:ASP:OD1	2.26	0.62
1:C:330:ARG:NH2	1:C:380:ASP:OD2	2.32	0.62
1:D:236:ILE:HD12	1:D:236:ILE:H	1.63	0.62
1:A:439:VAL:HG12	1:A:444:ASP:HB3	1.81	0.62
1:B:441:SER:O	1:B:444:ASP:HB2	2.00	0.62
1:D:399:VAL:HG11	1:D:474:PHE:CZ	2.34	0.62
1:D:418:LYS:O	1:D:419:LEU:HD13	1.99	0.62
1:B:297:LYS:HG3	1:B:299:ASP:OD1	1.99	0.62
1:B:267:PRO:HA	1:B:317:GLU:HB2	1.80	0.62
1:B:406:ASN:C	1:B:408:LYS:H	2.07	0.62
1:B:245:CYS:HB3	1:B:284:PRO:C	2.22	0.62
1:D:395:LEU:CA	1:D:479:ARG:O	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:395:LEU:CB	1:D:479:ARG:O	2.47	0.62
1:B:233:ALA:CA	1:B:278:ILE:CD1	2.75	0.62
1:C:524:LYS:CG	1:C:585:VAL:CG2	2.52	0.62
1:B:355:THR:HG22	1:B:355:THR:O	2.01	0.61
1:B:410:PHE:CD1	1:B:418:LYS:CG	2.83	0.61
1:C:243:LEU:HD12	1:D:287:CYS:SG	2.39	0.61
1:D:526:CYS:SG	1:D:537:THR:HB	2.40	0.61
1:B:388:PRO:HA	1:B:391:ARG:HD2	1.75	0.61
1:D:384:LEU:HD23	1:D:390:TYR:HD2	1.63	0.61
1:A:229:ASN:HB2	1:D:383:LEU:HD21	1.83	0.61
1:A:582:ALA:O	1:A:585:VAL:HG22	2.00	0.61
1:B:393:LEU:O	1:B:395:LEU:HG	2.00	0.61
1:B:539:PHE:CG	1:B:549:ARG:HD2	2.35	0.60
1:C:248:LEU:CD1	1:C:286:LYS:CA	2.77	0.60
1:D:495:GLY:N	5:D:703:HOH:O	2.33	0.60
1:A:414:ASN:HB2	1:A:417:ALA:HB2	1.83	0.60
1:D:270:LYS:O	1:D:274:ALA:N	2.22	0.60
1:A:229:ASN:HD21	1:A:278:ILE:HD11	1.66	0.60
1:B:413:LEU:CD1	1:B:437:HIS:NE2	2.52	0.60
1:C:268:LEU:HD11	1:C:279:ASP:HB2	1.84	0.60
1:D:347:TYR:HB2	1:D:493:LEU:CD1	2.29	0.60
1:D:269:ASN:O	1:D:273:LEU:N	2.35	0.60
1:D:379:ARG:HH11	1:D:379:ARG:CG	2.15	0.60
1:C:423:GLU:OE1	1:C:429:VAL:HB	2.02	0.60
1:C:543:LYS:O	1:C:546:GLN:HB2	2.02	0.60
1:D:384:LEU:HD23	1:D:390:TYR:CD2	2.33	0.60
1:D:399:VAL:HG13	1:D:475:GLN:O	2.01	0.60
1:D:332:LEU:HD11	1:D:560:CYS:HB3	1.84	0.59
1:D:382:PHE:CE1	1:D:397:VAL:HG21	2.38	0.59
1:A:267:PRO:HG3	1:A:317:GLU:HB3	1.85	0.59
1:B:372:GLY:O	1:B:376:MET:HG3	2.03	0.59
1:B:561:MET:HE1	1:B:581:TYR:CD1	2.38	0.59
1:B:400:THR:HG23	1:B:400:THR:O	2.03	0.59
1:D:354:LYS:HZ3	1:D:495:GLY:HA2	1.65	0.59
1:B:358:MET:HE2	1:B:373:ILE:HB	1.85	0.59
1:D:395:LEU:HA	1:D:479:ARG:O	2.03	0.59
1:B:441:SER:HB2	1:B:444:ASP:CG	2.29	0.58
1:C:331:PRO:HA	5:C:701:HOH:O	2.03	0.58
1:C:561:MET:CA	1:C:562:ILE:N	2.67	0.58
1:C:571:SER:O	1:C:575:THR:OG1	2.18	0.58
1:D:244:GLU:OE1	1:D:244:GLU:HA	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:ILE:HD11	1:D:487:LYS:C	2.29	0.58
1:B:264:ARG:HH11	1:B:357:THR:CG2	2.09	0.58
1:A:265:LYS:HG3	1:A:316:ASP:HA	1.84	0.58
1:D:410:PHE:HD2	1:D:417:ALA:HB1	1.68	0.58
1:B:577:ASN:OD1	1:B:580:ARG:NH1	2.34	0.58
1:B:349:GLN:HA	1:B:496:ASN:OD1	2.03	0.57
1:B:404:ILE:HG13	1:B:471:HIS:HD2	1.67	0.57
1:B:356:HIS:O	1:B:357:THR:HB	2.05	0.57
1:D:328:THR:O	1:D:332:LEU:HG	2.03	0.57
1:D:512:GLU:N	1:D:513:GLY:HA3	2.19	0.57
1:B:322:GLU:HA	1:B:376:MET:HE1	1.85	0.57
1:C:235:MET:HE1	1:C:303:TYR:HA	1.87	0.57
1:B:391:ARG:HB3	1:B:391:ARG:CZ	2.33	0.57
1:D:468:SER:O	5:D:703:HOH:O	2.18	0.57
1:D:236:ILE:CD1	1:D:304:LEU:HD21	2.34	0.56
1:D:413:LEU:HG	1:D:414:ASN:H	1.70	0.56
1:A:246:HIS:HB2	1:B:246:HIS:NE2	2.20	0.56
1:B:399:VAL:HG23	1:B:439:VAL:HG13	1.87	0.56
1:D:410:PHE:HB3	1:D:417:ALA:HB1	1.87	0.56
1:A:396:GLU:HB3	1:A:438:LEU:HD11	1.87	0.56
1:B:399:VAL:HG21	1:B:439:VAL:CG1	2.36	0.56
1:C:429:VAL:HG21	1:C:546:GLN:HG3	1.87	0.56
1:D:232:PHE:O	1:D:236:ILE:HD13	2.05	0.56
1:D:277:GLU:OE2	1:D:570:SER:N	2.30	0.56
1:D:346:ALA:HB2	1:D:358:MET:HE3	1.87	0.56
1:D:524:LYS:HD2	1:D:584:ARG:HB2	1.86	0.56
1:B:409:LEU:HD12	1:B:419:LEU:HB2	1.71	0.56
1:C:332:LEU:HD13	1:C:342:ALA:HB1	1.87	0.56
1:D:236:ILE:H	1:D:236:ILE:CD1	2.19	0.56
1:D:321:ASN:ND2	1:D:371:LYS:O	2.39	0.56
1:D:236:ILE:HD12	1:D:304:LEU:HD21	1.88	0.56
1:D:264:ARG:HE	1:D:324:VAL:HG11	1.71	0.56
1:C:281:ILE:HD13	1:C:567:PRO:HA	1.89	0.55
1:C:475:GLN:HE21	1:C:487:LYS:HD3	1.72	0.55
1:D:495:GLY:HA3	5:D:703:HOH:O	2.06	0.55
1:C:250:MET:HG3	1:C:326:ARG:NH1	1.96	0.55
1:D:509:THR:HA	1:D:511:MET:H	1.72	0.55
1:D:353:GLY:C	4:D:602:ADP:O1A	2.50	0.55
1:A:377:ALA:O	1:A:381:VAL:N	2.36	0.55
1:B:431:VAL:CG2	1:B:432:VAL:H	2.10	0.55
1:B:285:SER:HB2	1:B:288:LEU:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:GLN:O	1:B:391:ARG:HG2	2.07	0.55
1:D:292:HIS:ND1	1:D:306:ASN:OD1	2.19	0.55
1:D:332:LEU:HD13	1:D:488:PHE:CZ	2.42	0.55
1:D:336:ILE:O	1:D:478:LEU:HD12	2.07	0.55
1:D:410:PHE:CD2	1:D:417:ALA:HB1	2.42	0.55
1:B:388:PRO:CA	1:B:391:ARG:CD	2.71	0.55
1:C:263:VAL:HA	1:C:563:ALA:O	2.07	0.55
1:C:479:ARG:HG2	1:C:484:MET:HA	1.88	0.55
1:A:338:GLU:OE1	1:A:556:ASN:ND2	2.40	0.55
1:D:537:THR:CB	1:D:538:PRO:HA	2.37	0.55
1:C:308:ALA:C	1:C:309:PHE:CD1	2.86	0.54
1:D:537:THR:CB	1:D:538:PRO:CA	2.86	0.54
1:A:290:LEU:HD11	1:A:306:ASN:HB3	1.88	0.54
1:A:312:ASP:O	5:A:701:HOH:O	2.18	0.54
1:A:413:LEU:HD23	1:A:437:HIS:CD2	2.42	0.54
1:B:466:ASN:C	1:B:468:SER:H	2.15	0.54
1:B:248:LEU:HB2	1:B:286:LYS:CB	2.36	0.54
1:B:315:PHE:CE2	1:B:324:VAL:HG23	2.42	0.54
1:B:357:THR:O	1:B:357:THR:HG22	2.06	0.54
1:B:401:PHE:H	1:B:413:LEU:HD21	1.72	0.54
1:D:329:ALA:HA	1:D:332:LEU:HD12	1.87	0.54
1:A:527:ILE:HD13	1:A:552:PHE:HE1	1.72	0.54
1:C:521:LEU:O	1:C:525:GLU:HG2	2.08	0.54
1:D:354:LYS:HB2	4:D:602:ADP:O2B	2.07	0.54
1:C:324:VAL:HG23	1:C:325:TYR:N	2.22	0.54
1:D:395:LEU:HD13	1:D:480:ALA:CA	2.24	0.54
1:C:231:GLU:O	1:C:235:MET:HG3	2.07	0.54
1:A:282:SER:OG	1:A:292:HIS:NE2	2.41	0.54
1:B:399:VAL:CG2	1:B:439:VAL:HG13	2.37	0.54
1:D:349:GLN:CA	1:D:496:ASN:OD1	2.43	0.54
1:D:320:SER:O	1:D:324:VAL:HG13	2.08	0.54
4:D:602:ADP:PB	5:D:701:HOH:O	2.53	0.53
1:C:477:ILE:HG23	1:C:484:MET:HE3	1.90	0.53
1:C:524:LYS:O	1:C:528:ARG:HG2	2.08	0.53
1:C:546:GLN:C	1:C:548:LEU:N	2.64	0.53
1:D:332:LEU:CD1	1:D:488:PHE:HZ	2.22	0.53
1:A:412:LEU:HD22	1:A:455[A]:CYS:SG	2.49	0.53
1:B:539:PHE:CD2	1:B:549:ARG:CD	2.83	0.53
1:A:312:ASP:O	1:A:313:PHE:CD1	2.61	0.53
1:B:353:GLY:O	1:B:357:THR:HB	2.09	0.53
1:D:325:TYR:OH	1:D:380:ASP:OD2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:304:LEU:HG	1:B:306:ASN:OD1	2.09	0.53
1:B:413:LEU:HD11	1:B:437:HIS:CD2	2.08	0.53
1:A:291:VAL:HG21	1:A:576:LEU:HD21	1.90	0.53
1:A:267:PRO:HD2	4:A:602:ADP:C2	2.44	0.53
1:B:409:LEU:HD11	1:B:419:LEU:CA	2.38	0.53
1:D:398:TYR:CD2	1:D:436:GLU:OE2	2.62	0.53
1:D:400:THR:HB	1:D:434:LEU:HD21	1.91	0.53
1:D:400:THR:HG1	1:D:475:GLN:HG3	1.74	0.53
1:D:347:TYR:HB3	1:D:561:MET:HE3	1.90	0.53
1:C:304:LEU:HB3	1:C:306:ASN:ND2	2.23	0.52
1:B:477:ILE:HG13	1:B:487:LYS:HG3	1.90	0.52
1:D:307:GLN:OE1	1:D:576:LEU:HD11	2.09	0.52
1:D:269:ASN:OD1	1:D:272:GLU:HB3	2.09	0.52
1:A:491:VAL:HG21	1:A:548:LEU:HD11	1.91	0.52
1:A:248:LEU:O	1:A:248:LEU:HD12	2.10	0.52
1:B:273:LEU:O	1:B:276:LYS:N	2.41	0.52
1:B:336:ILE:HG21	1:B:488:PHE:HB2	1.91	0.52
1:B:431:VAL:HG11	1:B:434:LEU:CD2	2.39	0.52
1:D:347:TYR:CB	1:D:493:LEU:HD13	2.35	0.52
1:D:493:LEU:HD22	1:D:520:LEU:CD2	2.32	0.52
1:B:272:GLU:O	1:B:277:GLU:CB	2.57	0.52
1:C:527:ILE:CG2	1:C:585:VAL:CG1	2.88	0.52
1:D:400:THR:CG2	1:D:436:GLU:CG	2.85	0.52
1:A:267:PRO:HD2	4:A:602:ADP:N1	2.25	0.52
1:B:275:LYS:O	1:B:275:LYS:NZ	2.30	0.52
1:C:296:LEU:HD13	1:C:302:LYS:HG2	1.92	0.52
1:C:429:VAL:HG11	1:C:546:GLN:CG	2.27	0.52
1:C:540:ARG:CB	1:C:545:THR:HB	2.40	0.52
1:D:446:ILE:HD12	1:D:449:ILE:HB	1.92	0.52
1:A:350:THR:OG1	1:A:497:GLU:OE2	2.28	0.51
1:B:351:GLY:O	1:B:566:SER:OG	2.28	0.51
1:D:236:ILE:N	1:D:236:ILE:CD1	2.73	0.51
1:D:495:GLY:CA	5:D:703:HOH:O	2.57	0.51
1:B:353:GLY:O	1:B:356:HIS:C	2.51	0.51
1:C:429:VAL:HG21	1:C:546:GLN:CG	2.40	0.51
1:D:289:LEU:HD22	1:D:579:LEU:HD11	1.91	0.51
1:A:349:GLN:HG2	1:A:350:THR:N	2.24	0.51
1:C:248:LEU:HD11	1:C:286:LYS:HB3	1.93	0.51
1:C:382:PHE:HZ	1:C:439:VAL:HG23	1.74	0.51
1:D:537:THR:N	1:D:538:PRO:HA	2.24	0.51
1:C:576:LEU:O	1:C:580:ARG:N	2.32	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:379:ARG:CG	1:D:379:ARG:NH1	2.74	0.51
1:B:399:VAL:CG2	1:B:439:VAL:CG1	2.88	0.51
1:D:512:GLU:H	1:D:513:GLY:HA3	1.76	0.51
1:A:397:VAL:HG22	1:A:478:LEU:HD23	1.93	0.51
1:B:233:ALA:CB	1:B:278:ILE:CD1	2.88	0.51
1:B:410:PHE:HE1	1:B:418:LYS:CG	2.23	0.51
1:B:422:LEU:C	1:B:422:LEU:HD12	2.35	0.51
1:C:321:ASN:HA	1:C:324:VAL:HG22	1.93	0.51
1:C:330:ARG:HA	1:C:333:VAL:HG23	1.93	0.51
1:D:398:TYR:HE1	1:D:438:LEU:CB	2.24	0.51
1:A:245:CYS:SG	2:P:714:ALA:HB2	2.50	0.51
1:D:395:LEU:HB3	1:D:479:ARG:C	2.35	0.51
1:A:414:ASN:HB2	1:A:417:ALA:CB	2.41	0.50
1:B:299:ASP:OD1	1:B:300:LEU:N	2.43	0.50
1:B:231:GLU:C	1:B:233:ALA:H	2.19	0.50
1:B:303:TYR:CD1	1:B:303:TYR:C	2.89	0.50
1:C:254:ILE:CG2	1:C:331:PRO:HG3	2.41	0.50
1:C:337:PHE:HZ	1:C:381:VAL:HG13	1.76	0.50
1:B:248:LEU:HD23	1:B:248:LEU:C	2.36	0.50
1:B:267:PRO:CA	1:B:317:GLU:HB2	2.40	0.50
1:B:343:THR:HG23	1:B:559:THR:OG1	2.11	0.50
1:B:496:ASN:ND2	1:B:578:THR:OG1	2.44	0.50
1:D:519:SER:OG	1:D:542:SER:HB2	2.11	0.50
1:D:530:LEU:HD22	1:D:552:PHE:HA	1.94	0.50
1:B:431:VAL:HG11	1:B:434:LEU:HD22	1.94	0.50
1:B:259:ILE:CD1	1:B:530:LEU:HD23	2.40	0.50
1:C:304:LEU:HB3	1:C:306:ASN:HD21	1.77	0.50
1:A:542:SER:HG	1:A:545:THR:HG23	1.75	0.50
1:D:316:ASP:OD1	1:D:316:ASP:N	2.34	0.50
1:C:401:PHE:CE1	1:C:412:LEU:HD12	2.47	0.49
1:A:411:ASP:OD2	1:A:435:GLN:CB	2.59	0.49
1:B:264:ARG:HG3	1:B:315:PHE:HB2	1.93	0.49
1:C:331:PRO:CA	5:C:701:HOH:O	2.60	0.49
1:C:375:ALA:HB2	1:C:446:ILE:HD13	1.95	0.49
1:A:249:THR:OG1	1:A:251:THR:OG1	2.22	0.49
1:B:471:HIS:ND1	1:B:493:LEU:HD23	2.27	0.49
1:A:414:ASN:ND2	1:A:435:GLN:OE1	2.45	0.49
1:D:525:GLU:O	1:D:528:ARG:HB3	2.11	0.49
1:B:274:ALA:C	1:B:276:LYS:H	2.20	0.49
1:C:335:THR:HG21	1:C:558:ARG:HD2	1.94	0.49
1:D:328:THR:HB	1:D:560:CYS:SG	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:565:ILE:HB	1:D:575:THR:HG23	1.95	0.49
1:D:318:THR:OG1	1:D:319:ALA:N	2.46	0.49
1:A:292:HIS:ND1	1:A:306:ASN:OD1	2.43	0.49
1:C:431:VAL:HG12	1:C:432:VAL:N	2.28	0.48
1:B:391:ARG:NH1	1:B:391:ARG:CB	2.73	0.48
1:C:321:ASN:O	1:C:324:VAL:HG22	2.14	0.48
1:D:400:THR:HG1	1:D:475:GLN:HE21	1.50	0.48
1:B:358:MET:O	1:B:372:GLY:CA	2.62	0.48
1:A:338:GLU:CD	1:A:556:ASN:HD21	2.21	0.48
1:B:404:ILE:HA	1:B:409:LEU:HA	1.95	0.48
1:C:248:LEU:CD1	1:C:286:LYS:CB	2.92	0.48
5:C:704:HOH:O	1:D:586:LYS:NZ	2.40	0.48
1:D:472:ALA:HB3	1:D:492:ASP:HB3	1.94	0.48
1:A:286:LYS:O	1:A:314:ALA:N	2.45	0.48
1:D:233:ALA:O	1:D:237:LYS:HB2	2.13	0.48
1:D:393:LEU:CG	1:D:395:LEU:HD11	2.44	0.48
1:B:321:ASN:O	1:B:324:VAL:CG1	2.60	0.48
1:B:390:TYR:O	1:B:392:LYS:O	2.31	0.48
1:D:233:ALA:HB1	1:D:278:ILE:HD12	1.95	0.48
1:D:373:ILE:HA	1:D:376:MET:HB2	1.96	0.48
1:D:559:THR:OG1	1:D:560:CYS:N	2.47	0.48
1:A:440:ASN:O	1:A:441:SER:HB3	2.12	0.48
1:A:248:LEU:HD12	1:A:248:LEU:C	2.38	0.48
1:B:280:VAL:HG21	1:B:572:CYS:HG	1.79	0.48
1:B:566:SER:H	1:B:575:THR:HG21	1.77	0.48
1:C:527:ILE:HB	1:C:585:VAL:CG1	2.43	0.48
1:D:322:GLU:N	1:D:376:MET:HE1	2.27	0.48
1:D:543:LYS:HD2	1:D:546:GLN:NE2	2.27	0.48
1:A:265:LYS:HD2	1:A:316:ASP:HB2	1.96	0.47
1:D:248:LEU:HD12	1:D:249:THR:O	2.14	0.47
1:A:229:ASN:HD21	1:A:278:ILE:CD1	2.27	0.47
1:B:268:LEU:HD13	1:B:567:PRO:HG2	1.95	0.47
1:B:359:GLY:HA2	1:B:372:GLY:CA	2.42	0.47
1:B:406:ASN:O	1:B:408:LYS:N	2.47	0.47
1:C:281:ILE:HG21	1:C:565:ILE:HD11	1.96	0.47
1:D:303:TYR:O	1:D:304:LEU:HD12	2.14	0.47
1:D:550:ASP:O	1:D:553:ILE:HG13	2.14	0.47
1:A:545:THR:OG1	1:A:546:GLN:N	2.47	0.47
1:D:353:GLY:CA	4:D:602:ADP:O1A	2.62	0.47
1:D:354:LYS:N	4:D:602:ADP:O1A	2.46	0.47
1:A:278:ILE:HD12	1:A:569:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:ASN:C	1:B:468:SER:N	2.71	0.47
1:B:479:ARG:NH1	1:B:482:GLY:O	2.47	0.47
1:D:527:ILE:HG13	1:D:552:PHE:HE1	1.80	0.47
1:D:398:TYR:HB2	1:D:477:ILE:HB	1.96	0.47
1:D:543:LYS:HA	1:D:546:GLN:HE21	1.80	0.47
1:A:348:GLY:N	1:A:354:LYS:HD3	2.29	0.47
1:A:411:ASP:OD1	1:A:413:LEU:N	2.47	0.47
1:A:413:LEU:HD23	1:A:437:HIS:HD2	1.80	0.47
1:C:266:ARG:NH1	1:C:351:GLY:O	2.48	0.47
1:D:248:LEU:HD12	1:D:249:THR:N	2.29	0.47
1:D:260:CYS:HA	1:D:312:ASP:OD2	2.14	0.47
1:D:541:GLU:O	1:D:542:SER:HB3	2.14	0.47
1:A:534:LYS:O	1:A:553:ILE:CD1	2.63	0.47
1:B:282:SER:OG	1:B:292:HIS:NE2	2.47	0.47
1:C:232:PHE:O	1:C:236:ILE:HG13	2.14	0.47
1:D:337:PHE:HA	1:D:478:LEU:CD1	2.45	0.47
1:A:239:PHE:CZ	1:A:290:LEU:HD21	2.50	0.46
1:A:264:ARG:HB3	1:A:564:THR:HG22	1.97	0.46
1:D:321:ASN:HA	1:D:324:VAL:HG22	1.97	0.46
1:D:358:MET:HB3	1:D:374:TYR:CZ	2.49	0.46
1:B:431:VAL:HG11	1:B:434:LEU:HB2	1.97	0.46
1:B:580:ARG:O	1:B:584:ARG:HG2	2.16	0.46
1:A:280:VAL:HG22	1:A:292:HIS:O	2.15	0.46
1:C:263:VAL:HG21	1:C:289:LEU:HD13	1.97	0.46
1:C:287:CYS:SG	1:D:243:LEU:HA	2.56	0.46
1:D:279:ASP:OD1	1:D:567:PRO:HB3	2.16	0.46
1:D:382:PHE:CE1	1:D:397:VAL:HG11	2.51	0.46
1:B:478:LEU:HB2	1:B:485:HIS:HB3	1.97	0.46
1:C:527:ILE:CB	1:C:585:VAL:HG11	2.46	0.46
1:D:539:PHE:HD1	1:D:539:PHE:O	1.98	0.46
1:A:431:VAL:HG13	1:A:434:LEU:HG	1.98	0.46
1:D:315:PHE:CD1	1:D:324:VAL:HG12	2.50	0.46
1:A:382:PHE:HZ	1:A:439:VAL:CG2	2.25	0.46
1:A:550:ASP:OD1	1:A:551:SER:N	2.48	0.46
1:B:299:ASP:O	1:B:300:LEU:HB2	2.15	0.46
1:B:315:PHE:CZ	1:B:324:VAL:HA	2.51	0.46
1:C:574:TYR:O	1:C:578:THR:OG1	2.21	0.46
1:A:264:ARG:HB2	1:A:315:PHE:HE1	1.80	0.45
1:A:439:VAL:HG12	1:A:444:ASP:CB	2.47	0.45
1:B:576:LEU:HA	1:B:576:LEU:HD23	1.77	0.45
1:C:229:ASN:OD1	1:C:569:ILE:HD13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:248:LEU:CD1	1:C:286:LYS:HB3	2.46	0.45
1:D:336:ILE:HD12	1:D:336:ILE:HA	1.83	0.45
1:A:299:ASP:O	1:A:300:LEU:HB2	2.15	0.45
1:B:282:SER:O	1:B:290:LEU:N	2.48	0.45
1:B:537:THR:O	1:B:539:PHE:HD1	1.98	0.45
1:C:239:PHE:CE1	1:C:292:HIS:HE1	2.33	0.45
1:C:443:ASP:HA	1:C:446:ILE:CG2	2.46	0.45
1:D:384:LEU:HD23	1:D:384:LEU:O	2.16	0.45
1:B:231:GLU:C	1:B:233:ALA:N	2.73	0.45
1:B:250:MET:SD	1:B:326:ARG:NE	2.83	0.45
1:C:297:LYS:HG3	1:C:298:VAL:H	1.80	0.45
1:C:332:LEU:O	1:C:335:THR:OG1	2.26	0.45
1:B:249:THR:HG22	1:B:250:MET:N	2.30	0.45
1:D:395:LEU:CD2	1:D:395:LEU:N	2.65	0.45
1:A:379:ARG:HG3	1:A:442:ALA:HB2	1.95	0.45
1:B:296:LEU:HD12	1:B:296:LEU:HA	1.80	0.45
1:B:388:PRO:CA	1:B:391:ARG:HD2	2.40	0.45
1:B:400:THR:HG22	1:B:475:GLN:O	2.16	0.45
1:B:539:PHE:CB	5:B:706:HOH:O	2.51	0.45
1:C:337:PHE:CZ	1:C:381:VAL:HG13	2.52	0.45
1:B:354:LYS:O	1:B:356:HIS:O	2.35	0.45
1:C:248:LEU:HD13	1:C:286:LYS:CA	2.42	0.45
1:C:307:GLN:OE1	1:D:305:GLU:OE2	2.34	0.45
1:C:527:ILE:HB	1:C:585:VAL:HG11	1.99	0.45
1:D:332:LEU:HD13	1:D:488:PHE:CE1	2.52	0.45
1:D:347:TYR:HB2	1:D:561:MET:HE1	1.99	0.45
1:B:394:GLY:O	1:B:480:ALA:O	2.35	0.45
1:D:230:TRP:O	1:D:231:GLU:OE2	2.35	0.45
1:B:398:TYR:C	1:B:399:VAL:HG23	2.42	0.45
1:C:428:GLN:C	1:C:429:VAL:HG12	2.42	0.45
1:D:229:ASN:N	1:D:230:TRP:HA	2.31	0.45
1:D:235:MET:HE1	1:D:304:LEU:CD1	2.29	0.45
1:D:243:LEU:HD21	1:D:284:PRO:HB3	1.99	0.45
1:D:232:PHE:C	1:D:236:ILE:HD13	2.42	0.45
1:C:337:PHE:HB3	1:C:390:TYR:HE2	1.82	0.44
1:A:322:GLU:HA	1:A:376:MET:HE1	1.99	0.44
1:A:538:PRO:O	1:A:539:PHE:CD1	2.70	0.44
1:C:232:PHE:HZ	1:C:302:LYS:HE2	1.83	0.44
1:B:231:GLU:OE1	1:B:231:GLU:HA	2.16	0.44
1:D:332:LEU:CD1	1:D:488:PHE:CZ	2.99	0.44
1:D:443:ASP:O	1:D:446:ILE:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:446:ILE:O	1:D:450:ASP:N	2.35	0.44
1:A:351:GLY:H	4:A:602:ADP:PB	2.41	0.44
1:A:445:VAL:O	1:A:449:ILE:HD12	2.16	0.44
1:B:396:GLU:O	1:B:398:TYR:CD1	2.71	0.44
1:D:232:PHE:O	1:D:236:ILE:CD1	2.65	0.44
1:C:265:LYS:NZ	1:C:281:ILE:O	2.32	0.44
1:D:402:PHE:HB2	1:D:410:PHE:O	2.18	0.44
1:A:397:VAL:HG22	1:A:478:LEU:CD2	2.48	0.44
1:C:355:THR:OG1	4:C:602:ADP:O2A	2.36	0.44
1:A:583:ASP:O	1:A:584:ARG:HB2	2.16	0.44
1:B:349:GLN:CA	1:B:496:ASN:OD1	2.66	0.44
1:A:276:LYS:HG3	1:A:276:LYS:O	2.17	0.43
1:A:536:HIS:CD2	1:A:537:THR:N	2.86	0.43
1:B:435:GLN:O	1:B:435:GLN:HG2	2.17	0.43
1:C:398:TYR:HD2	1:C:436:GLU:O	2.01	0.43
1:C:421:VAL:HG12	1:C:431:VAL:HA	2.00	0.43
1:A:534:LYS:O	1:A:553:ILE:HD13	2.18	0.43
1:B:387:GLN:C	1:B:391:ARG:HD2	2.43	0.43
1:C:351:GLY:H	4:C:602:ADP:PB	2.41	0.43
1:B:358:MET:HB2	1:B:358:MET:HE3	1.76	0.43
1:B:391:ARG:NH1	1:B:391:ARG:CG	2.72	0.43
1:D:239:PHE:HE1	1:D:243:LEU:HD13	1.83	0.43
1:C:546:GLN:C	1:C:548:LEU:H	2.27	0.43
1:A:229:ASN:ND2	1:A:278:ILE:HD11	2.32	0.43
1:C:277:GLU:CD	1:C:568:GLY:HA2	2.43	0.43
1:C:287:CYS:HB2	1:C:311:PHE:O	2.19	0.43
1:D:509:THR:HA	1:D:511:MET:N	2.33	0.43
1:A:343:THR:OG1	1:A:559:THR:HG22	2.18	0.43
1:A:540:ARG:C	1:A:542:SER:H	2.25	0.43
1:C:261:VAL:HG11	1:C:582:ALA:O	2.18	0.43
1:C:321:ASN:C	1:C:324:VAL:HG22	2.44	0.43
1:D:329:ALA:O	1:D:332:LEU:HB2	2.18	0.43
1:A:229:ASN:OD1	1:A:229:ASN:C	2.61	0.43
1:A:535:ALA:HA	1:A:553:ILE:HD11	2.00	0.43
1:B:347:TYR:CE1	1:B:496:ASN:HB3	2.53	0.43
1:B:348:GLY:N	1:B:354:LYS:HD3	2.27	0.43
1:B:387:GLN:O	1:B:391:ARG:HG3	2.16	0.43
1:C:347:TYR:HE1	1:C:520:LEU:HD13	1.82	0.43
1:D:281:ILE:HD12	1:D:289:LEU:HD21	2.01	0.43
1:D:537:THR:CB	1:D:539:PHE:N	2.81	0.43
1:A:275:LYS:HE2	1:A:275:LYS:HB2	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:ILE:HD13	1:A:552:PHE:CE1	2.53	0.43
1:D:343:THR:O	1:D:559:THR:OG1	2.25	0.43
1:B:303:TYR:C	1:B:303:TYR:HD1	2.27	0.43
1:B:404:ILE:HG13	1:B:404:ILE:O	2.19	0.43
1:C:397:VAL:O	1:C:438:LEU:HD12	2.19	0.43
1:D:475:GLN:HB3	1:D:489:SER:HA	2.01	0.43
1:A:527:ILE:CD1	1:A:552:PHE:HE1	2.31	0.43
1:C:250:MET:HE3	1:C:323:VAL:CG1	2.43	0.43
1:C:336:ILE:HG22	1:C:478:LEU:HD12	2.01	0.43
1:C:484:MET:HE3	1:C:484:MET:HB2	1.81	0.43
1:D:234:ARG:O	1:D:238:GLU:N	2.42	0.43
1:A:584:ARG:CD	1:B:235:MET:HE2	2.49	0.42
1:B:248:LEU:HD12	1:B:286:LYS:HD3	1.93	0.42
1:A:330:ARG:O	1:A:333:VAL:HG12	2.19	0.42
1:A:348:GLY:HA2	1:A:578:THR:HG23	2.01	0.42
1:D:371:LYS:HB3	1:D:372:GLY:H	1.47	0.42
1:B:349:GLN:O	1:B:352:SER:OG	2.30	0.42
1:B:474:PHE:HD2	1:B:490:LEU:HD13	1.84	0.42
1:C:320:SER:O	1:C:323:VAL:HG22	2.19	0.42
1:D:262:CYS:SG	1:D:562:ILE:HD13	2.59	0.42
1:D:328:THR:OG1	1:D:329:ALA:N	2.52	0.42
1:D:356:HIS:C	1:D:356:HIS:CD2	2.97	0.42
1:A:347:TYR:O	1:A:563:ALA:HA	2.19	0.42
1:B:281:ILE:HD13	1:B:291:VAL:HG22	2.02	0.42
1:B:292:HIS:HB3	1:B:304:LEU:CD2	2.47	0.42
1:C:279:ASP:OD1	1:C:567:PRO:HB2	2.19	0.42
1:A:579:LEU:O	1:A:582:ALA:N	2.49	0.42
1:B:434:LEU:HD12	1:B:434:LEU:HA	1.85	0.42
1:C:237:LYS:HA	1:C:237:LYS:HD3	1.66	0.42
1:C:248:LEU:HD12	1:C:286:LYS:HA	1.96	0.42
1:A:381:VAL:HG21	1:A:476:ILE:HD13	2.01	0.42
1:C:345:PHE:CE2	1:C:523:LEU:HD21	2.54	0.42
1:C:348:GLY:HA2	1:C:578:THR:HG21	2.02	0.42
1:B:299:ASP:OD2	1:B:301:THR:HB	2.19	0.42
1:B:355:THR:O	1:B:355:THR:CG2	2.68	0.42
1:B:379:ARG:O	1:B:383:LEU:HG	2.20	0.42
1:D:398:TYR:HB3	1:D:436:GLU:OE2	2.19	0.42
1:B:268:LEU:HD12	1:B:268:LEU:HA	1.81	0.42
1:C:401:PHE:HB3	1:C:413:LEU:HG	2.01	0.42
1:D:307:GLN:OE1	1:D:576:LEU:HD21	2.19	0.42
1:D:401:PHE:HD2	1:D:474:PHE:HD1	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:530:LEU:HD12	1:C:530:LEU:HA	1.78	0.42
1:D:356:HIS:CD2	1:D:356:HIS:O	2.73	0.42
1:D:413:LEU:HG	1:D:414:ASN:N	2.35	0.42
1:B:245:CYS:CA	1:B:284:PRO:O	2.68	0.42
1:A:310:CYS:HB2	1:B:239:PHE:CE1	2.55	0.41
1:A:351:GLY:N	4:A:602:ADP:O3B	2.53	0.41
1:B:353:GLY:HA2	4:B:601:ADP:H8	1.85	0.41
1:B:399:VAL:HG12	1:B:400:THR:N	2.35	0.41
1:C:299:ASP:O	1:C:300:LEU:HB2	2.19	0.41
1:A:530:LEU:HD12	1:A:530:LEU:HA	1.86	0.41
1:C:242:THR:HG21	1:D:586:LYS:HD2	2.02	0.41
1:B:278:ILE:CG2	1:B:569:ILE:HB	2.50	0.41
1:B:400:THR:HG23	1:B:475:GLN:HB2	1.98	0.41
1:B:556:ASN:OD1	1:B:556:ASN:N	2.54	0.41
1:C:324:VAL:CG2	1:C:325:TYR:N	2.83	0.41
1:D:418:LYS:C	1:D:419:LEU:HD22	2.40	0.41
1:D:471:HIS:CE1	1:D:493:LEU:HD23	2.55	0.41
1:A:259:ILE:HD11	1:A:530:LEU:HB3	2.03	0.41
1:B:353:GLY:O	1:B:357:THR:CB	2.69	0.41
1:C:232:PHE:CZ	1:C:302:LYS:HE2	2.55	0.41
1:D:261:VAL:HG11	1:D:582:ALA:O	2.20	0.41
1:C:250:MET:HE3	1:C:323:VAL:HA	2.02	0.41
1:A:278:ILE:HG22	1:A:279:ASP:O	2.21	0.41
1:D:275:LYS:HB2	1:D:275:LYS:HE2	1.93	0.41
1:D:399:VAL:CG1	1:D:474:PHE:CZ	3.03	0.41
1:D:537:THR:HB	1:D:538:PRO:C	2.45	0.41
1:A:401:PHE:HB3	1:A:413:LEU:HD13	2.03	0.41
1:A:476:ILE:HB	1:A:488:PHE:HB3	2.03	0.41
1:B:262[A]:CYS:SG	1:B:313:PHE:HB2	2.61	0.41
1:B:347:TYR:O	1:B:563:ALA:HA	2.21	0.41
1:C:288:LEU:HD22	1:D:243:LEU:HD11	2.03	0.41
1:C:319:ALA:HB1	1:C:323:VAL:HG21	2.01	0.41
1:D:337:PHE:CD1	1:D:478:LEU:HD11	2.56	0.41
1:A:450:ASP:OD1	1:A:450:ASP:N	2.53	0.41
1:C:348:GLY:O	1:C:354:LYS:NZ	2.50	0.41
1:C:401:PHE:HD1	1:C:402:PHE:N	2.19	0.41
1:C:530:LEU:HD11	1:C:557:SER:OG	2.21	0.41
1:D:385:LYS:HB3	1:D:385:LYS:HE3	1.88	0.41
1:B:403:GLU:O	1:B:410:PHE:N	2.53	0.40
1:D:406:ASN:ND2	1:D:512:GLU:O	2.36	0.40
1:D:507:ARG:O	1:D:508:GLN:C	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:VAL:HG23	1:A:563:ALA:O	2.21	0.40
1:A:456:ARG:H	1:A:456:ARG:HG2	1.72	0.40
1:A:576:LEU:HD23	1:A:576:LEU:HA	1.91	0.40
1:D:418:LYS:O	1:D:419:LEU:CD1	2.67	0.40
1:D:566:SER:HA	1:D:567:PRO:HD3	1.81	0.40
1:A:406:ASN:C	1:A:408:LYS:H	2.28	0.40
1:A:493:LEU:HD13	1:A:520:LEU:HD22	2.02	0.40
1:B:267:PRO:HB3	1:B:317:GLU:HB2	2.03	0.40
1:B:299:ASP:OD1	1:B:299:ASP:C	2.64	0.40
1:C:309:PHE:CD1	1:C:309:PHE:N	2.89	0.40
1:A:245:CYS:SG	2:P:714:ALA:CB	3.10	0.40
1:A:267:PRO:HG3	1:A:317:GLU:CB	2.52	0.40
1:B:258:ARG:HA	1:B:558:ARG:HG2	2.04	0.40
1:C:576:LEU:HD23	1:C:579:LEU:HD12	2.03	0.40
1:D:352:SER:N	4:D:602:ADP:O3B	2.49	0.40
1:D:586:LYS:HE3	1:D:586:LYS:HB3	1.85	0.40
1:A:357:THR:O	1:A:373:ILE:HG13	2.21	0.40
1:B:249:THR:HG22	1:B:251:THR:H	1.86	0.40
1:B:315:PHE:CZ	1:B:324:VAL:HG23	2.56	0.40
1:B:401:PHE:O	1:B:413:LEU:HD23	2.22	0.40
1:B:439:VAL:HG21	1:B:445:VAL:HG23	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	300/387 (78%)	261 (87%)	36 (12%)	3 (1%)	12	45
1	B	306/387 (79%)	265 (87%)	40 (13%)	1 (0%)	36	70
1	C	309/387 (80%)	278 (90%)	30 (10%)	1 (0%)	36	70
1	D	308/387 (80%)	266 (86%)	38 (12%)	4 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	5/12 (42%)	4 (80%)	1 (20%)	0	100	100
All	All	1228/1560 (79%)	1074 (88%)	145 (12%)	9 (1%)	18	53

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	230	TRP
1	A	353	GLY
1	A	455[A]	CYS
1	A	455[B]	CYS
1	D	330	ARG
1	D	455	CYS
1	B	407	GLY
1	D	253	PRO
1	D	247	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	238/332 (72%)	222 (93%)	16 (7%)	15	46
1	B	244/332 (74%)	227 (93%)	17 (7%)	14	44
1	C	244/332 (74%)	232 (95%)	12 (5%)	22	56
1	D	225/332 (68%)	201 (89%)	24 (11%)	6	26
2	P	4/11 (36%)	2 (50%)	2 (50%)	0	0
All	All	955/1339 (71%)	884 (93%)	71 (7%)	12	42

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	LYS
1	A	275	LYS
1	A	282	SER

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Mol	Chain	Res	Type
1	A	288	LEU
1	A	291	VAL
1	A	310	CYS
1	A	315	PHE
1	A	324	VAL
1	A	395	LEU
1	A	413	LEU
1	A	431	VAL
1	A	434	LEU
1	A	523	LEU
1	A	541	GLU
1	A	548	LEU
1	A	561	MET
1	B	229	ASN
1	B	245	CYS
1	B	246	HIS
1	B	248	LEU
1	B	250	MET
1	B	289	LEU
1	B	303	TYR
1	B	358	MET
1	B	391	ARG
1	B	393	LEU
1	B	395	LEU
1	B	397	VAL
1	B	413	LEU
1	B	414	ASN
1	B	436	GLU
1	B	471	HIS
1	B	527	ILE
1	C	242	THR
1	C	246	HIS
1	C	248	LEU
1	C	249	THR
1	C	305	GLU
1	C	307	GLN
1	C	355	THR
1	C	378	SER
1	C	424	ASP
1	C	523	LEU
1	C	546	GLN
1	C	583	ASP

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Mol	Chain	Res	Type
1	D	231	GLU
1	D	236	ILE
1	D	237	LYS
1	D	242	THR
1	D	248	LEU
1	D	258	ARG
1	D	263	VAL
1	D	303	TYR
1	D	305	GLU
1	D	336	ILE
1	D	352	SER
1	D	357	THR
1	D	378	SER
1	D	379	ARG
1	D	395	LEU
1	D	409	LEU
1	D	412	LEU
1	D	413	LEU
1	D	419	LEU
1	D	432	VAL
1	D	497	GLU
1	D	537	THR
1	D	539	PHE
1	D	565	ILE
2	P	712	GLU
2	P	713	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	257	HIS
1	A	321	ASN
1	A	349	GLN
1	A	440	ASN
1	A	536	HIS
1	A	556	ASN
1	B	437	HIS
1	C	257	HIS
1	C	306	ASN
1	D	246	HIS
1	D	356	HIS
1	D	475	GLN

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Mol	Chain	Res	Type
1	D	546	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 7 are monoatomic - leaving 4 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	$\# Z > 2$
4	ADP	D	602	3	28,29,29	1.46	5 (17%)	43,45,45	1.83	8 (18%)
4	ADP	B	601	3	28,29,29	1.46	5 (17%)	43,45,45	1.84	8 (18%)
4	ADP	A	602	3	28,29,29	1.41	3 (10%)	43,45,45	1.97	10 (23%)
4	ADP	C	602	-	28,29,29	1.44	5 (17%)	43,45,45	1.78	8 (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
4	ADP	D	602	3	-	2/16/32/32	0/3/3/3
4	ADP	B	601	3	-	1/16/32/32	0/3/3/3
4	ADP	A	602	3	-	7/16/32/32	0/3/3/3
4	ADP	C	602	-	-	4/16/32/32	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	ADP	C5-C4	4.85	1.47	1.39
4	B	601	ADP	C5-C4	4.84	1.47	1.39
4	D	602	ADP	C5-C4	4.81	1.47	1.39
4	C	602	ADP	C5-C4	4.80	1.47	1.39
4	C	602	ADP	C5-C6	2.81	1.48	1.41
4	D	602	ADP	C5-C6	2.78	1.48	1.41
4	B	601	ADP	C5-C6	2.76	1.48	1.41
4	A	602	ADP	C5-C6	2.57	1.48	1.41
4	A	602	ADP	C5-N7	-2.53	1.34	1.39
4	D	602	ADP	PA-O3A	2.48	1.62	1.59
4	C	602	ADP	C8-N7	2.37	1.36	1.31
4	B	601	ADP	C8-N7	2.34	1.36	1.31
4	B	601	ADP	C5-N7	-2.27	1.34	1.39
4	B	601	ADP	PA-O3A	2.27	1.61	1.59
4	D	602	ADP	C5-N7	-2.26	1.35	1.39
4	D	602	ADP	C8-N7	2.26	1.36	1.31
4	C	602	ADP	C5-N7	-2.21	1.35	1.39
4	C	602	ADP	PA-O3A	2.05	1.61	1.59

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	602	ADP	C5-C4-N3	-6.14	118.26	126.72
4	B	601	ADP	C5-C4-N3	-6.07	118.36	126.72
4	D	602	ADP	C5-C4-N3	-6.03	118.41	126.72
4	C	602	ADP	C5-C4-N3	-5.87	118.64	126.72
4	A	602	ADP	N3-C4-N9	5.22	136.04	127.17
4	B	601	ADP	N3-C4-N9	4.80	135.33	127.17
4	D	602	ADP	N3-C4-N9	4.79	135.31	127.17
4	C	602	ADP	N3-C4-N9	4.52	134.85	127.17
4	D	602	ADP	C2-N3-C4	3.74	120.97	111.83
4	B	601	ADP	C2-N3-C4	3.74	120.96	111.83
4	C	602	ADP	C2-N3-C4	3.71	120.89	111.83
4	C	602	ADP	C4-C5-N7	-3.62	106.45	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602	ADP	C4-C5-N7	-3.56	106.51	110.58
4	A	602	ADP	O4'-C1'-N9	3.54	114.89	108.09
4	A	602	ADP	C2-N3-C4	3.53	120.46	111.83
4	B	601	ADP	C4-C5-N7	-3.47	106.61	110.58
4	A	602	ADP	C4-C5-N7	-3.20	106.92	110.58
4	C	602	ADP	N3-C2-N1	-3.18	123.76	128.58
4	D	602	ADP	N3-C2-N1	-3.17	123.79	128.58
4	B	601	ADP	N3-C2-N1	-3.15	123.81	128.58
4	A	602	ADP	N3-C2-N1	-2.94	124.14	128.58
4	D	602	ADP	C5-N7-C8	2.64	107.61	103.45
4	A	602	ADP	C4-N9-C8	2.64	108.51	105.74
4	A	602	ADP	C2'-C1'-N9	-2.57	106.91	113.30
4	A	602	ADP	C5-N7-C8	2.54	107.45	103.45
4	C	602	ADP	C5-N7-C8	2.54	107.44	103.45
4	D	602	ADP	C4-N9-C8	2.53	108.40	105.74
4	B	601	ADP	C5-N7-C8	2.50	107.38	103.45
4	C	602	ADP	C4-N9-C8	2.40	108.26	105.74
4	B	601	ADP	C4-N9-C8	2.39	108.25	105.74
4	B	601	ADP	C3'-C2'-C1'	2.30	105.82	101.46
4	C	602	ADP	C6-C5-N7	2.16	136.26	132.09
4	A	602	ADP	C1'-N9-C8	-2.15	122.32	127.09
4	D	602	ADP	C6-C5-N7	2.01	135.97	132.09

There are no chirality outliers.

All (14) torsion outliers are listed below:

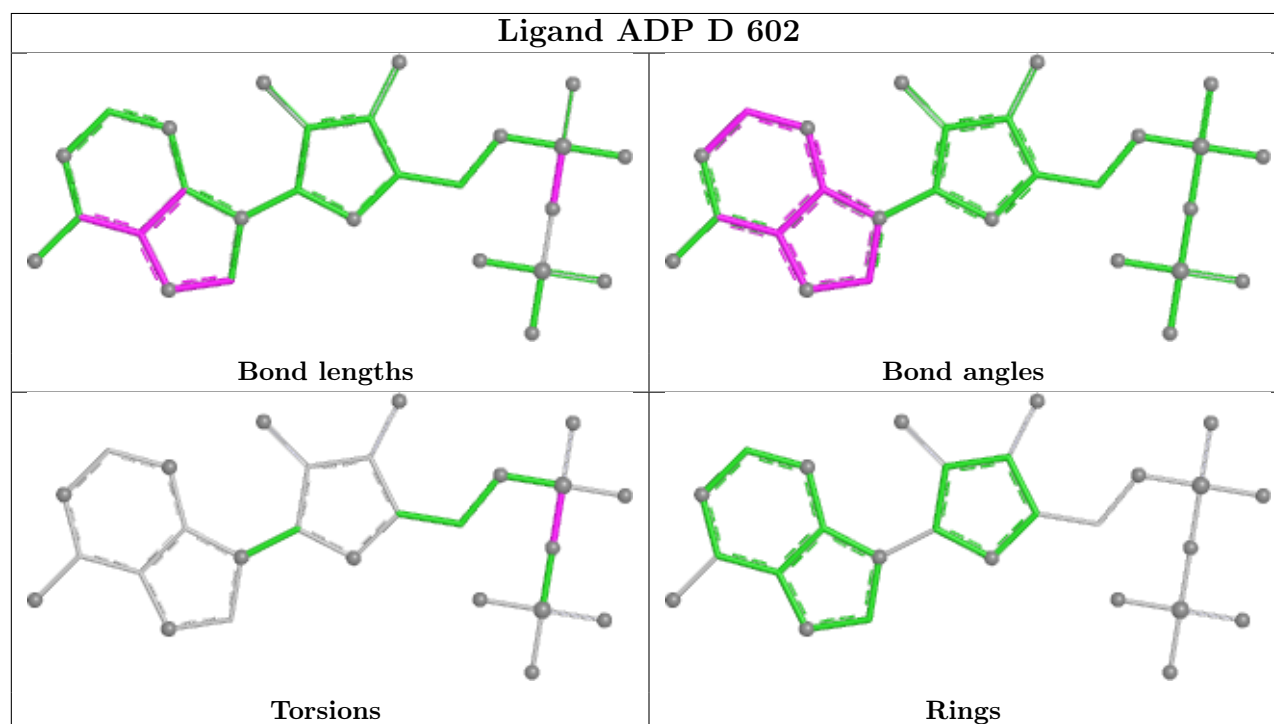
Mol	Chain	Res	Type	Atoms
4	A	602	ADP	PA-O3A-PB-O2B
4	A	602	ADP	PA-O3A-PB-O3B
4	A	602	ADP	O4'-C4'-C5'-O5'
4	A	602	ADP	C3'-C4'-C5'-O5'
4	A	602	ADP	C2'-C1'-N9-C8
4	D	602	ADP	PB-O3A-PA-O1A
4	C	602	ADP	C5'-O5'-PA-O1A
4	C	602	ADP	C5'-O5'-PA-O2A
4	C	602	ADP	C5'-O5'-PA-O3A
4	C	602	ADP	PB-O3A-PA-O2A
4	A	602	ADP	C2'-C1'-N9-C4
4	A	602	ADP	O4'-C1'-N9-C8
4	B	601	ADP	PB-O3A-PA-O2A
4	D	602	ADP	PB-O3A-PA-O2A

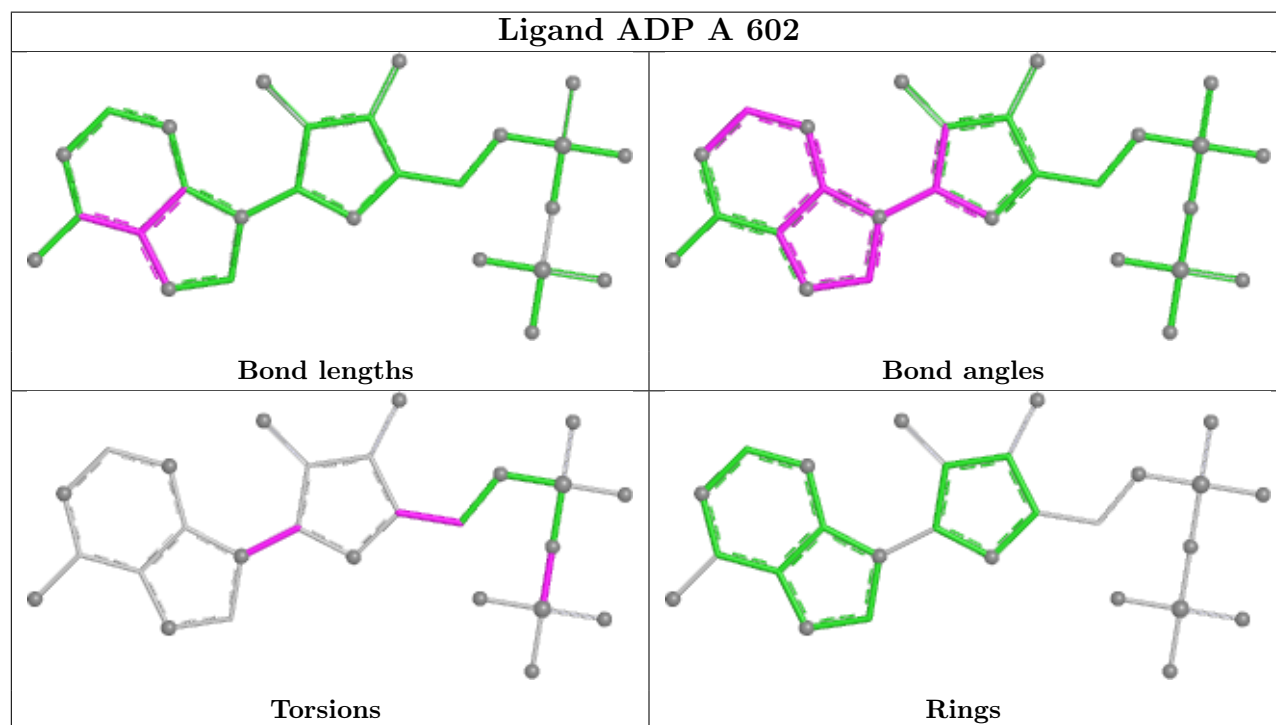
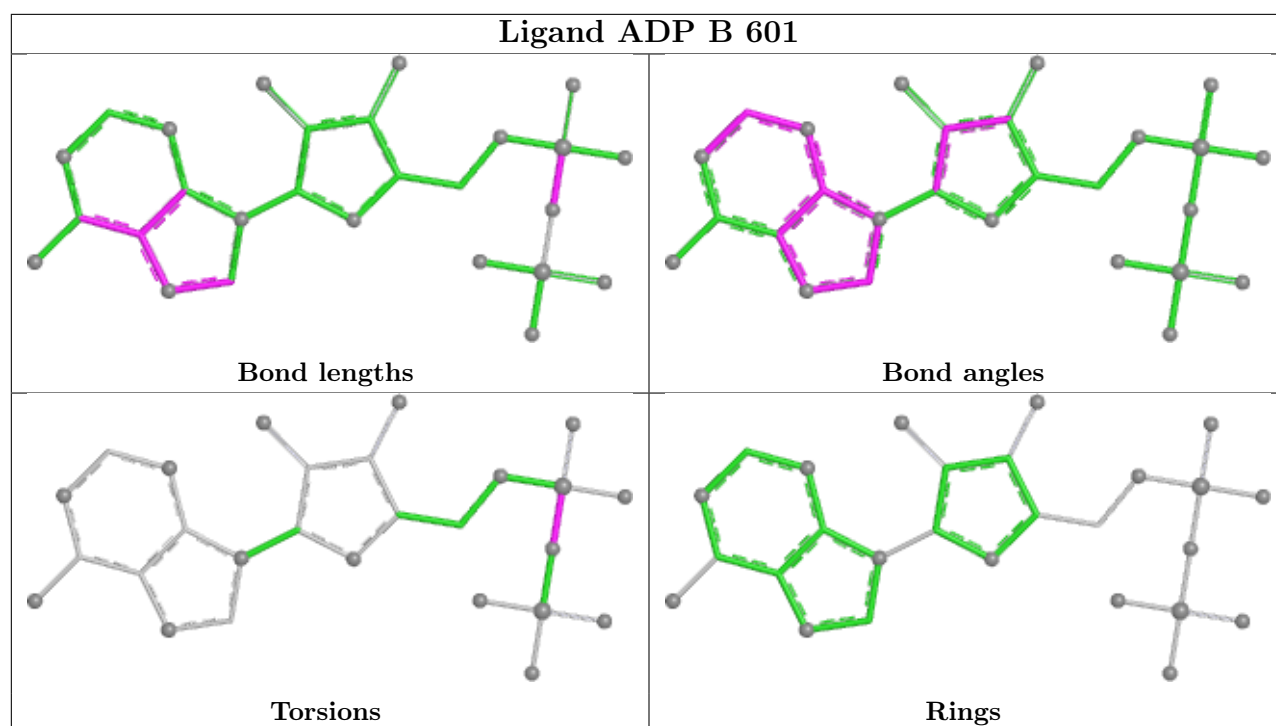
There are no ring outliers.

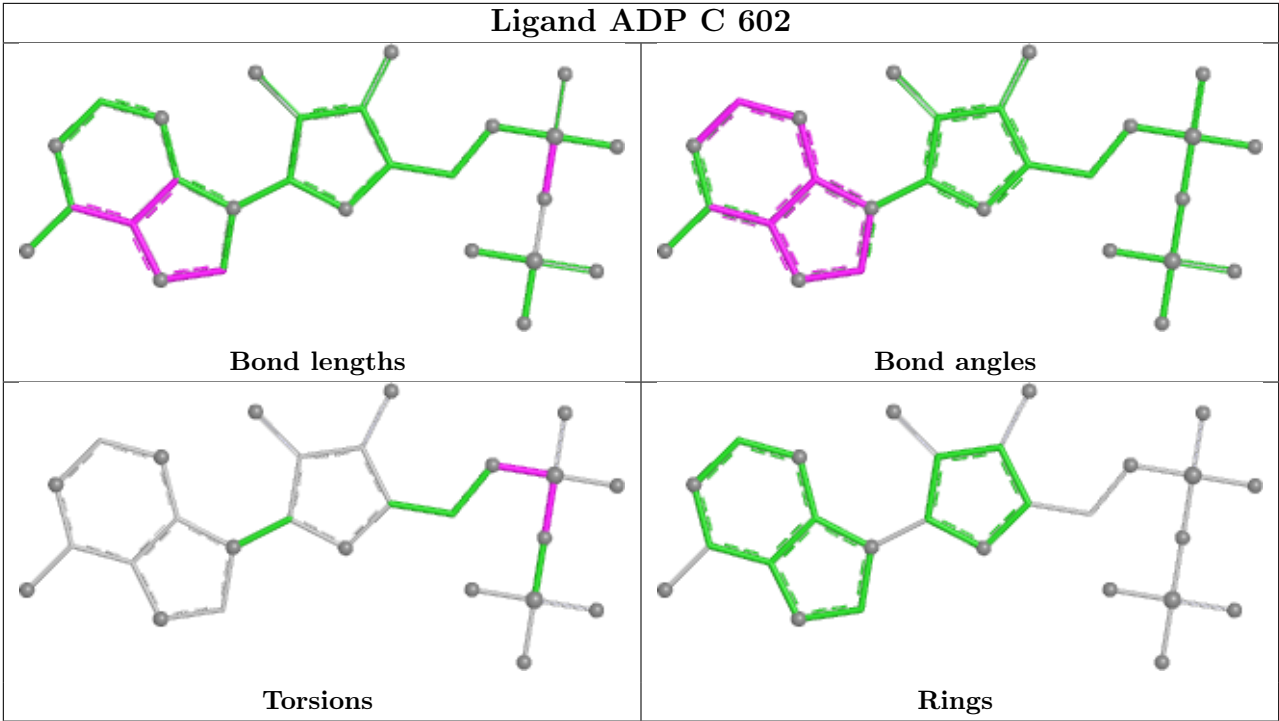
4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	602	ADP	7	0
4	B	601	ADP	1	0
4	A	602	ADP	5	0
4	C	602	ADP	3	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	229:ASN	C	230:TRP	N	1.00

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	309/387 (79%)	0.08	3 (0%) 79 59	28, 65, 100, 114	3 (0%)
1	B	319/387 (82%)	0.32	9 (2%) 55 32	29, 64, 93, 113	1 (0%)
1	C	322/387 (83%)	0.28	7 (2%) 62 39	25, 74, 118, 149	1 (0%)
1	D	322/387 (83%)	0.41	10 (3%) 51 30	30, 77, 117, 129	0
2	P	7/12 (58%)	0.40	1 (14%) 6 3	43, 54, 66, 67	0
All	All	1279/1560 (81%)	0.28	30 (2%) 61 38	25, 70, 111, 149	5 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	585	VAL	5.1
1	C	433	GLY	4.5
1	B	399	VAL	4.2
1	C	298	VAL	4.0
1	B	397	VAL	3.8
1	C	582	ALA	3.5
1	B	247	PRO	3.1
1	B	473	CYS	3.1
1	D	430	GLN	3.0
1	B	428	GLN	2.9
1	D	495	GLY	2.9
1	A	531	GLY	2.8
1	D	332	LEU	2.8
2	P	710	LEU	2.7
1	C	412	LEU	2.5
1	A	587	GLU	2.5
1	D	442	ALA	2.3
1	B	561	MET	2.3
1	B	357	THR	2.3
1	A	433	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	260	CYS	2.2
1	D	249	THR	2.2
1	C	429	VAL	2.1
1	D	398	TYR	2.1
1	D	532	GLN	2.1
1	B	407	GLY	2.1
1	B	398	TYR	2.1
1	C	551	SER	2.1
1	D	537	THR	2.1
1	D	561	MET	2.1

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.

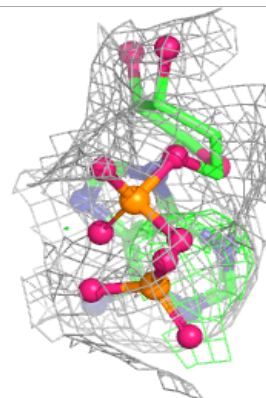
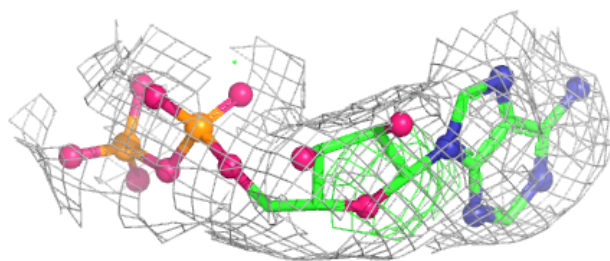
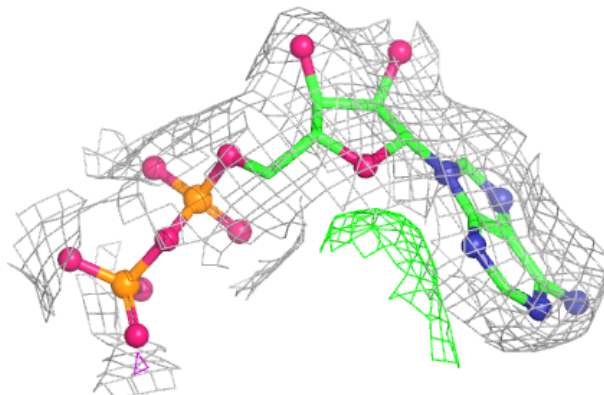
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	C	603	1/1	0.64	0.28	78,78,78,78	0
3	MG	D	601	1/1	0.79	0.12	49,49,49,49	0
4	ADP	A	602	27/27	0.87	0.09	54,79,94,105	0
3	MG	A	601	1/1	0.89	0.06	54,54,54,54	0
4	ADP	C	602	27/27	0.90	0.08	48,66,75,81	0
3	MG	C	601	1/1	0.92	0.16	53,53,53,53	0
4	ADP	D	602	27/27	0.94	0.08	49,74,85,92	0
4	ADP	B	601	27/27	0.95	0.08	38,50,57,59	0
3	MG	A	603	1/1	0.95	0.12	42,42,42,42	0
3	MG	B	603	1/1	0.95	0.04	30,30,30,30	0
3	MG	B	602	1/1	0.96	0.20	41,41,41,41	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.

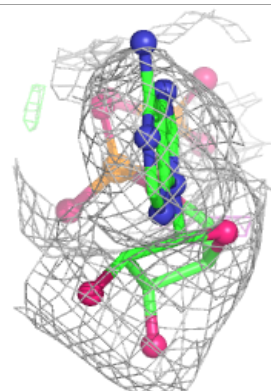
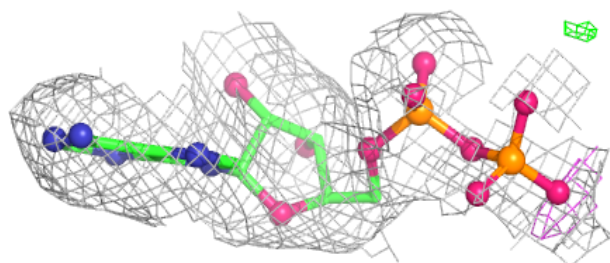
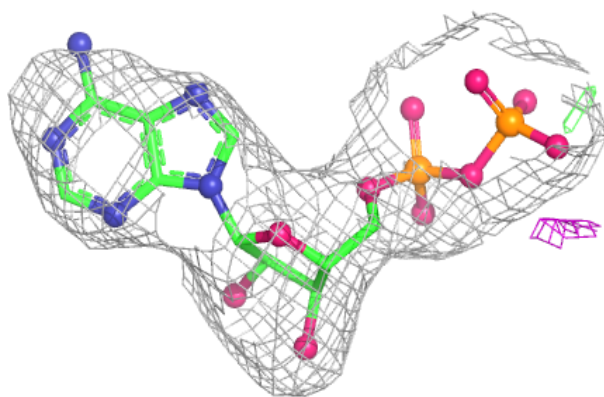
Electron density around ADP A 602:

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

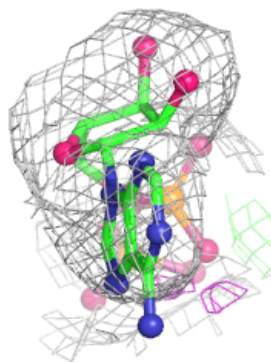
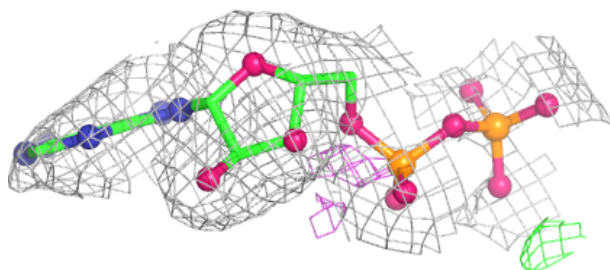
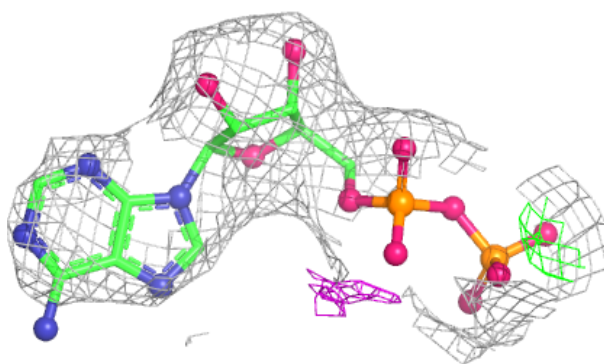


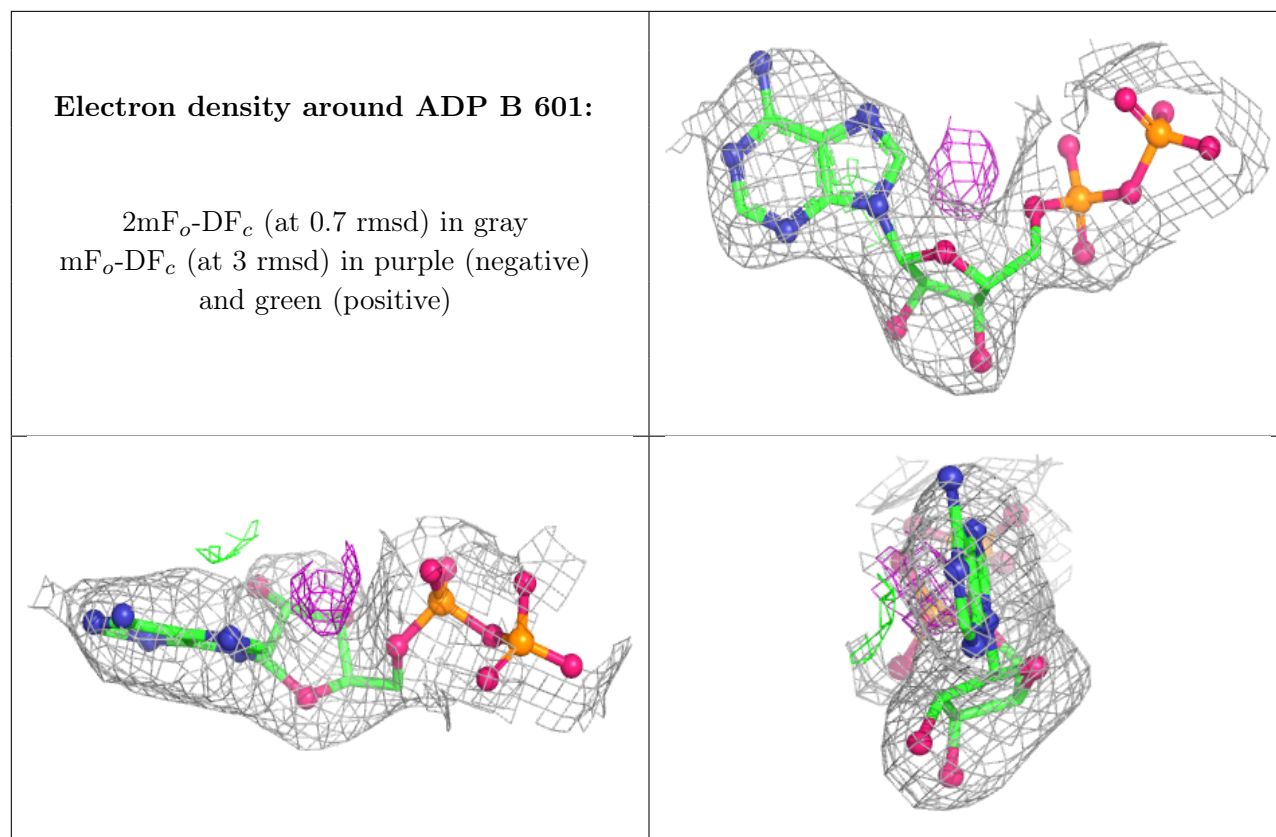
Electron density around ADP C 602:

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

**Electron density around ADP D 602:**

$2mF_o-DF_c$ (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.