



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:36 AM UTC

PDB ID : 4FT4 / pdb_00004ft4
Title : crystal structure of Zea mays ZMET2 in complex H3(1-32)K9me2 peptide and SAH
Authors : Du, J.; Patel, D.J.
Deposited on : 2012-06-27
Resolution : 2.70 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:

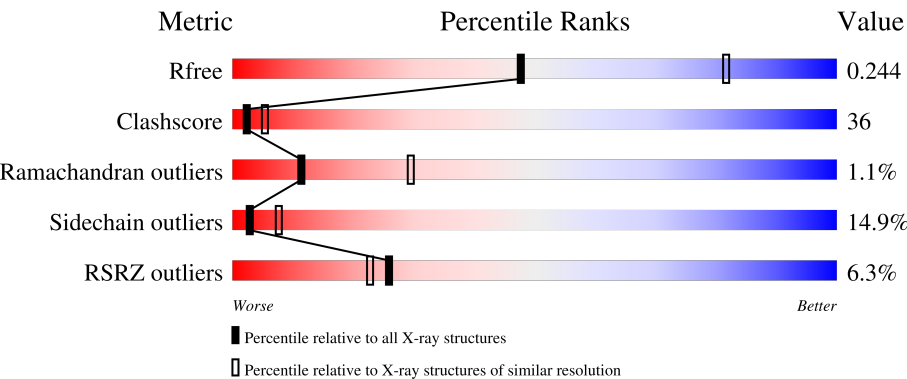
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	784	8% 35% 41% 12% • 12%
1	B	784	3% 57% 25% 6% • 12%
2	P	32	9% 6% 12% • 78%
2	Q	32	3% • • 6% • 84%

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
2	MLY	P	9	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11265 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 DNA (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	693	Total	C	N	O	S	0	0	0
			5514	3521	939	1021	33			
1	A	688	Total	C	N	O	S	0	0	0
			5443	3476	931	1003	33			

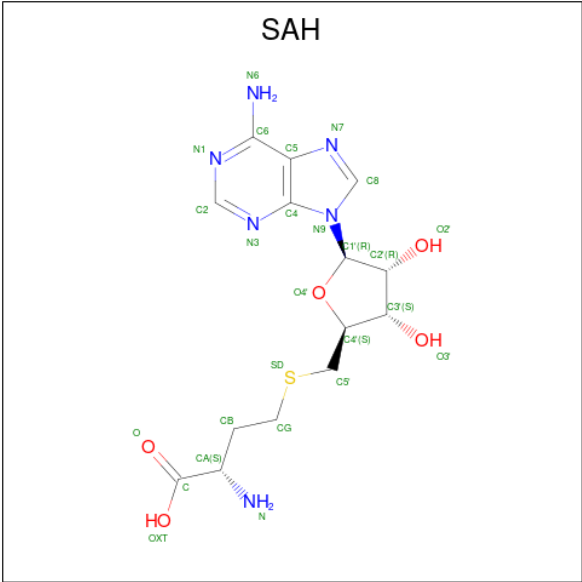
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	129	SER	-	expression tag	UNP Q9AXT8
A	129	SER	-	expression tag	UNP Q9AXT8

- Molecule 2 is a protein called H3(1-32)K9me2 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	0	0	0
			56	33	12	11			
2	Q	5	Total	C	N	O	0	0	0
			40	24	9	7			

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
3	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

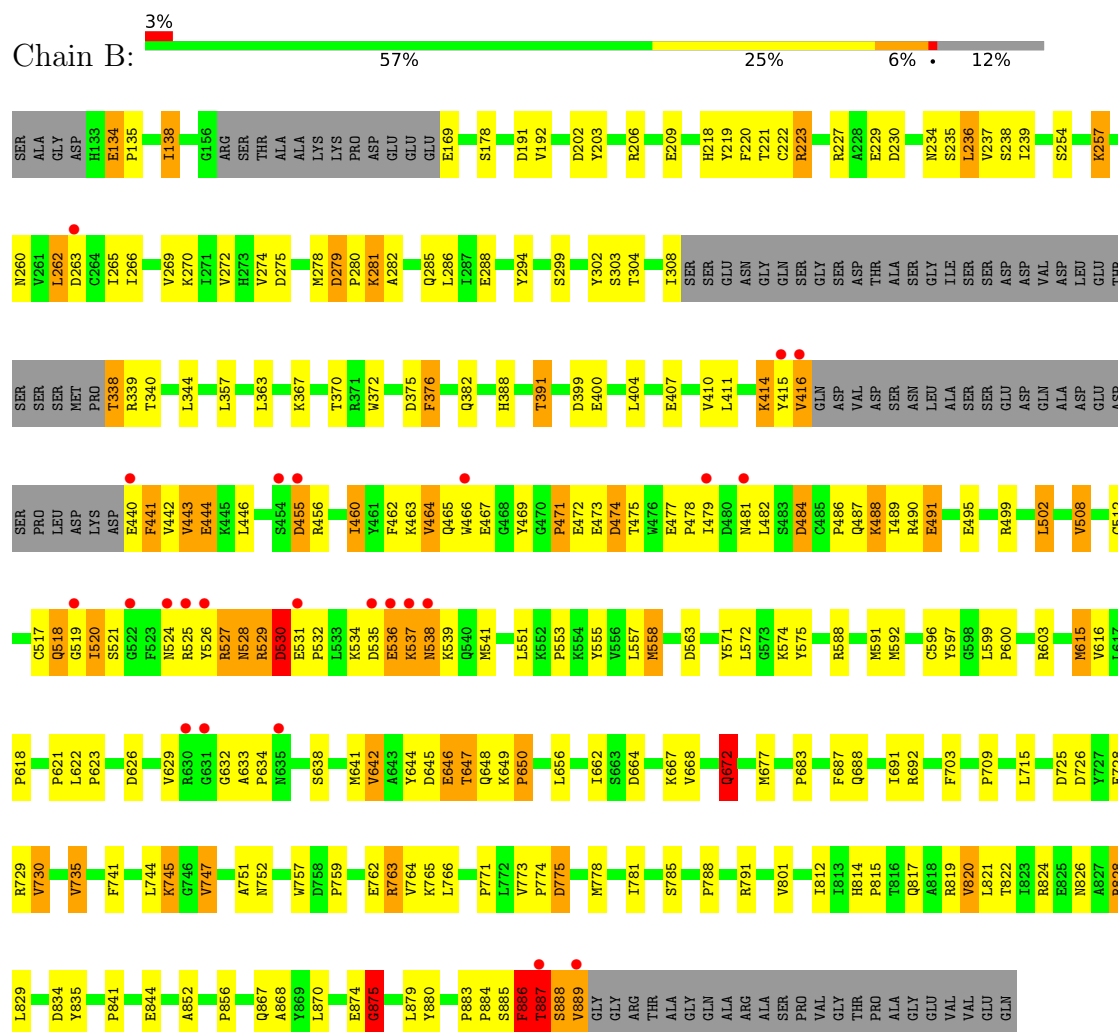
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	132	Total	O	0	0
			132	132		
4	A	27	Total	O	0	0
			27	27		
4	Q	1	Total	O	0	0
			1	1		

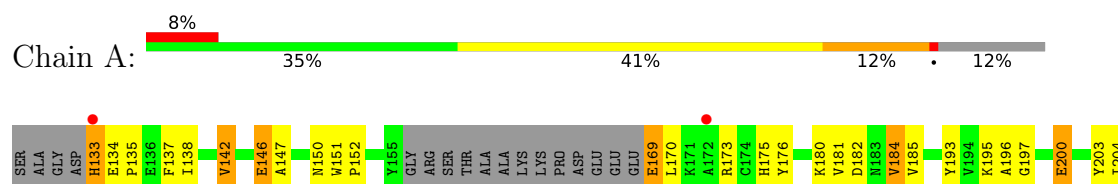
3 Residue-property plots

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: DNA (cytosine-5)-methyltransferase 1



• Molecule 1: DNA (cytosine-5)-methyltransferase 1





ALA	ARG	THR	LYS	GLN	T6	A7	R8	K9	S10	THR	GLY	GLY	LYS	ALA	PRO	ARG	LYS	GLN	LEU	ALA	THR	LYS	ALA	ALA	ARG	LYS	SER	ALA	PRO	ALA	THR
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.64Å 111.56Å 151.48Å 90.00° 101.98° 90.00°	Depositor
Resolution (Å)	43.82 – 2.70 43.82 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.4 (43.82-2.70) 98.5 (43.82-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.206 , 0.248 0.200 , 0.244	Depositor DCC
R_{free} test set	2894 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtriage
Anisotropy	0.512	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 63.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11265	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.53	0/5577	0.96	36/7555 (0.5%)
1	B	0.59	0/5649	0.85	16/7650 (0.2%)
2	P	0.26	0/44	0.66	0/58
2	Q	0.24	0/28	1.12	1/36 (2.8%)
All	All	0.56	0/11298	0.91	53/15299 (0.3%)

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	1

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	538	ASN	N-CA-C	-11.44	98.85	112.92
1	A	483	SER	N-CA-C	-11.02	99.26	111.28
1	A	284	ALA	N-CA-C	-9.93	100.45	111.28
1	A	648	GLN	N-CA-C	9.92	121.92	108.23
1	A	538	ASN	N-CA-C	-9.73	99.22	112.94
1	A	480	ASP	N-CA-C	-9.56	98.53	111.54
1	A	479	ILE	N-CA-C	8.77	121.20	108.58
1	A	793	TRP	N-CA-C	8.74	119.44	107.73
1	B	529	ARG	N-CA-C	7.19	119.98	111.71
1	B	234	ASN	CB-CA-C	-6.99	107.73	117.23
1	A	883	PRO	N-CA-C	6.94	119.17	110.70
1	B	530	ASP	N-CA-C	6.66	118.62	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	ILE	CB-CA-C	-6.62	102.70	110.91
1	A	478	PRO	N-CA-C	6.52	125.90	112.47
1	A	525	ARG	N-CA-C	-6.47	100.86	110.23
1	A	536	GLU	N-CA-C	6.42	121.82	108.53
1	A	478	PRO	CA-C-N	6.39	130.62	122.37
1	A	478	PRO	C-N-CA	6.39	130.62	122.37
1	B	444	GLU	N-CA-C	6.36	118.29	111.36
1	A	586	GLN	N-CA-C	-6.34	100.89	110.28
1	B	672	GLN	CA-C-N	6.33	126.87	120.04
1	B	672	GLN	C-N-CA	6.33	126.87	120.04
1	A	564	ILE	CB-CA-C	-6.12	104.05	111.88
1	A	535	ASP	N-CA-C	6.04	120.51	112.30
1	A	615	MET	N-CA-C	5.82	116.24	108.38
1	A	672	GLN	CA-C-N	5.76	125.86	119.87
1	A	672	GLN	C-N-CA	5.76	125.86	119.87
1	B	775	ASP	N-CA-C	5.68	117.47	111.28
1	A	755	VAL	N-CA-C	5.61	116.38	108.36
1	A	622	LEU	CA-C-N	5.56	125.57	119.89
1	A	622	LEU	C-N-CA	5.56	125.57	119.89
1	A	388	HIS	CA-C-N	5.52	126.74	119.84
1	A	388	HIS	C-N-CA	5.52	126.74	119.84
1	B	745	LYS	N-CA-C	5.41	118.07	110.23
1	B	887	THR	N-CA-C	-5.40	100.10	108.31
1	A	773	VAL	CA-C-N	5.35	125.27	119.76
1	A	773	VAL	C-N-CA	5.35	125.27	119.76
1	B	886	PHE	N-CA-C	-5.29	99.53	110.80
1	A	470	GLY	CA-C-N	5.26	124.88	119.05
1	A	470	GLY	C-N-CA	5.26	124.88	119.05
1	A	682	SER	CA-C-N	5.18	124.94	119.76
1	A	682	SER	C-N-CA	5.18	124.94	119.76
1	B	534	LYS	N-CA-C	-5.17	105.65	111.28
1	A	535	ASP	CA-C-N	-5.15	114.86	123.04
1	A	535	ASP	C-N-CA	-5.15	114.86	123.04
1	A	151	TRP	CA-C-N	5.11	124.90	119.28
1	A	151	TRP	C-N-CA	5.11	124.90	119.28
1	B	662	ILE	N-CA-C	5.10	117.12	112.43
1	B	471	PRO	N-CA-C	-5.08	103.46	111.34
2	Q	7	ALA	N-CA-C	5.05	117.18	111.11
1	A	415	TYR	N-CA-CB	-5.05	109.05	114.10
1	B	471	PRO	CA-C-N	-5.04	118.94	126.86
1	B	471	PRO	C-N-CA	-5.04	118.94	126.86

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	875	GLY	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	5443	0	5326	536	0
1	B	5514	0	5427	237	0
2	P	56	0	59	11	0
2	Q	40	0	45	9	0
3	A	26	0	19	5	0
3	B	26	0	19	5	0
4	A	27	0	0	2	0
4	B	132	0	0	5	0
4	Q	1	0	0	0	0
All	All	11265	0	10895	784	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 36.

All (784) 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:483:SER:O	1:A:486:PRO:HD3	1.31	1.26
1:A:533:LEU:HD12	1:A:534:LYS:N	1.52	1.22
1:A:589:LEU:C	1:A:589:LEU:HD12	1.64	1.22
1:A:481:ASN:C	1:A:481:ASN:HD22	1.47	1.20
1:A:589:LEU:HD12	1:A:589:LEU:O	1.34	1.20
1:A:878:PRO:C	1:A:879:LEU:HD13	1.65	1.20
1:A:285:GLN:CA	1:A:285:GLN:HE21	1.56	1.18
1:A:285:GLN:HE21	1:A:285:GLN:HA	1.07	1.15
1:A:526:TYR:HA	1:A:529:ARG:HD2	1.21	1.14
1:A:667:LYS:HD3	1:A:667:LYS:H	1.12	1.13
1:B:260:ASN:HD21	2:Q:7:ALA:HA	0.91	1.07
1:B:416:VAL:HG22	1:B:489:ILE:HG22	1.35	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:ASN:C	1:A:481:ASN:ND2	2.07	1.06
1:B:471:PRO:O	1:B:472:GLU:HB2	1.55	1.05
1:A:533:LEU:HD12	1:A:534:LYS:CA	1.85	1.05
1:A:203:TYR:CD1	2:P:9:MLY:HD3	1.91	1.04
1:A:533:LEU:CD1	1:A:533:LEU:C	2.30	1.04
1:A:781:ILE:HG22	1:A:781:ILE:O	1.57	1.04
1:A:589:LEU:C	1:A:589:LEU:CD1	2.30	1.04
1:A:878:PRO:C	1:A:879:LEU:CD1	2.30	1.03
1:A:203:TYR:HD1	2:P:9:MLY:HD3	1.13	1.03
1:B:883:PRO:HB2	1:B:884:PRO:HD2	1.39	1.02
1:A:879:LEU:HD13	1:A:879:LEU:N	1.63	1.02
1:B:886:PHE:HD1	1:B:887:THR:H	1.03	1.02
1:A:209:GLU:HB2	1:A:221:THR:HB	1.38	1.02
1:B:528:ASN:ND2	1:B:535:ASP:HB3	1.76	1.01
1:A:413:LYS:HB2	1:A:413:LYS:NZ	1.75	1.00
1:A:536:GLU:O	1:A:537:LYS:HG2	1.62	1.00
1:A:793:TRP:HB3	1:A:815:PRO:HB3	1.41	1.00
1:B:886:PHE:CD1	1:B:887:THR:N	2.29	1.00
1:B:260:ASN:ND2	2:Q:7:ALA:HA	1.77	0.98
1:A:749:VAL:CG1	1:A:756:GLU:CB	2.41	0.97
1:B:279:ASP:OD2	1:B:280:PRO:HD2	1.64	0.97
1:A:414:LYS:O	1:A:415:TYR:HB2	1.65	0.96
1:A:169:GLU:OE1	1:A:169:GLU:N	1.98	0.95
1:A:533:LEU:CD1	1:A:534:LYS:N	2.30	0.95
1:A:749:VAL:O	1:A:749:VAL:HG22	1.63	0.95
1:A:285:GLN:HA	1:A:285:GLN:NE2	1.71	0.95
1:B:528:ASN:ND2	1:B:536:GLU:CD	2.25	0.95
1:B:466:TRP:HH2	1:B:475:THR:HG1	0.96	0.94
1:A:481:ASN:ND2	1:A:482:LEU:HG	1.81	0.94
1:A:537:LYS:O	1:A:537:LYS:HG3	1.64	0.93
1:A:203:TYR:CE1	2:P:9:MLY:HD2	2.04	0.92
1:A:735:VAL:HG22	1:A:791:ARG:HH22	1.35	0.92
1:A:749:VAL:HG12	1:A:756:GLU:CB	1.99	0.92
1:A:371:ARG:HH11	1:A:371:ARG:CG	1.84	0.91
1:B:508:VAL:HG11	1:B:551:LEU:HD13	1.52	0.91
1:A:485:CYS:HB3	1:A:488:LYS:HB2	1.53	0.91
1:A:481:ASN:HD21	1:A:482:LEU:HG	1.35	0.91
1:A:203:TYR:CD1	2:P:9:MLY:CD	2.55	0.90
1:B:442:VAL:HG13	1:B:467:GLU:HB3	1.52	0.90
1:A:536:GLU:OE1	1:A:537:LYS:HG2	1.72	0.90
1:A:879:LEU:CD1	1:A:879:LEU:N	2.30	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:GLU:O	1:A:536:GLU:HG3	1.73	0.89
1:A:533:LEU:CD1	1:A:534:LYS:HA	2.02	0.89
1:B:443:VAL:HG22	1:B:443:VAL:O	1.72	0.89
1:A:285:GLN:HE21	1:A:285:GLN:N	1.70	0.89
1:A:671:HIS:HB2	1:A:721:ARG:HE	1.37	0.88
1:A:203:TYR:HE1	2:P:9:MLY:HD2	1.38	0.88
1:B:519:GLY:HA2	1:B:524:ASN:CB	2.04	0.88
1:A:533:LEU:C	1:A:533:LEU:HD13	1.98	0.87
1:A:724:ASN:O	1:A:725:ASP:HB2	1.74	0.87
1:A:749:VAL:HG11	1:A:756:GLU:CB	2.05	0.86
1:A:635:ASN:O	1:A:636:ALA:HB3	1.76	0.85
1:A:485:CYS:HA	1:A:488:LYS:HD3	1.59	0.85
1:A:770:LYS:CG	1:A:771:PRO:HD2	2.05	0.85
1:A:793:TRP:CB	1:A:815:PRO:HB3	2.06	0.85
1:A:859:ARG:HH11	1:A:859:ARG:CG	1.90	0.85
1:A:877:ASP:OD2	1:A:878:PRO:HD2	1.76	0.85
1:B:260:ASN:HD21	2:Q:7:ALA:CA	1.83	0.85
1:A:525:ARG:O	1:A:526:TYR:CG	2.30	0.84
1:A:525:ARG:O	1:A:526:TYR:CD2	2.30	0.84
1:B:528:ASN:HD22	1:B:535:ASP:HB3	1.43	0.84
1:A:748:ARG:HD2	1:A:759:PRO:HD3	1.59	0.83
1:B:745:LYS:HG2	1:B:764:VAL:HG21	1.58	0.83
1:A:283:LYS:HA	1:A:283:LYS:HE2	1.59	0.83
1:A:283:LYS:HA	1:A:283:LYS:CE	2.09	0.82
1:A:484:ASP:O	1:A:486:PRO:HD2	1.78	0.82
1:A:602:PHE:HE2	1:A:630:ARG:HH12	1.21	0.82
1:A:533:LEU:CD1	1:A:534:LYS:CA	2.56	0.82
1:A:196:ALA:HA	1:A:203:TYR:HE2	1.43	0.82
1:A:667:LYS:HD3	1:A:667:LYS:N	1.94	0.81
1:A:285:GLN:CA	1:A:285:GLN:NE2	2.30	0.81
1:B:191:ASP:OD1	1:B:206:ARG:HD3	1.81	0.81
1:B:883:PRO:HB2	1:B:884:PRO:CD	2.11	0.81
1:B:528:ASN:HB2	1:B:535:ASP:CG	2.06	0.81
1:A:485:CYS:CA	1:A:488:LYS:HD3	2.12	0.80
1:A:261:VAL:HG23	1:A:263:ASP:H	1.45	0.80
1:A:536:GLU:OE1	1:A:537:LYS:CE	2.30	0.79
1:B:416:VAL:HG21	1:B:490:ARG:CA	2.13	0.79
1:B:443:VAL:O	1:B:443:VAL:CG2	2.30	0.79
1:B:279:ASP:OD2	1:B:280:PRO:CD	2.30	0.79
1:A:735:VAL:HG22	1:A:791:ARG:NH2	1.97	0.79
1:B:275:ASP:O	1:B:278:MET:HG2	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:811:VAL:HG22	1:A:811:VAL:O	1.81	0.79
1:A:133:HIS:HE2	1:A:180:LYS:HG2	1.47	0.79
1:A:283:LYS:CE	1:A:283:LYS:CA	2.60	0.79
1:B:209:GLU:HB2	1:B:221:THR:HB	1.63	0.79
1:A:811:VAL:O	1:A:811:VAL:CG2	2.31	0.79
1:A:536:GLU:O	1:A:537:LYS:CG	2.30	0.79
1:B:886:PHE:HD1	1:B:887:THR:N	1.75	0.78
1:A:142:VAL:CG2	1:A:147:ALA:HB2	2.13	0.78
1:A:415:TYR:O	1:A:416:VAL:HG13	1.83	0.78
1:B:519:GLY:HA2	1:B:524:ASN:HB2	1.65	0.78
1:B:715:LEU:O	1:B:824:ARG:HD2	1.82	0.78
1:A:602:PHE:CE2	1:A:630:ARG:NH1	2.50	0.78
1:A:651:SER:O	1:A:652:LEU:HD23	1.84	0.78
1:A:413:LYS:HB2	1:A:413:LYS:HZ3	1.45	0.78
1:A:485:CYS:C	1:A:488:LYS:HD3	2.08	0.78
1:B:416:VAL:CG2	1:B:490:ARG:HA	2.13	0.78
1:A:794:TRP:HH2	1:A:816:THR:HG23	1.49	0.78
1:A:536:GLU:O	1:A:536:GLU:CG	2.29	0.78
1:A:283:LYS:HE2	1:A:283:LYS:CA	2.12	0.77
1:A:536:GLU:OE1	1:A:537:LYS:HE2	1.84	0.77
1:B:236:LEU:HD22	1:B:575:TYR:HA	1.66	0.77
1:A:781:ILE:O	1:A:781:ILE:CG2	2.30	0.77
1:A:728:GLU:OE1	1:A:766:LEU:HD23	1.85	0.77
1:A:819:ARG:HG2	1:A:820:VAL:O	1.84	0.77
1:B:442:VAL:CG1	1:B:467:GLU:HB3	2.14	0.77
1:B:528:ASN:HB2	1:B:535:ASP:OD1	1.82	0.77
1:A:203:TYR:CE1	2:P:9:MLY:CD	2.66	0.77
1:A:196:ALA:HA	1:A:203:TYR:CE2	2.19	0.77
1:B:645:ASP:OD2	1:B:647:THR:HG23	1.86	0.76
1:A:725:ASP:OD1	1:A:768:SER:CB	2.34	0.76
1:A:415:TYR:O	1:A:416:VAL:HG22	1.86	0.76
1:A:460:ILE:O	1:A:461:TYR:HD2	1.69	0.75
1:A:483:SER:O	1:A:486:PRO:CD	2.25	0.75
1:A:823:ILE:HD11	1:A:842:ILE:HG23	1.67	0.75
1:A:223:ARG:HB3	1:A:257:LYS:HG2	1.67	0.75
1:A:565:LEU:HD12	1:A:591:MET:HE2	1.69	0.75
1:B:279:ASP:OD2	1:B:279:ASP:C	2.29	0.75
1:B:645:ASP:CG	1:B:647:THR:HG23	2.11	0.74
1:A:867:GLN:NE2	1:A:872:GLU:O	2.20	0.74
1:A:371:ARG:HH11	1:A:371:ARG:HG3	1.50	0.74
1:A:770:LYS:HG3	1:A:771:PRO:HD2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:ILE:O	1:A:480:ASP:C	2.30	0.74
1:A:443:VAL:HG21	1:A:485:CYS:SG	2.27	0.74
1:A:347:TYR:O	3:A:1000:SAH:HG1	1.88	0.73
1:A:555:TYR:HE2	1:A:618:PRO:HD3	1.52	0.73
1:B:763:ARG:NH1	1:B:773:VAL:O	2.22	0.73
1:A:748:ARG:O	1:A:749:VAL:HG13	1.88	0.73
1:A:748:ARG:HG2	1:A:749:VAL:H	1.54	0.72
1:B:888:SER:O	1:B:889:VAL:C	2.30	0.72
1:A:508:VAL:HG21	1:A:551:LEU:HD13	1.72	0.72
1:A:343:LEU:HD13	1:A:510:VAL:HG22	1.71	0.72
1:B:763:ARG:NH2	1:B:775:ASP:OD1	2.21	0.72
1:A:481:ASN:ND2	1:A:482:LEU:CG	2.51	0.72
1:A:659:GLY:HA3	1:A:794:TRP:HD1	1.54	0.72
1:B:223:ARG:HD2	1:B:254:SER:O	1.90	0.72
1:A:691:ILE:HG12	1:A:828:ARG:HG2	1.70	0.72
1:A:279:ASP:HB3	1:A:280:PRO:HD2	1.72	0.72
1:A:748:ARG:O	1:A:749:VAL:CG1	2.38	0.72
1:A:196:ALA:HB1	1:A:200:GLU:HB3	1.72	0.71
1:A:415:TYR:C	1:A:416:VAL:HG22	2.15	0.71
1:A:501:ILE:O	1:A:502:LEU:HD23	1.90	0.71
1:A:746:GLY:O	1:A:757:TRP:HA	1.90	0.71
1:B:471:PRO:O	1:B:472:GLU:CB	2.30	0.71
1:A:555:TYR:CE2	1:A:618:PRO:HD3	2.24	0.71
1:A:794:TRP:CH2	1:A:816:THR:HG23	2.24	0.71
1:A:485:CYS:O	1:A:488:LYS:HB2	1.90	0.71
1:B:741:PHE:HE1	1:B:778:MET:CE	2.04	0.71
1:A:766:LEU:HB2	1:A:770:LYS:O	1.90	0.71
1:A:635:ASN:O	1:A:636:ALA:CB	2.35	0.71
1:A:747:VAL:O	1:A:748:ARG:HB2	1.91	0.71
1:A:770:LYS:HG2	1:A:771:PRO:HD2	1.72	0.70
1:A:793:TRP:HB2	1:A:794:TRP:CE3	2.25	0.70
1:A:560:ASN:HB3	1:A:564:ILE:HD11	1.73	0.70
1:B:192:VAL:HG21	1:B:265:ILE:HG23	1.73	0.70
1:B:527:ARG:N	4:B:1190:HOH:O	2.23	0.70
1:B:883:PRO:CB	1:B:884:PRO:CD	2.68	0.70
1:A:231:THR:OG1	1:A:233:ILE:HG12	1.91	0.70
1:A:601:GLN:NE2	1:A:830:GLN:OE1	2.24	0.69
1:A:371:ARG:HB3	1:A:372:TRP:CE3	2.28	0.69
1:A:359:LEU:C	1:A:859:ARG:HH12	2.00	0.69
1:A:766:LEU:CD1	1:A:772:LEU:HA	2.23	0.69
1:A:737:LYS:NZ	1:A:795:ASP:OD1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:VAL:HG12	1:A:489:ILE:HG22	1.75	0.69
1:A:481:ASN:HD21	1:A:482:LEU:CG	2.06	0.69
1:A:488:LYS:CD	1:A:488:LYS:H	2.05	0.69
1:A:560:ASN:CB	1:A:564:ILE:HD11	2.23	0.68
1:A:819:ARG:NH2	1:A:825:GLU:OE1	2.25	0.68
1:B:488:LYS:HA	1:B:491:GLU:HG3	1.74	0.68
1:B:603:ARG:NH2	1:B:801:VAL:O	2.27	0.68
1:A:749:VAL:O	1:A:749:VAL:CG2	2.37	0.68
1:B:416:VAL:HG21	1:B:490:ARG:HA	1.73	0.68
1:B:528:ASN:OD1	1:B:528:ASN:C	2.36	0.68
1:A:279:ASP:HB3	1:A:280:PRO:CD	2.24	0.68
1:A:484:ASP:C	1:A:486:PRO:CD	2.65	0.68
1:A:671:HIS:CB	1:A:721:ARG:HE	2.06	0.68
1:B:462:PHE:HE2	1:B:479:ILE:HD13	1.59	0.68
1:A:659:GLY:HA3	1:A:794:TRP:CD1	2.29	0.68
1:A:744:LEU:HD13	1:A:772:LEU:HD22	1.76	0.68
1:A:283:LYS:HE3	1:A:286:LEU:HD12	1.74	0.68
1:B:528:ASN:HD22	1:B:536:GLU:HG3	1.59	0.68
1:A:859:ARG:HH11	1:A:859:ARG:HG3	1.58	0.68
1:A:791:ARG:NH2	1:A:815:PRO:O	2.27	0.67
1:A:728:GLU:CD	1:A:766:LEU:CD2	2.68	0.67
1:A:819:ARG:NH2	1:A:825:GLU:CD	2.53	0.67
1:A:878:PRO:O	1:A:879:LEU:HD12	1.94	0.67
1:A:533:LEU:HD12	1:A:534:LYS:HA	1.61	0.67
1:A:604:MET:SD	1:A:641:MET:HE1	2.34	0.67
1:A:878:PRO:C	1:A:879:LEU:HD12	2.19	0.67
1:A:878:PRO:CB	1:A:879:LEU:HD13	2.25	0.67
1:A:456:ARG:HD2	1:A:461:TYR:HD1	1.59	0.67
2:Q:7:ALA:O	2:Q:8:ARG:HB3	1.94	0.67
1:A:371:ARG:HH11	1:A:371:ARG:HG2	1.59	0.67
1:A:485:CYS:HA	1:A:488:LYS:CD	2.25	0.66
1:A:659:GLY:CA	1:A:794:TRP:CD1	2.78	0.66
1:A:195:LYS:HA	1:A:266:ILE:HD11	1.78	0.66
1:A:867:GLN:HE21	1:A:872:GLU:C	2.02	0.66
1:A:481:ASN:ND2	1:A:482:LEU:CB	2.58	0.66
1:A:748:ARG:C	1:A:749:VAL:HG12	2.21	0.66
1:B:466:TRP:HZ3	1:B:475:THR:HG23	1.61	0.66
1:B:645:ASP:OD2	1:B:647:THR:CG2	2.43	0.66
1:A:278:MET:HB3	1:A:283:LYS:HD3	1.77	0.66
1:A:882:LEU:N	1:A:882:LEU:HD12	2.10	0.66
1:B:541:MET:SD	1:B:558:MET:HE1	2.37	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:LEU:HD12	1:A:344:LEU:N	2.10	0.65
1:A:617:LEU:HD12	1:A:618:PRO:HD2	1.77	0.65
1:A:384:LEU:HD23	1:A:393:VAL:HG22	1.77	0.65
1:B:591:MET:O	1:B:642:VAL:HG13	1.97	0.65
1:B:664:ASP:OD1	1:B:828:ARG:NH1	2.30	0.65
1:A:737:LYS:NZ	1:A:795:ASP:OD2	2.28	0.65
1:B:279:ASP:OD2	1:B:281:LYS:N	2.30	0.65
1:A:285:GLN:NE2	1:A:285:GLN:N	2.42	0.65
1:A:748:ARG:C	1:A:749:VAL:CG1	2.70	0.65
1:A:794:TRP:CZ3	1:A:815:PRO:HB2	2.31	0.65
1:B:455:ASP:N	1:B:455:ASP:OD1	2.29	0.65
1:B:645:ASP:OD1	1:B:645:ASP:N	2.29	0.65
1:A:275:ASP:OD2	1:A:277:ASN:N	2.30	0.64
1:A:295:ASP:OD1	1:A:296:MET:HG3	1.96	0.64
1:A:560:ASN:HB3	1:A:564:ILE:CD1	2.27	0.64
2:P:11:THR:O	2:P:11:THR:OG1	2.16	0.64
1:A:808:HIS:C	1:A:809:ASN:OD1	2.40	0.64
1:B:460:ILE:HG22	1:B:479:ILE:HB	1.80	0.64
1:B:887:THR:OG1	1:B:888:SER:N	2.29	0.64
1:A:137:PHE:C	1:A:138:ILE:HD12	2.23	0.64
1:A:596:CYS:HB3	1:A:623:PRO:HB3	1.80	0.64
1:A:485:CYS:HB3	1:A:488:LYS:CB	2.26	0.64
1:B:495:GLU:OE2	1:B:499:ARG:NH1	2.30	0.64
1:A:481:ASN:ND2	1:A:482:LEU:HB2	2.11	0.64
1:A:484:ASP:C	1:A:486:PRO:HD2	2.22	0.64
1:B:304:THR:HG21	1:B:588:ARG:HH21	1.63	0.64
1:A:565:LEU:CD1	1:A:591:MET:HE2	2.28	0.64
1:B:528:ASN:HD22	1:B:536:GLU:CG	2.12	0.63
1:A:533:LEU:HD13	1:A:533:LEU:O	1.98	0.63
1:A:737:LYS:NZ	1:A:795:ASP:CG	2.56	0.63
1:A:359:LEU:C	1:A:859:ARG:NH1	2.57	0.63
1:B:279:ASP:CG	1:B:280:PRO:HD2	2.23	0.63
1:B:466:TRP:HB2	1:B:469:TYR:HD2	1.63	0.63
1:A:414:LYS:CG	1:A:416:VAL:O	2.46	0.63
1:A:664:ASP:HB2	1:A:688:GLN:CD	2.24	0.63
1:A:642:VAL:HG12	1:A:642:VAL:O	1.99	0.63
1:A:645:ASP:OD1	1:A:648:GLN:HG3	1.97	0.63
1:A:748:ARG:N	1:A:756:GLU:O	2.31	0.63
1:A:647:THR:O	1:A:648:GLN:NE2	2.32	0.63
1:B:481:ASN:OD1	1:A:527:ARG:NE	2.32	0.62
1:B:474:ASP:N	1:B:474:ASP:OD1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:766:LEU:HD12	1:A:772:LEU:HA	1.80	0.62
1:B:884:PRO:CD	1:B:885:SER:H	2.13	0.62
1:A:526:TYR:HA	1:A:529:ARG:CD	2.14	0.62
1:B:525:ARG:HG3	1:B:526:TYR:CE2	2.34	0.62
1:A:343:LEU:HD12	1:A:344:LEU:H	1.63	0.62
1:A:600:PRO:HG2	1:A:661:ALA:HB2	1.81	0.62
1:A:684:LYS:N	1:A:688:GLN:OE1	2.27	0.62
1:B:375:ASP:CG	3:B:1000:SAH:O3'	2.43	0.62
1:B:791:ARG:HD3	1:B:815:PRO:O	2.00	0.62
1:A:481:ASN:CG	1:A:482:LEU:HG	2.24	0.62
1:B:416:VAL:HG23	1:B:490:ARG:HA	1.81	0.62
1:A:802:VAL:HG22	1:A:803:THR:N	2.15	0.62
1:B:399:ASP:OD2	1:B:400:GLU:N	2.33	0.62
1:B:519:GLY:CA	1:B:524:ASN:CB	2.76	0.61
1:B:236:LEU:HD22	1:B:575:TYR:CA	2.29	0.61
1:B:415:TYR:O	1:B:416:VAL:HB	2.00	0.61
1:B:683:PRO:HB3	1:B:692:ARG:HD3	1.81	0.61
1:A:747:VAL:C	1:A:756:GLU:O	2.43	0.61
1:B:791:ARG:NH2	1:B:814:HIS:O	2.34	0.61
1:A:482:LEU:N	1:A:482:LEU:HD23	2.13	0.61
1:B:528:ASN:ND2	1:B:535:ASP:CB	2.60	0.61
1:A:877:ASP:CG	1:A:878:PRO:HD2	2.24	0.61
1:A:632:GLY:O	1:A:634:PRO:HD3	2.00	0.61
1:B:370:THR:O	1:B:391:THR:HB	2.00	0.61
1:A:583:MET:O	1:A:584:LYS:HG2	2.01	0.61
1:B:202:ASP:O	1:B:227:ARG:NH2	2.32	0.61
1:A:728:GLU:CD	1:A:766:LEU:HD21	2.26	0.61
1:B:388:HIS:O	1:B:391:THR:HG23	2.01	0.61
1:A:408:TRP:O	1:A:412:CYS:SG	2.53	0.61
1:A:633:ALA:HB2	1:A:641:MET:CE	2.31	0.61
2:P:8:ARG:NH2	2:P:10:SER:OG	2.34	0.61
1:A:449:ILE:HD11	1:A:460:ILE:HG13	1.83	0.60
1:B:440:GLU:HG2	1:B:441:PHE:H	1.66	0.60
1:A:356:GLY:HA3	1:A:858:ALA:HB3	1.83	0.60
1:A:449:ILE:HG22	1:A:492:PHE:HZ	1.66	0.60
1:A:878:PRO:HB2	1:A:879:LEU:CD1	2.31	0.60
1:B:134:GLU:HG3	1:B:135:PRO:HD2	1.82	0.60
1:A:203:TYR:HD1	2:P:9:MLY:CD	1.96	0.60
1:A:763:ARG:HH22	1:A:775:ASP:CG	2.08	0.60
1:B:526:TYR:C	4:B:1190:HOH:O	2.43	0.60
1:A:340:THR:HA	1:A:367:LYS:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:744:LEU:O	1:B:747:VAL:CG1	2.49	0.60
1:A:748:ARG:CG	1:A:749:VAL:H	2.14	0.60
1:A:859:ARG:HH11	1:A:859:ARG:HG2	1.65	0.60
1:B:218:HIS:HB3	1:B:262:LEU:HD22	1.83	0.60
1:A:284:ALA:C	1:A:285:GLN:HE21	2.10	0.60
1:A:196:ALA:CA	1:A:203:TYR:HE2	2.15	0.59
1:A:636:ALA:O	1:A:639:GLN:NE2	2.29	0.59
1:A:307:ASN:O	1:A:308:ILE:HB	2.01	0.59
1:A:463:LYS:HA	1:A:475:THR:O	2.02	0.59
2:Q:8:ARG:HG2	2:Q:8:ARG:O	2.02	0.59
1:B:672:GLN:HG3	1:B:672:GLN:O	2.02	0.59
1:A:594:ALA:HB3	1:A:603:ARG:HB3	1.85	0.59
1:B:407:GLU:O	1:B:410:VAL:HG22	2.01	0.59
1:A:757:TRP:NE1	1:A:763:ARG:HG2	2.18	0.59
1:A:371:ARG:HG3	1:A:371:ARG:NH1	2.16	0.59
1:A:601:GLN:HB2	1:A:798:VAL:O	2.01	0.59
1:B:466:TRP:CZ3	1:B:475:THR:HG23	2.38	0.59
1:B:528:ASN:HD22	1:B:536:GLU:CD	2.09	0.59
1:B:874:GLU:CD	1:B:875:GLY:N	2.61	0.58
1:A:456:ARG:HD2	1:A:461:TYR:CD1	2.38	0.58
1:A:481:ASN:ND2	1:A:481:ASN:O	2.16	0.58
1:A:781:ILE:HG21	1:A:784:LYS:O	2.02	0.58
1:B:519:GLY:CA	1:B:524:ASN:HB3	2.34	0.58
1:B:520:ILE:HG13	1:B:563:ASP:HB3	1.84	0.58
1:A:650:PRO:HD2	1:A:651:SER:H	1.68	0.58
1:A:728:GLU:CD	1:A:766:LEU:HD23	2.29	0.58
1:A:387:ASN:HD21	1:A:837:ARG:H	1.51	0.58
1:B:192:VAL:CG2	1:B:265:ILE:HG23	2.34	0.58
1:B:728:GLU:HB3	1:B:766:LEU:HD22	1.85	0.58
1:A:672:GLN:HG3	1:A:718:GLN:HG2	1.84	0.58
1:B:191:ASP:OD2	1:B:206:ARG:NH1	2.37	0.57
1:B:229:GLU:HG3	1:B:237:VAL:HG11	1.86	0.57
1:A:757:TRP:CZ2	1:A:763:ARG:CZ	2.87	0.57
1:B:278:MET:HE2	1:B:282:ALA:HB3	1.85	0.57
1:B:519:GLY:O	1:B:524:ASN:HB3	2.03	0.57
1:B:744:LEU:O	1:B:747:VAL:HG12	2.04	0.57
1:A:460:ILE:C	1:A:461:TYR:CD2	2.82	0.57
1:A:792:LEU:C	1:A:792:LEU:HD12	2.29	0.57
1:A:878:PRO:O	1:A:879:LEU:CD1	2.49	0.57
1:B:668:VAL:HG11	1:B:677:MET:HE1	1.86	0.57
1:A:664:ASP:OD2	1:A:692:ARG:NH1	2.32	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:874:GLU:CD	1:B:875:GLY:H	2.13	0.57
1:A:414:LYS:O	1:A:415:TYR:CB	2.45	0.57
1:A:671:HIS:HB2	1:A:721:ARG:NE	2.14	0.57
1:B:239:ILE:C	1:B:239:ILE:HD12	2.29	0.57
1:A:878:PRO:HB2	1:A:879:LEU:HD13	1.85	0.57
1:B:629:VAL:HG11	1:B:641:MET:SD	2.45	0.57
1:A:488:LYS:H	1:A:488:LYS:HD2	1.67	0.57
2:P:8:ARG:NH1	2:P:10:SER:OG	2.38	0.57
1:A:677:MET:HE3	1:A:717:HIS:HB3	1.86	0.56
1:A:748:ARG:CD	1:A:759:PRO:HD3	2.32	0.56
1:A:736:LYS:HA	1:A:793:TRP:CH2	2.40	0.56
1:A:781:ILE:CG2	1:A:784:LYS:O	2.53	0.56
1:A:349:GLY:C	1:A:351:GLY:H	2.14	0.56
1:A:695:ARG:NE	1:A:835:TYR:CD1	2.74	0.56
1:A:859:ARG:HG3	1:A:859:ARG:NH1	2.20	0.56
1:B:473:GLU:OE1	1:B:473:GLU:HA	2.04	0.56
1:A:415:TYR:CE1	1:A:494:GLN:HG2	2.41	0.56
2:Q:8:ARG:O	2:Q:8:ARG:CG	2.54	0.56
1:A:375:ASP:O	1:A:395:ASN:HA	2.06	0.56
1:A:564:ILE:O	1:A:570:GLY:HA2	2.06	0.56
1:A:664:ASP:HB3	1:A:828:ARG:HH12	1.71	0.56
1:A:774:PRO:HB3	1:A:776:TYR:CE2	2.40	0.56
1:A:209:GLU:HB2	1:A:221:THR:CB	2.26	0.56
1:A:589:LEU:HA	1:A:620:TYR:OH	2.05	0.56
1:A:263:ASP:OD2	1:A:263:ASP:N	2.38	0.55
1:B:741:PHE:CD2	1:B:788:PRO:HB2	2.41	0.55
1:A:645:ASP:HB2	1:A:648:GLN:HG2	1.88	0.55
1:A:695:ARG:HG3	1:A:700:ASP:HB3	1.87	0.55
1:A:814:HIS:CG	1:A:815:PRO:HD2	2.41	0.55
1:B:279:ASP:OD2	1:B:280:PRO:N	2.39	0.55
1:B:828:ARG:NH2	1:B:834:ASP:OD2	2.39	0.55
1:A:659:GLY:HA2	1:A:794:TRP:CD1	2.40	0.55
1:A:802:VAL:CG2	1:A:803:THR:N	2.69	0.55
1:A:195:LYS:NZ	1:A:197:GLY:HA2	2.21	0.55
1:A:234:ASN:OD1	1:A:235:SER:N	2.39	0.55
1:A:855:VAL:HG22	1:A:856:PRO:HD3	1.89	0.55
1:B:884:PRO:HD2	1:B:885:SER:H	1.71	0.55
1:A:715:LEU:O	1:A:824:ARG:HD2	2.06	0.55
1:A:283:LYS:N	1:A:283:LYS:CD	2.68	0.55
1:A:650:PRO:CD	1:A:651:SER:H	2.20	0.55
1:A:828:ARG:HD2	1:A:834:ASP:OD1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:872:GLU:OE1	1:A:872:GLU:N	2.39	0.55
1:A:659:GLY:CA	1:A:794:TRP:HD1	2.17	0.55
1:B:512:CYS:HA	1:B:557:LEU:O	2.07	0.54
1:A:279:ASP:OD1	1:A:279:ASP:N	2.39	0.54
1:B:416:VAL:HG21	1:B:490:ARG:N	2.22	0.54
1:A:345:ASP:OD2	1:A:354:SER:HB3	2.06	0.54
1:A:133:HIS:ND1	1:A:134:GLU:N	2.56	0.54
1:A:133:HIS:ND1	1:A:133:HIS:C	2.65	0.54
1:A:287:ILE:HD13	1:A:293:TYR:CE2	2.43	0.54
2:P:8:ARG:CZ	2:P:10:SER:OG	2.56	0.54
1:A:173:ARG:HG3	1:A:214:THR:HA	1.90	0.54
1:A:739:ALA:HB3	1:A:791:ARG:HG2	1.90	0.54
1:A:416:VAL:HG12	1:A:489:ILE:CG2	2.37	0.54
1:B:527:ARG:HB2	4:B:1190:HOH:O	2.08	0.53
1:A:537:LYS:O	1:A:537:LYS:CG	2.45	0.53
1:B:375:ASP:OD2	3:B:1000:SAH:O3'	2.25	0.53
1:A:749:VAL:CG1	1:A:756:GLU:N	2.71	0.53
1:A:770:LYS:HG2	1:A:771:PRO:CD	2.38	0.53
1:B:191:ASP:CG	1:B:206:ARG:HH11	2.16	0.53
1:B:508:VAL:HG22	1:B:553:PRO:HB3	1.90	0.53
1:A:235:SER:C	1:A:237:VAL:H	2.15	0.53
1:A:415:TYR:CD1	1:A:494:GLN:HG2	2.43	0.53
1:A:602:PHE:O	1:A:799:PRO:O	2.26	0.53
1:A:882:LEU:HD12	1:A:882:LEU:H	1.72	0.53
1:A:758:ASP:O	1:A:761:ILE:O	2.27	0.53
1:B:541:MET:SD	1:B:558:MET:CE	2.97	0.53
1:A:481:ASN:ND2	1:A:482:LEU:N	2.55	0.53
1:A:592:MET:SD	1:A:861:LEU:HD21	2.49	0.53
1:A:878:PRO:HG2	1:A:879:LEU:HD22	1.91	0.53
1:B:487:GLN:O	1:B:491:GLU:HG2	2.09	0.53
1:A:146:GLU:OE1	1:A:146:GLU:C	2.52	0.53
1:A:446:LEU:HD23	1:A:462:PHE:HB3	1.91	0.53
1:A:449:ILE:HG12	1:A:450:CYS:N	2.23	0.53
1:A:469:TYR:HD1	1:A:473:GLU:HG2	1.73	0.53
1:A:792:LEU:O	1:A:793:TRP:HB3	2.07	0.53
1:A:802:VAL:CG2	1:A:803:THR:H	2.21	0.53
1:B:735:VAL:O	1:B:735:VAL:CG2	2.56	0.53
1:A:740:ASN:HA	1:A:790:GLY:HA2	1.90	0.53
1:A:832:PHE:HA	1:A:855:VAL:HG11	1.91	0.53
1:B:416:VAL:CG2	1:B:490:ARG:CA	2.79	0.52
1:B:530:ASP:C	1:B:532:PRO:HD3	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:622:LEU:HD13	1:B:644:TYR:CE1	2.44	0.52
1:A:414:LYS:HG2	1:A:416:VAL:O	2.08	0.52
1:A:460:ILE:O	1:A:461:TYR:CD2	2.57	0.52
1:B:555:TYR:CE1	1:B:615:MET:HG2	2.44	0.52
1:A:229:GLU:OE2	1:A:229:GLU:N	2.23	0.52
1:A:609:TRP:CD1	1:A:620:TYR:CE1	2.97	0.52
1:A:819:ARG:HH22	1:A:825:GLU:CD	2.15	0.52
1:A:371:ARG:HB3	1:A:372:TRP:CD2	2.44	0.52
1:A:588:ARG:HG3	1:A:589:LEU:N	2.23	0.52
1:A:460:ILE:C	1:A:461:TYR:HD2	2.16	0.52
1:A:469:TYR:CD1	1:A:473:GLU:HG2	2.44	0.52
1:A:513:GLY:HA3	1:A:544:PHE:HE1	1.75	0.52
1:A:536:GLU:OE1	1:A:537:LYS:HE3	2.07	0.52
1:A:545:MET:HA	1:A:548:VAL:HG12	1.92	0.52
1:B:484:ASP:C	1:B:486:PRO:HD3	2.34	0.52
1:B:519:GLY:C	1:B:524:ASN:HB3	2.35	0.52
1:B:596:CYS:HB3	1:B:623:PRO:HB3	1.91	0.52
1:B:751:ALA:O	1:B:752:ASN:HB2	2.09	0.52
1:A:744:LEU:HD13	1:A:772:LEU:CD2	2.40	0.52
1:A:195:LYS:HZ3	1:A:197:GLY:HA2	1.75	0.52
1:A:513:GLY:HA3	1:A:544:PHE:CE1	2.45	0.52
1:A:671:HIS:ND1	1:A:721:ARG:NE	2.58	0.52
1:B:388:HIS:HB3	1:B:391:THR:CG2	2.39	0.52
1:A:226:PHE:O	1:A:251:VAL:HG12	2.10	0.52
1:A:344:LEU:HG	1:A:346:LEU:CD1	2.40	0.52
1:B:886:PHE:C	1:B:887:THR:HG23	2.35	0.52
1:A:376:PHE:C	1:A:376:PHE:CD2	2.86	0.52
1:A:484:ASP:C	1:A:486:PRO:HD3	2.34	0.51
1:B:415:TYR:O	1:B:416:VAL:CB	2.58	0.51
1:B:762:GLU:O	1:B:763:ARG:C	2.50	0.51
1:A:619:LYS:NZ	1:A:875:GLY:O	2.43	0.51
1:B:525:ARG:HG3	1:B:526:TYR:CD2	2.46	0.51
1:A:236:LEU:HG	1:A:574:LYS:HB2	1.93	0.51
1:A:657:LEU:HD23	1:A:795:ASP:HA	1.93	0.51
1:A:414:LYS:HG3	1:A:416:VAL:O	2.10	0.51
1:A:703:PHE:O	1:A:704:GLY:C	2.53	0.51
1:A:803:THR:HB	1:A:847:ILE:HG12	1.92	0.51
1:A:536:GLU:O	1:A:537:LYS:CB	2.58	0.50
1:B:404:LEU:HD21	1:B:502:LEU:HD21	1.93	0.50
1:A:481:ASN:HD21	1:A:482:LEU:HB2	1.76	0.50
1:A:241:VAL:HG13	1:A:241:VAL:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:CYS:HA	1:A:488:LYS:CE	2.42	0.50
1:A:269:VAL:HG13	1:A:271:ILE:HG13	1.94	0.50
1:A:283:LYS:N	1:A:283:LYS:HD2	2.26	0.50
1:A:363:LEU:HB2	1:A:863:TYR:CD1	2.46	0.50
1:A:279:ASP:CB	1:A:280:PRO:CD	2.88	0.50
1:A:282:ALA:O	1:A:285:GLN:HB2	2.11	0.50
1:A:536:GLU:O	1:A:536:GLU:OE1	2.30	0.50
1:A:635:ASN:O	1:A:635:ASN:OD1	2.30	0.50
1:A:349:GLY:O	1:A:350:CYS:SG	2.70	0.50
1:A:415:TYR:O	1:A:416:VAL:CG1	2.57	0.50
1:A:852:ALA:HA	3:A:1000:SAH:C	2.40	0.50
1:A:591:MET:HE1	1:A:634:PRO:HD2	1.93	0.50
1:A:732:GLN:OE1	1:A:772:LEU:HD21	2.12	0.50
1:B:134:GLU:HG3	1:B:135:PRO:CD	2.41	0.49
1:B:667:LYS:HG2	1:B:817:GLN:CD	2.37	0.49
1:B:781:ILE:O	1:B:781:ILE:HG22	2.11	0.49
1:B:529:ARG:O	1:B:532:PRO:HD3	2.12	0.49
1:B:888:SER:O	1:B:889:VAL:O	2.30	0.49
1:A:276:PRO:O	1:A:278:MET:O	2.30	0.49
1:B:741:PHE:CE1	1:B:778:MET:CE	2.91	0.49
1:A:182:ASP:O	1:A:184:VAL:HG12	2.11	0.49
1:A:384:LEU:HD23	1:A:393:VAL:CG2	2.41	0.49
1:A:624:THR:HG22	1:A:624:THR:O	2.12	0.49
1:A:650:PRO:CD	1:A:651:SER:N	2.73	0.49
1:A:667:LYS:H	1:A:667:LYS:CD	1.90	0.49
1:A:812:ILE:O	1:A:812:ILE:CG1	2.61	0.49
1:A:449:ILE:HD11	1:A:460:ILE:CG1	2.41	0.49
1:B:375:ASP:OD1	3:B:1000:SAH:O3'	2.30	0.49
1:A:555:TYR:OH	1:A:616:VAL:O	2.23	0.49
1:A:622:LEU:HD13	1:A:644:TYR:CE1	2.47	0.49
1:A:645:ASP:OD1	1:A:648:GLN:CG	2.60	0.49
1:A:657:LEU:HG	1:A:795:ASP:C	2.38	0.49
1:B:236:LEU:HD13	1:B:574:LYS:HB2	1.95	0.49
1:A:793:TRP:O	1:A:796:GLU:HG2	2.11	0.49
1:A:281:LYS:HD2	1:A:282:ALA:N	2.27	0.49
1:B:555:TYR:HE2	1:B:618:PRO:HD3	1.78	0.49
1:B:741:PHE:HE1	1:B:778:MET:HE2	1.77	0.49
1:A:449:ILE:HG22	1:A:492:PHE:CZ	2.46	0.49
1:A:479:ILE:C	1:A:481:ASN:N	2.65	0.49
1:A:586:GLN:NE2	1:A:615:MET:O	2.44	0.49
1:B:446:LEU:CD2	1:B:464:VAL:HG12	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:688:GLN:HA	1:B:691:ILE:HD11	1.94	0.49
1:A:633:ALA:HB2	1:A:641:MET:HE3	1.94	0.49
1:A:645:ASP:O	1:A:646:GLU:HB2	2.12	0.49
1:A:867:GLN:NE2	1:A:873:SER:HA	2.27	0.48
1:B:338:THR:HG21	1:B:367:LYS:HE3	1.94	0.48
1:B:339:ARG:HD3	1:B:870:LEU:CD2	2.43	0.48
1:A:481:ASN:HD21	1:A:482:LEU:CB	2.24	0.48
1:A:867:GLN:NE2	1:A:872:GLU:C	2.66	0.48
1:B:440:GLU:HG2	1:B:441:PHE:N	2.28	0.48
1:B:525:ARG:CG	1:B:526:TYR:CE2	2.96	0.48
1:B:622:LEU:HD21	1:B:879:LEU:HD13	1.94	0.48
1:A:275:ASP:O	1:A:278:MET:HB2	2.13	0.48
1:A:385:LYS:HB2	1:A:393:VAL:HG21	1.96	0.48
1:A:488:LYS:CD	1:A:488:LYS:N	2.74	0.48
1:B:528:ASN:ND2	1:B:536:GLU:CG	2.74	0.48
1:A:229:GLU:H	1:A:229:GLU:CD	2.12	0.48
1:A:239:ILE:C	1:A:239:ILE:HD12	2.38	0.48
1:A:349:GLY:HA3	4:A:1114:HOH:O	2.13	0.48
1:A:884:PRO:O	1:A:885:SER:C	2.57	0.48
1:B:828:ARG:HD2	1:B:834:ASP:OD1	2.13	0.48
1:A:415:TYR:O	1:A:416:VAL:CG2	2.59	0.48
1:A:633:ALA:HB2	1:A:641:MET:HE2	1.95	0.48
1:A:137:PHE:O	1:A:138:ILE:HD12	2.14	0.48
1:A:463:LYS:HB2	1:A:476:TRP:CZ3	2.49	0.48
1:A:477:GLU:HA	1:A:478:PRO:HD3	1.26	0.48
1:A:566:LYS:HD2	1:A:566:LYS:HA	1.61	0.48
1:A:641:MET:HG3	1:A:643:ALA:H	1.78	0.48
1:A:307:ASN:O	1:A:308:ILE:CB	2.61	0.48
1:A:619:LYS:HD3	1:A:877:ASP:O	2.14	0.48
1:A:235:SER:O	1:A:237:VAL:N	2.47	0.47
1:A:663:SER:OG	1:A:688:GLN:NE2	2.39	0.47
1:A:729:ARG:O	1:A:732:GLN:N	2.43	0.47
1:B:521:SER:HB3	1:B:563:ASP:OD2	2.13	0.47
1:A:488:LYS:HD2	1:A:488:LYS:N	2.28	0.47
1:A:512:CYS:HA	1:A:557:LEU:O	2.13	0.47
3:B:1000:SAH:HG2	3:B:1000:SAH:H4'	1.68	0.47
1:B:886:PHE:O	1:B:887:THR:C	2.57	0.47
1:A:142:VAL:HG22	1:A:147:ALA:HB2	1.94	0.47
1:B:220:PHE:HE1	1:B:222:CYS:HG	1.60	0.47
1:A:181:VAL:O	1:A:184:VAL:HG13	2.14	0.47
1:A:650:PRO:HD2	1:A:651:SER:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:VAL:HG21	1:B:286:LEU:HG	1.97	0.47
1:A:353:MET:O	1:A:357:LEU:HG	2.15	0.47
1:B:841:PRO:HG2	1:B:844:GLU:CG	2.44	0.47
1:A:667:LYS:HA	1:A:817:GLN:HE22	1.79	0.47
1:A:878:PRO:CA	1:A:879:LEU:HD13	2.39	0.47
1:A:235:SER:OG	1:A:236:LEU:N	2.45	0.47
1:A:483:SER:C	1:A:486:PRO:HD3	2.27	0.47
1:B:481:ASN:C	1:B:482:LEU:HD23	2.40	0.47
1:B:535:ASP:HB3	1:B:536:GLU:HG3	1.97	0.47
1:B:884:PRO:CG	1:B:885:SER:N	2.78	0.47
1:A:415:TYR:C	1:A:416:VAL:CG2	2.85	0.47
1:B:382:GLN:NE2	4:B:1201:HOH:O	2.27	0.46
1:B:826:ASN:ND2	4:B:1187:HOH:O	2.46	0.46
1:B:294:TYR:HE1	1:B:308:ILE:HD13	1.80	0.46
1:A:877:ASP:CG	1:A:878:PRO:CD	2.88	0.46
3:A:1000:SAH:O3'	4:A:1114:HOH:O	2.20	0.46
1:B:525:ARG:HD2	1:B:525:ARG:O	2.15	0.46
1:B:725:ASP:O	1:B:729:ARG:HG3	2.15	0.46
1:B:531:GLU:N	1:B:532:PRO:HD3	2.30	0.46
1:B:781:ILE:HB	1:B:785:SER:HB2	1.97	0.46
1:A:176:TYR:O	1:A:210:PHE:HB2	2.16	0.46
1:A:485:CYS:O	1:A:488:LYS:CB	2.61	0.46
1:B:219:TYR:HA	1:B:260:ASN:O	2.16	0.46
1:A:560:ASN:CG	1:A:564:ILE:HD11	2.40	0.46
1:A:619:LYS:HE3	1:A:875:GLY:O	2.15	0.46
1:A:291:ASP:O	1:A:292:LEU:HD23	2.16	0.46
1:A:536:GLU:O	1:A:536:GLU:CD	2.58	0.46
1:A:479:ILE:HG13	1:A:480:ASP:N	2.22	0.46
1:A:482:LEU:C	1:A:484:ASP:N	2.70	0.46
1:A:630:ARG:C	1:A:632:GLY:N	2.73	0.46
1:A:645:ASP:O	1:A:646:GLU:CB	2.64	0.46
1:B:376:PHE:C	1:B:376:PHE:CD2	2.90	0.46
1:A:135:PRO:HG3	1:A:263:ASP:OD2	2.15	0.46
1:B:304:THR:HG21	1:B:588:ARG:NH2	2.31	0.46
1:B:632:GLY:O	1:B:634:PRO:HD3	2.16	0.46
1:A:696:LYS:HZ3	1:A:706:GLY:H	1.64	0.46
1:A:485:CYS:O	1:A:488:LYS:N	2.48	0.46
1:A:622:LEU:HD13	1:A:644:TYR:HE1	1.81	0.46
1:B:227:ARG:HB2	1:B:230:ASP:OD2	2.16	0.45
1:A:133:HIS:CE1	1:A:134:GLU:O	2.69	0.45
1:A:444:GLU:HG3	1:A:445:LYS:N	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:416:VAL:HG22	1:B:489:ILE:CG2	2.26	0.45
1:A:630:ARG:C	1:A:632:GLY:H	2.23	0.45
1:B:411:LEU:O	1:B:415:TYR:N	2.50	0.45
1:B:482:LEU:C	1:B:484:ASP:N	2.73	0.45
1:A:569:ASP:O	1:A:574:LYS:HE3	2.16	0.45
1:A:612:LEU:C	1:A:614:SER:H	2.24	0.45
1:B:517:CYS:C	1:B:518:GLN:HG2	2.41	0.45
1:A:387:ASN:HD21	1:A:837:ARG:N	2.13	0.45
1:A:813:ILE:HA	1:A:820:VAL:HA	1.99	0.45
1:A:822:THR:OG1	1:A:825:GLU:HG3	2.15	0.45
1:B:528:ASN:HD21	1:B:536:GLU:CD	2.17	0.45
1:A:349:GLY:H	3:A:1000:SAH:HG2	1.81	0.45
1:A:413:LYS:CG	1:A:414:LYS:N	2.77	0.45
1:A:513:GLY:C	1:A:515:PRO:HD3	2.42	0.45
1:A:808:HIS:CD2	1:A:808:HIS:N	2.84	0.45
1:A:545:MET:HA	1:A:548:VAL:CG1	2.46	0.45
1:A:589:LEU:CD1	1:A:640:CYS:HB3	2.46	0.45
1:B:599:LEU:HD11	1:B:856:PRO:HD2	1.99	0.45
1:A:283:LYS:O	1:A:287:ILE:HG13	2.17	0.45
1:A:356:GLY:HA3	1:A:858:ALA:CB	2.45	0.45
1:A:485:CYS:N	1:A:486:PRO:CD	2.80	0.45
1:A:612:LEU:C	1:A:614:SER:N	2.73	0.45
1:A:626:ASP:N	1:A:652:LEU:HB3	2.32	0.45
1:A:657:LEU:HB3	1:A:794:TRP:O	2.17	0.45
1:A:788:PRO:O	1:A:790:GLY:N	2.50	0.45
1:B:357:LEU:HD11	1:B:557:LEU:HD23	1.99	0.45
1:B:626:ASP:OD1	1:B:626:ASP:C	2.60	0.45
1:B:835:TYR:CD1	1:B:835:TYR:C	2.95	0.45
1:B:886:PHE:C	1:B:887:THR:CG2	2.90	0.45
1:A:363:LEU:N	1:A:363:LEU:HD23	2.32	0.45
1:A:732:GLN:OE1	1:A:772:LEU:HD11	2.17	0.45
2:Q:6:THR:O	2:Q:6:THR:OG1	2.32	0.45
1:B:338:THR:CG2	1:B:367:LYS:HE3	2.47	0.45
1:A:749:VAL:O	1:A:754:ILE:O	2.35	0.45
1:B:812:ILE:HG23	1:B:820:VAL:HG22	1.99	0.45
1:A:279:ASP:CB	1:A:280:PRO:HD2	2.45	0.45
1:A:449:ILE:CG1	1:A:450:CYS:N	2.80	0.45
1:A:463:LYS:HB2	1:A:476:TRP:CE3	2.52	0.45
1:A:763:ARG:NH1	1:A:773:VAL:O	2.49	0.45
1:B:735:VAL:O	1:B:735:VAL:HG23	2.16	0.44
1:B:648:GLN:O	1:B:650:PRO:HD3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:LEU:O	1:A:483:SER:C	2.58	0.44
1:B:488:LYS:HA	1:B:491:GLU:CG	2.43	0.44
1:A:283:LYS:HA	1:A:283:LYS:HE3	1.93	0.44
1:A:531:GLU:OE2	1:A:534:LYS:NZ	2.38	0.44
1:A:598:GLY:C	1:A:656:LEU:HD12	2.42	0.44
1:B:481:ASN:OD1	1:B:481:ASN:O	2.36	0.44
1:A:486:PRO:O	1:A:487:GLN:C	2.58	0.44
1:A:781:ILE:HB	1:A:785:SER:HB2	2.00	0.44
1:B:302:TYR:O	1:B:303:SER:C	2.60	0.44
1:B:538:ASN:ND2	1:B:572:LEU:HD11	2.33	0.44
1:B:571:TYR:C	1:B:571:TYR:CD2	2.95	0.44
1:B:642:VAL:HG22	1:B:642:VAL:O	2.17	0.44
1:A:621:PRO:HD3	1:A:864:CYS:SG	2.58	0.44
1:A:687:PHE:CE1	1:A:691:ILE:HD13	2.52	0.44
1:B:741:PHE:CE1	1:B:778:MET:HE2	2.52	0.44
1:A:724:ASN:O	1:A:725:ASP:CB	2.54	0.44
1:A:883:PRO:HG2	1:A:884:PRO:HD3	1.99	0.44
3:A:1000:SAH:HG2	3:A:1000:SAH:H4'	1.51	0.44
1:A:368:LEU:HD23	1:A:368:LEU:HA	1.81	0.44
1:A:499:ARG:HD2	1:A:499:ARG:HA	1.68	0.44
1:A:748:ARG:CG	1:A:749:VAL:N	2.80	0.44
1:A:275:ASP:OD2	1:A:275:ASP:C	2.61	0.44
1:A:522:GLY:O	1:A:525:ARG:HB2	2.18	0.44
1:A:664:ASP:CG	1:A:692:ARG:HH11	2.22	0.43
1:A:819:ARG:CG	1:A:820:VAL:O	2.60	0.43
1:B:528:ASN:CB	1:B:535:ASP:OD1	2.59	0.43
1:B:599:LEU:HA	1:B:600:PRO:HD3	1.83	0.43
1:A:133:HIS:HE2	1:A:180:LYS:HE3	1.84	0.43
1:B:884:PRO:CD	1:B:885:SER:N	2.77	0.43
1:A:235:SER:C	1:A:237:VAL:N	2.74	0.43
1:A:371:ARG:CG	1:A:371:ARG:NH1	2.54	0.43
1:A:487:GLN:O	1:A:490:ARG:HB3	2.18	0.43
1:B:462:PHE:CE2	1:B:479:ILE:HD13	2.48	0.43
1:A:740:ASN:OD1	1:A:740:ASN:C	2.60	0.43
1:A:196:ALA:CB	1:A:200:GLU:HB3	2.47	0.43
1:A:388:HIS:ND1	1:A:702:SER:OG	2.32	0.43
1:A:589:LEU:HD11	1:A:640:CYS:HB3	2.00	0.43
1:A:236:LEU:HD13	1:A:236:LEU:HA	1.90	0.43
1:A:500:LYS:C	1:A:502:LEU:N	2.74	0.43
1:B:535:ASP:O	1:B:536:GLU:C	2.62	0.43
1:A:609:TRP:CD2	1:A:618:PRO:HG2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:ASN:O	1:A:784:LYS:HB3	2.19	0.43
1:A:787:LYS:N	1:A:788:PRO:CD	2.82	0.43
1:A:876:SER:O	1:A:876:SER:OG	2.30	0.43
1:A:882:LEU:HA	1:A:883:PRO:HD3	1.88	0.43
1:B:202:ASP:OD2	1:B:266:ILE:HD13	2.18	0.43
1:B:220:PHE:HE1	1:B:222:CYS:SG	2.40	0.43
1:A:599:LEU:C	1:A:601:GLN:H	2.26	0.43
1:A:878:PRO:HB2	1:A:879:LEU:HD11	2.01	0.43
1:B:416:VAL:HG21	1:B:490:ARG:HG3	2.00	0.42
1:A:490:ARG:O	1:A:491:GLU:C	2.62	0.42
1:B:646:GLU:O	1:B:647:THR:C	2.60	0.42
1:B:703:PHE:CE1	1:B:709:PRO:HD3	2.54	0.42
1:A:346:LEU:HD21	1:A:547:ILE:HG21	2.01	0.42
1:A:564:ILE:HG23	1:A:572:LEU:HB2	2.01	0.42
1:A:649:LYS:HA	1:A:650:PRO:HD3	1.82	0.42
1:A:671:HIS:CD2	1:A:673:PRO:HD3	2.54	0.42
1:A:689:ARG:HB2	1:A:689:ARG:CZ	2.48	0.42
1:A:804:ARG:HB3	1:A:806:GLU:OE1	2.20	0.42
1:B:687:PHE:O	1:B:691:ILE:HG13	2.18	0.42
1:B:819:ARG:NH1	1:B:822:THR:HG23	2.35	0.42
1:A:359:LEU:O	1:A:859:ARG:NH1	2.37	0.42
1:A:398:ALA:O	1:A:401:PHE:HB3	2.18	0.42
1:A:589:LEU:CD1	1:A:590:GLY:N	2.81	0.42
1:A:798:VAL:O	1:A:799:PRO:C	2.63	0.42
1:A:821:LEU:O	1:A:846:TYR:OH	2.34	0.42
1:A:794:TRP:HH2	1:A:816:THR:CG2	2.24	0.42
1:A:882:LEU:N	1:A:882:LEU:CD1	2.79	0.42
2:Q:7:ALA:O	2:Q:8:ARG:CB	2.65	0.42
1:B:463:LYS:HE2	1:B:474:ASP:HB2	2.01	0.42
1:A:367:LYS:NZ	1:A:369:GLU:OE2	2.52	0.42
1:A:664:ASP:HB3	1:A:828:ARG:NH1	2.34	0.42
1:B:416:VAL:HG21	1:B:490:ARG:CB	2.50	0.42
1:B:527:ARG:HB2	1:B:527:ARG:HE	1.40	0.42
1:A:399:ASP:OD1	1:A:400:GLU:N	2.53	0.42
1:A:447:VAL:O	1:A:447:VAL:HG12	2.18	0.42
1:B:664:ASP:CG	1:B:828:ARG:HH12	2.27	0.42
1:A:348:SER:O	1:A:350:CYS:N	2.53	0.42
1:A:356:GLY:O	1:A:859:ARG:HA	2.19	0.42
1:A:728:GLU:OE1	1:A:766:LEU:CD2	2.57	0.42
1:B:222:CYS:O	1:B:257:LYS:HA	2.19	0.42
1:A:536:GLU:OE1	1:A:537:LYS:CG	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:735:VAL:HA	1:A:791:ARG:NH2	2.34	0.42
1:B:633:ALA:HA	1:B:634:PRO:HD2	1.79	0.42
1:B:885:SER:C	1:B:886:PHE:O	2.58	0.42
1:A:273:HIS:HB2	1:A:294:TYR:CE2	2.55	0.42
1:A:479:ILE:H	1:A:479:ILE:HG22	1.55	0.42
1:B:414:LYS:O	1:B:414:LYS:HG3	2.15	0.41
1:A:369:GLU:HG3	1:A:371:ARG:HD3	2.01	0.41
1:B:275:ASP:OD1	1:B:275:ASP:C	2.63	0.41
1:A:353:MET:HG3	1:A:853:VAL:HG11	2.01	0.41
1:A:387:ASN:ND2	1:A:837:ARG:H	2.17	0.41
1:A:622:LEU:HG	1:A:879:LEU:HB3	2.03	0.41
1:A:792:LEU:HD23	1:A:811:VAL:HG23	2.00	0.41
1:B:537:LYS:HG2	1:B:539:LYS:HB2	2.01	0.41
1:B:592:MET:HE3	1:B:597:TYR:OH	2.20	0.41
1:A:415:TYR:O	1:A:416:VAL:CB	2.69	0.41
1:A:447:VAL:O	1:A:447:VAL:CG1	2.67	0.41
1:A:594:ALA:CB	1:A:603:ARG:HB3	2.50	0.41
1:A:696:LYS:HE2	1:A:706:GLY:HA2	2.03	0.41
1:A:758:ASP:HA	1:A:759:PRO:HD3	1.93	0.41
1:A:855:VAL:N	1:A:856:PRO:CD	2.84	0.41
1:B:757:TRP:O	1:B:759:PRO:HD3	2.21	0.41
1:A:344:LEU:HD13	1:A:372:TRP:HB2	2.03	0.41
1:A:740:ASN:OD1	1:A:742:ARG:N	2.38	0.41
1:A:204:ILE:HG22	1:A:225:PHE:CD2	2.56	0.41
1:A:150:ASN:C	1:A:152:PRO:HD3	2.45	0.41
1:B:344:LEU:CD1	1:B:372:TRP:HB2	2.51	0.41
1:B:477:GLU:HA	1:B:478:PRO:HD3	1.95	0.41
1:B:672:GLN:O	1:B:672:GLN:CG	2.68	0.41
1:A:802:VAL:HG22	1:A:803:THR:H	1.82	0.41
1:B:203:TYR:CE2	2:Q:7:ALA:HB3	2.56	0.41
1:B:209:GLU:HB2	1:B:221:THR:CB	2.43	0.41
1:B:616:VAL:O	1:B:868:ALA:HB1	2.20	0.41
1:B:621:PRO:HA	1:B:880:TYR:O	2.20	0.41
1:A:196:ALA:CB	1:A:203:TYR:CE2	3.03	0.41
1:A:233:ILE:O	1:A:233:ILE:HG13	2.20	0.41
1:A:482:LEU:HD23	1:A:482:LEU:H	1.81	0.41
1:A:497:HIS:CD2	1:A:497:HIS:C	2.98	0.41
1:A:658:LEU:CD2	1:A:792:LEU:HD13	2.50	0.41
1:A:677:MET:O	1:A:714:LEU:HB3	2.21	0.41
1:A:825:GLU:O	1:A:829:LEU:HD13	2.20	0.41
1:A:833:PRO:HG2	1:A:836:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:726:ASP:O	1:B:730:VAL:HG13	2.20	0.41
1:B:763:ARG:NH1	1:B:771:PRO:HB2	2.35	0.41
1:B:884:PRO:CG	1:B:885:SER:H	2.33	0.41
1:A:751:ALA:O	1:A:752:ASN:CB	2.69	0.41
1:B:202:ASP:OD2	1:B:266:ILE:CD1	2.69	0.40
1:B:491:GLU:HG2	1:B:491:GLU:H	1.54	0.40
1:A:175:HIS:CD2	1:A:211:PHE:HB3	2.56	0.40
1:A:564:ILE:CG2	1:A:573:GLY:N	2.84	0.40
1:B:814:HIS:CG	1:B:815:PRO:HD2	2.56	0.40
1:A:603:ARG:CZ	1:A:830:GLN:HE22	2.34	0.40
1:B:886:PHE:CG	1:B:887:THR:N	2.69	0.40
1:A:363:LEU:N	1:A:363:LEU:CD2	2.84	0.40
1:A:364:SER:OG	1:A:863:TYR:O	2.39	0.40
1:A:696:LYS:NZ	1:A:706:GLY:H	2.19	0.40
1:A:749:VAL:HG13	1:A:754:ILE:O	2.22	0.40
1:A:778:MET:O	1:A:783:GLY:HA2	2.22	0.40
1:B:138:ILE:HG12	1:B:178:SER:HB3	2.03	0.40
1:B:285:GLN:O	1:B:288:GLU:HB3	2.22	0.40
1:A:193:TYR:CE1	1:A:204:ILE:HG13	2.56	0.40
1:A:215:ASP:C	1:A:215:ASP:OD2	2.64	0.40
1:A:271:ILE:HA	1:A:292:LEU:O	2.20	0.40
1:A:631:GLY:C	1:A:633:ALA:H	2.29	0.40
1:A:722:LEU:CD1	1:A:730:VAL:HG21	2.52	0.40
1:B:751:ALA:O	1:B:752:ASN:CB	2.70	0.40
1:B:773:VAL:HA	1:B:774:PRO:HD2	1.93	0.40
1:B:852:ALA:HA	3:B:1000:SAH:C	2.52	0.40
1:A:133:HIS:NE2	1:A:180:LYS:HE3	2.37	0.40
1:A:302:TYR:O	1:A:303:SER:C	2.64	0.40
1:A:349:GLY:C	1:A:351:GLY:N	2.79	0.40
1:A:451:TYR:HA	1:A:459:GLY:O	2.22	0.40
1:A:482:LEU:O	1:A:485:CYS:N	2.54	0.40
1:A:649:LYS:HD2	1:A:650:PRO:HD2	2.02	0.40
1:A:671:HIS:CG	1:A:721:ARG:HE	2.40	0.40
1:A:682:SER:HB3	1:A:683:PRO:HD2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	680/784 (87%)	631 (93%)	38 (6%)	11 (2%)	7	20
1	B	685/784 (87%)	660 (96%)	22 (3%)	3 (0%)	30	54
2	P	4/32 (12%)	4 (100%)	0	0	100	100
2	Q	2/32 (6%)	1 (50%)	0	1 (50%)	0	0
All	All	1371/1632 (84%)	1296 (94%)	60 (4%)	15 (1%)	11	29

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	883	PRO
1	B	650	PRO
1	B	875	GLY
1	A	704	GLY
1	A	748	ARG
1	A	789	PHE
1	A	349	GLY
1	A	478	PRO
1	A	725	ASP
1	A	350	CYS
1	A	485	CYS
1	B	886	PHE
1	A	490	ARG
2	Q	8	ARG
1	A	650	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	580/668 (87%)	474 (82%)	106 (18%)	2	5
1	B	596/668 (89%)	530 (89%)	66 (11%)	6	15
2	P	5/21 (24%)	3 (60%)	2 (40%)	0	0
2	Q	3/21 (14%)	1 (33%)	2 (67%)	0	0
All	All	1184/1378 (86%)	1008 (85%)	176 (15%)	3	8

All (176) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	134	GLU
1	B	138	ILE
1	B	169	GLU
1	B	223	ARG
1	B	235	SER
1	B	236	LEU
1	B	238	SER
1	B	257	LYS
1	B	262	LEU
1	B	263	ASP
1	B	269	VAL
1	B	270	LYS
1	B	274	VAL
1	B	279	ASP
1	B	281	LYS
1	B	299	SER
1	B	338	THR
1	B	340	THR
1	B	363	LEU
1	B	376	PHE
1	B	391	THR
1	B	414	LYS
1	B	416	VAL
1	B	441	PHE
1	B	443	VAL
1	B	444	GLU
1	B	455	ASP
1	B	456	ARG
1	B	460	ILE
1	B	464	VAL
1	B	465	GLN

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Mol	Chain	Res	Type
1	B	474	ASP
1	B	484	ASP
1	B	488	LYS
1	B	491	GLU
1	B	502	LEU
1	B	508	VAL
1	B	518	GLN
1	B	520	ILE
1	B	527	ARG
1	B	528	ASN
1	B	530	ASP
1	B	536	GLU
1	B	537	LYS
1	B	558	MET
1	B	615	MET
1	B	638	SER
1	B	642	VAL
1	B	646	GLU
1	B	647	THR
1	B	649	LYS
1	B	656	LEU
1	B	672	GLN
1	B	730	VAL
1	B	735	VAL
1	B	747	VAL
1	B	763	ARG
1	B	765	LYS
1	B	820	VAL
1	B	821	LEU
1	B	828	ARG
1	B	829	LEU
1	B	867	GLN
1	B	887	THR
1	B	888	SER
1	B	889	VAL
1	A	133	HIS
1	A	142	VAL
1	A	146	GLU
1	A	169	GLU
1	A	170	LEU
1	A	184	VAL
1	A	185	VAL

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Mol	Chain	Res	Type
1	A	200	GLU
1	A	207	ILE
1	A	216	GLN
1	A	232	VAL
1	A	236	LEU
1	A	237	VAL
1	A	238	SER
1	A	251	VAL
1	A	261	VAL
1	A	263	ASP
1	A	270	LYS
1	A	278	MET
1	A	279	ASP
1	A	281	LYS
1	A	283	LYS
1	A	285	GLN
1	A	286	LEU
1	A	287	ILE
1	A	290	CYS
1	A	338	THR
1	A	363	LEU
1	A	368	LEU
1	A	371	ARG
1	A	376	PHE
1	A	384	LEU
1	A	407	GLU
1	A	410	VAL
1	A	411	LEU
1	A	413	LYS
1	A	416	VAL
1	A	442	VAL
1	A	444	GLU
1	A	455	ASP
1	A	457	GLU
1	A	460	ILE
1	A	464	VAL
1	A	475	THR
1	A	479	ILE
1	A	481	ASN
1	A	482	LEU
1	A	484	ASP
1	A	499	ARG

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Mol	Chain	Res	Type
1	A	502	LEU
1	A	508	VAL
1	A	510	VAL
1	A	521	SER
1	A	533	LEU
1	A	535	ASP
1	A	536	GLU
1	A	537	LYS
1	A	548	VAL
1	A	552	LYS
1	A	589	LEU
1	A	606	VAL
1	A	614	SER
1	A	627	VAL
1	A	629	VAL
1	A	644	TYR
1	A	647	THR
1	A	653	LYS
1	A	657	LEU
1	A	665	LEU
1	A	667	LYS
1	A	675	ASP
1	A	691	ILE
1	A	693	LEU
1	A	694	SER
1	A	697	ASP
1	A	699	LEU
1	A	716	ASP
1	A	747	VAL
1	A	749	VAL
1	A	754	ILE
1	A	763	ARG
1	A	765	LYS
1	A	766	LEU
1	A	767	SER
1	A	772	LEU
1	A	779	SER
1	A	781	ILE
1	A	782	LYS
1	A	801	VAL
1	A	802	VAL
1	A	808	HIS

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Mol	Chain	Res	Type
1	A	809	ASN
1	A	811	VAL
1	A	819	ARG
1	A	821	LEU
1	A	824	ARG
1	A	853	VAL
1	A	855	VAL
1	A	859	ARG
1	A	867	GLN
1	A	872	GLU
1	A	873	SER
1	A	874	GLU
1	A	876	SER
1	A	879	LEU
1	A	882	LEU
2	P	6	THR
2	P	11	THR
2	Q	6	THR
2	Q	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	216	GLN
1	B	234	ASN
1	B	528	ASN
1	B	752	ASN
1	B	810	GLN
1	A	285	GLN
1	A	465	GLN
1	A	481	ASN
1	A	487	GLN
1	A	648	GLN
1	A	867	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MLY	P	9	2	9,10,11	0.66	0	6,11,13	0.70	0
2	MLY	Q	9	2	9,10,11	0.73	0	6,11,13	1.63	1 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MLY	P	9	2	-	3/8/9/11	-
2	MLY	Q	9	2	-	4/8/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	Q	9	MLY	CD-CE-NZ	-3.87	103.70	113.71

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	9	MLY	C-CA-CB-CG
2	Q	9	MLY	C-CA-CB-CG
2	P	9	MLY	CD-CE-NZ-CH2
2	Q	9	MLY	CD-CE-NZ-CH1
2	Q	9	MLY	CD-CE-NZ-CH2
2	P	9	MLY	CD-CE-NZ-CH1
2	Q	9	MLY	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	9	MLY	7	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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	SAH	A	1000	-	27,28,28	1.45	4 (14%)	36,40,40	1.99	9 (25%)
3	SAH	B	1000	-	27,28,28	1.72	8 (29%)	36,40,40	4.49	21 (58%)

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	SAH	A	1000	-	-	4/15/31/31	0/3/3/3
3	SAH	B	1000	-	-	2/15/31/31	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1000	SAH	C5-C4	4.69	1.47	1.39
3	B	1000	SAH	C2-N3	3.47	1.40	1.33
3	B	1000	SAH	C2-N1	3.23	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1000	SAH	C5-C4	-3.12	1.33	1.39
3	B	1000	SAH	C5-N7	-3.07	1.33	1.39
3	A	1000	SAH	C5-C6	2.76	1.48	1.41
3	B	1000	SAH	C5-C6	-2.63	1.33	1.41
3	B	1000	SAH	O4'-C4'	2.63	1.50	1.45
3	B	1000	SAH	C8-N9	-2.53	1.33	1.37
3	A	1000	SAH	C8-N7	2.36	1.36	1.31
3	A	1000	SAH	C5-N7	-2.24	1.35	1.39
3	B	1000	SAH	C2'-C3'	-2.17	1.47	1.53

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1000	SAH	O4'-C1'-C2'	-15.36	73.74	106.62
3	B	1000	SAH	O4'-C4'-C5'	-12.34	77.06	108.83
3	B	1000	SAH	O4'-C4'-C3'	-7.45	90.36	105.15
3	B	1000	SAH	C5'-C4'-C3'	7.33	133.37	115.06
3	B	1000	SAH	N3-C2-N1	-6.78	118.31	128.58
3	A	1000	SAH	C5-C4-N3	-5.83	118.69	126.72
3	B	1000	SAH	C3'-C2'-C1'	-5.32	91.41	101.46
3	B	1000	SAH	C5-C4-N3	-4.64	120.32	126.72
3	A	1000	SAH	N3-C4-N9	4.58	134.95	127.17
3	B	1000	SAH	N9-C8-N7	-4.38	107.72	113.94
3	B	1000	SAH	C5'-SD-CG	-4.08	90.16	102.26
3	A	1000	SAH	C2-N3-C4	3.70	120.86	111.83
3	A	1000	SAH	C4-C5-N7	-3.46	106.63	110.58
3	B	1000	SAH	C2-N3-C4	3.31	119.92	111.83
3	A	1000	SAH	N3-C2-N1	-3.22	123.72	128.58
3	B	1000	SAH	C5-N7-C8	3.17	108.44	103.45
3	B	1000	SAH	C5-C6-N6	-2.84	116.25	123.29
3	B	1000	SAH	C6-C5-C4	2.70	120.86	117.18
3	B	1000	SAH	C4-C5-N7	-2.69	107.51	110.58
3	A	1000	SAH	C3'-C2'-C1'	2.54	106.27	101.46
3	A	1000	SAH	C4-N9-C8	2.53	108.39	105.74
3	A	1000	SAH	C5-N7-C8	2.52	107.41	103.45
3	B	1000	SAH	N3-C4-N9	2.42	131.29	127.17
3	B	1000	SAH	CB-CG-SD	2.34	118.67	113.45
3	B	1000	SAH	C4'-C5'-SD	-2.32	105.50	113.78
3	B	1000	SAH	C2'-C3'-C4'	-2.27	98.23	102.61
3	B	1000	SAH	C5-C4-N9	2.27	108.28	105.81
3	B	1000	SAH	C4-N9-C8	2.16	108.00	105.74
3	B	1000	SAH	C4-N9-C1'	-2.15	121.61	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1000	SAH	C6-C5-N7	2.06	136.06	132.09

There are no chirality outliers.

All (6) torsion outliers are listed below:

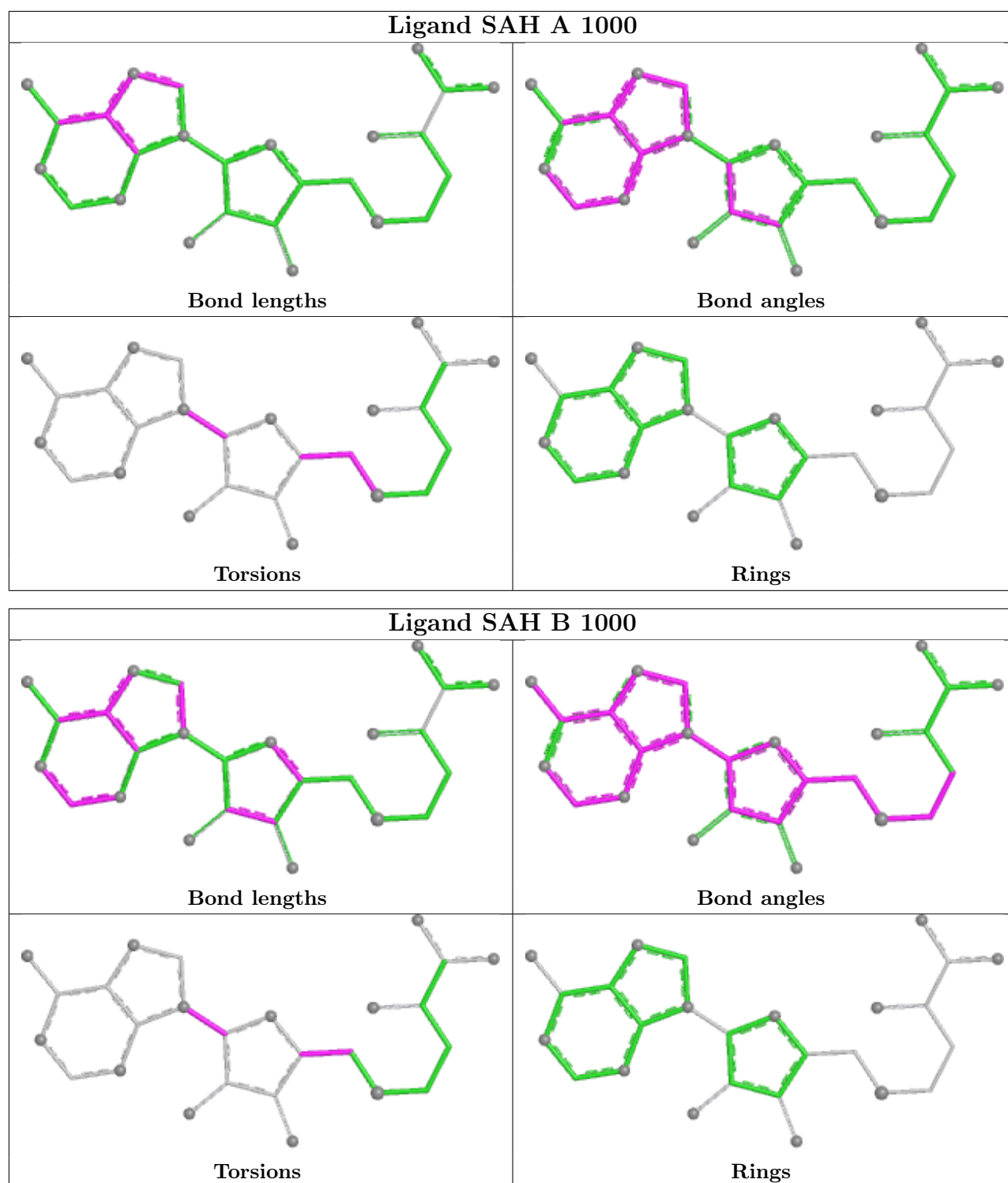
Mol	Chain	Res	Type	Atoms
3	B	1000	SAH	O4'-C4'-C5'-SD
3	A	1000	SAH	O4'-C4'-C5'-SD
3	A	1000	SAH	C3'-C4'-C5'-SD
3	B	1000	SAH	C2'-C1'-N9-C8
3	A	1000	SAH	C2'-C1'-N9-C8
3	A	1000	SAH	C4'-C5'-SD-CG

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1000	SAH	5	0
3	B	1000	SAH	5	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 ⓘ

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	688/784 (87%)	0.71	60 (8%) 16 13	56, 88, 149, 228	0
1	B	693/784 (88%)	-0.12	24 (3%) 47 43	24, 45, 106, 159	0
2	P	6/32 (18%)	1.99	3 (50%) 0 0	105, 130, 135, 135	0
2	Q	4/32 (12%)	2.47	1 (25%) 2 1	119, 128, 143, 164	0
All	All	1391/1632 (85%)	0.31	88 (6%) 26 23	24, 71, 137, 228	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	479	ILE	7.3
1	A	482	LEU	5.6
2	Q	6	THR	5.2
1	A	481	ASN	4.9
1	A	533	LEU	4.6
1	A	885	SER	4.1
1	A	627	VAL	4.1
1	A	884	PRO	3.8
1	A	349	GLY	3.7
1	A	526	TYR	3.7
1	A	416	VAL	3.7
1	B	481	ASN	3.6
1	B	536	GLU	3.5
1	B	889	VAL	3.4
2	P	11	THR	3.4
1	A	707	ALA	3.4
1	A	485	CYS	3.3
1	A	751	ALA	3.3
1	B	537	LYS	3.3
1	A	628	VAL	3.2
1	B	526	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	745	LYS	3.1
1	B	440	GLU	3.0
1	B	887	THR	2.9
1	A	650	PRO	2.9
1	A	632	GLY	2.8
1	A	461	TYR	2.8
1	B	538	ASN	2.8
1	A	441	PHE	2.8
1	A	278	MET	2.7
1	B	535	ASP	2.7
1	A	643	ALA	2.7
2	P	6	THR	2.7
1	B	454	SER	2.7
1	A	739	ALA	2.7
1	A	718	GLN	2.6
1	B	466	TRP	2.6
1	A	469	TYR	2.6
1	A	757	TRP	2.6
1	A	478	PRO	2.6
1	A	883	PRO	2.6
1	B	635	ASN	2.6
1	A	338	THR	2.5
1	B	630	ARG	2.5
1	B	531	GLU	2.5
1	B	415	TYR	2.5
1	A	454	SER	2.4
1	A	466	TRP	2.4
1	A	794	TRP	2.4
1	A	676	VAL	2.4
1	B	525	ARG	2.4
1	B	416	VAL	2.4
1	A	287	ILE	2.4
1	A	662	ILE	2.4
1	A	444	GLU	2.4
1	B	479	ILE	2.3
1	A	280	PRO	2.3
1	B	631	GLY	2.3
1	A	626	ASP	2.3
1	A	513	GLY	2.3
1	A	664	ASP	2.3
1	A	629	VAL	2.3
1	A	874	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	281	LYS	2.2
1	B	522	GLY	2.2
1	A	755	VAL	2.2
1	A	233	ILE	2.2
1	A	633	ALA	2.2
1	A	467	GLU	2.2
1	A	873	SER	2.2
1	A	749	VAL	2.2
1	A	793	TRP	2.2
1	A	750	GLY	2.2
1	B	455	ASP	2.2
1	A	741	PHE	2.2
1	A	243	GLY	2.1
1	A	448	GLY	2.1
1	A	464	VAL	2.1
1	A	770	LYS	2.1
1	B	524	ASN	2.1
1	A	752	ASN	2.1
1	A	769	GLY	2.1
1	A	172	ALA	2.1
1	A	744	LEU	2.0
1	A	133	HIS	2.0
1	B	519	GLY	2.0
2	P	8	ARG	2.0
1	B	263	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	MLY	Q	9	11/12	0.80	0.24	76,96,108,114	0
2	MLY	P	9	11/12	0.86	0.22	81,87,108,112	0

6.3 Carbohydrates [i](#)

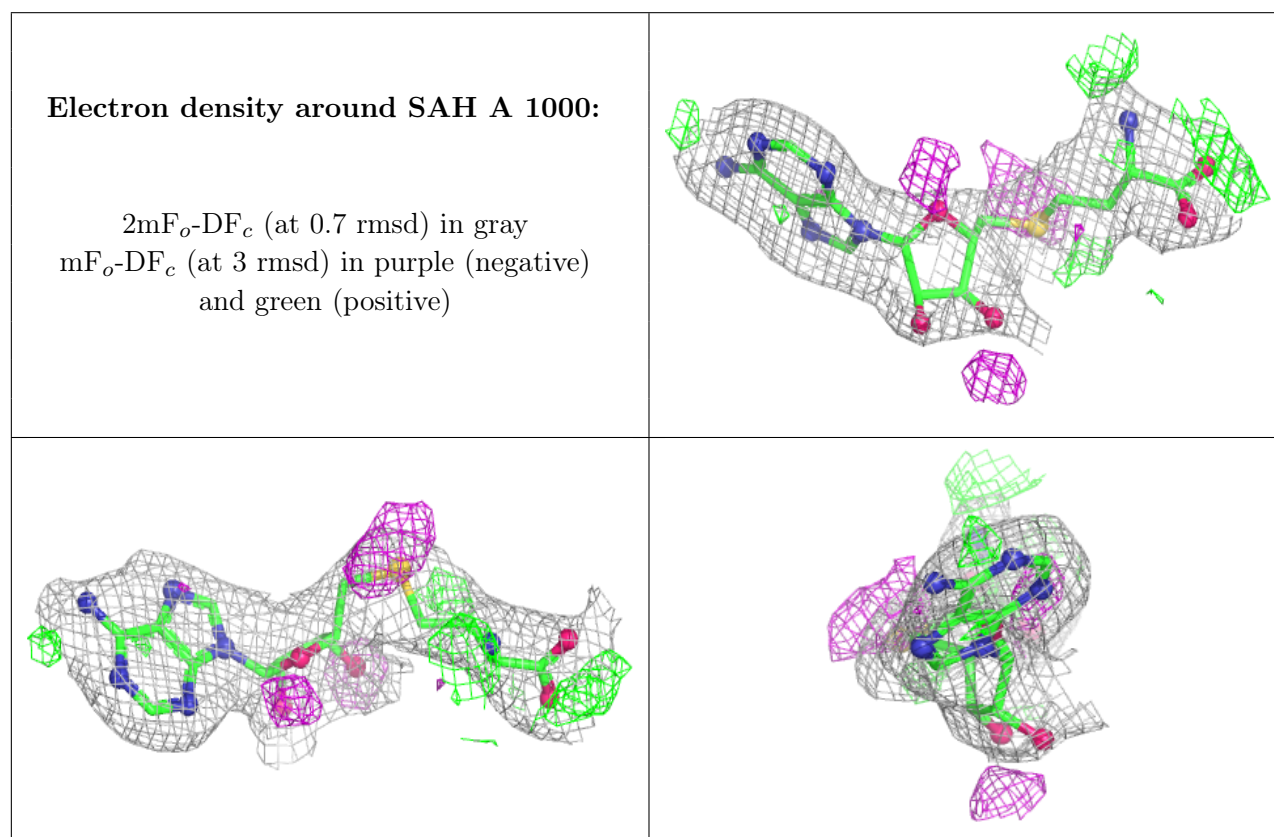
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

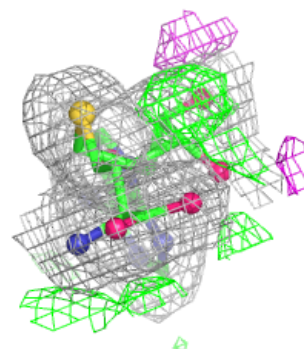
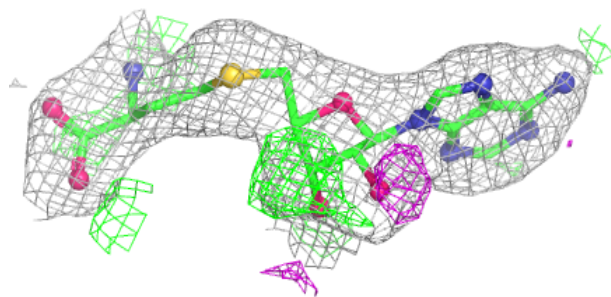
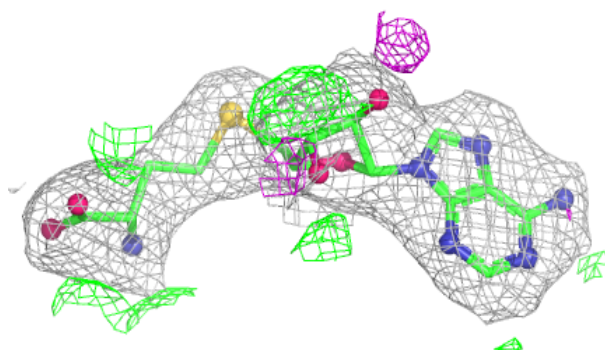
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SAH	A	1000	26/26	0.86	0.14	36,63,83,93	0
3	SAH	B	1000	26/26	0.96	0.08	11,36,55,67	0

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 SAH B 1000:

$2mF_o-DF_c$ (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.