



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Sep 17, 2017 – 05:45 AM EDT

PDB ID : 5KBS
EMDB ID: : EMD-8229
Title : Cryo-EM structure of GluA2-0xSTZ at 8.7 Angstrom resolution
Authors : Twomey, E.C.; Yelshanskaya, M.V.; Grassucci, R.A.; Frank, J.; Sobolevsky, A.I.
Deposited on : unknown
Resolution : 8.70 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

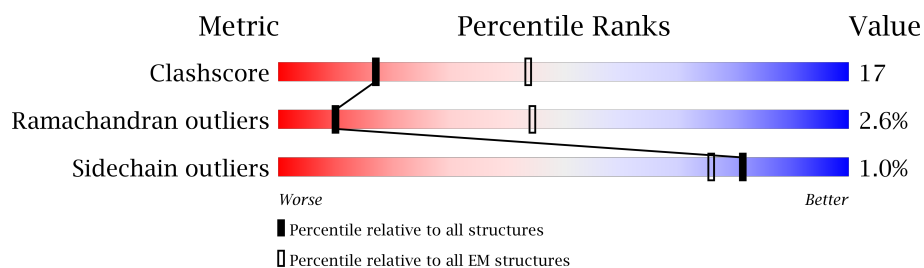
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.70 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1034	
1	B	1034	
1	C	1034	
1	D	1034	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22637 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Glutamate receptor 2, Voltage-dependent calcium channel gamma-2 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	782	Total	C	N	O	S	0	0
			5626	3620	898	1081	27		
1	B	779	Total	C	N	O	S	0	0
			5647	3635	902	1083	27		
1	C	779	Total	C	N	O	S	0	0
			5600	3605	891	1077	27		
1	D	779	Total	C	N	O	S	0	0
			5600	3605	891	1077	27		

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	GLU	ASN	engineered mutation	UNP P19491
A	382	LEU	VAL	engineered mutation	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	THR	deletion	UNP P19491
A	?	-	GLU	deletion	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	PRO	deletion	UNP P19491
A	?	-	SER	deletion	UNP P19491
A	384	GLU	GLY	engineered mutation	UNP P19491
A	385	ASP	ASN	engineered mutation	UNP P19491
A	392	GLN	ASN	conflict	UNP P19491
A	758	LEU	VAL	engineered mutation	UNP P19491
A	827	GLY	-	linker	UNP P19491
A	828	THR	-	linker	UNP P19491
A	875	ASP	ASN	conflict	UNP O88602
A	1036	THR	-	expression tag	UNP O88602
A	1037	GLY	-	expression tag	UNP O88602
A	1038	GLY	-	expression tag	UNP O88602
A	1039	LEU	-	expression tag	UNP O88602
A	1040	VAL	-	expression tag	UNP O88602
A	1041	PRO	-	expression tag	UNP O88602

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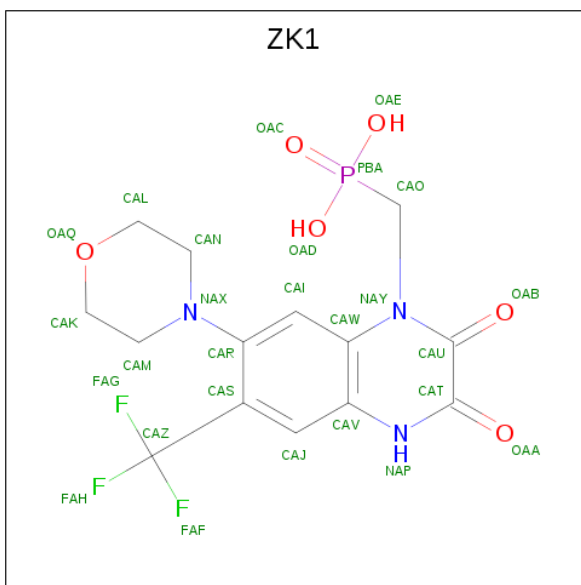
Chain	Residue	Modelled	Actual	Comment	Reference
A	1042	ARG	-	expression tag	UNP O88602
A	1043	GLY	-	expression tag	UNP O88602
B	241	GLU	ASN	engineered mutation	UNP P19491
B	382	LEU	VAL	engineered mutation	UNP P19491
B	?	-	LEU	deletion	UNP P19491
B	?	-	THR	deletion	UNP P19491
B	?	-	GLU	deletion	UNP P19491
B	?	-	LEU	deletion	UNP P19491
B	?	-	PRO	deletion	UNP P19491
B	?	-	SER	deletion	UNP P19491
B	384	GLU	GLY	engineered mutation	UNP P19491
B	385	ASP	ASN	engineered mutation	UNP P19491
B	392	GLN	ASN	conflict	UNP P19491
B	758	LEU	VAL	engineered mutation	UNP P19491
B	827	GLY	-	linker	UNP P19491
B	828	THR	-	linker	UNP P19491
B	875	ASP	ASN	conflict	UNP O88602
B	1036	THR	-	expression tag	UNP O88602
B	1037	GLY	-	expression tag	UNP O88602
B	1038	GLY	-	expression tag	UNP O88602
B	1039	LEU	-	expression tag	UNP O88602
B	1040	VAL	-	expression tag	UNP O88602
B	1041	PRO	-	expression tag	UNP O88602
B	1042	ARG	-	expression tag	UNP O88602
B	1043	GLY	-	expression tag	UNP O88602
C	241	GLU	ASN	engineered mutation	UNP P19491
C	382	LEU	VAL	engineered mutation	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	THR	deletion	UNP P19491
C	?	-	GLU	deletion	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	PRO	deletion	UNP P19491
C	?	-	SER	deletion	UNP P19491
C	384	GLU	GLY	engineered mutation	UNP P19491
C	385	ASP	ASN	engineered mutation	UNP P19491
C	392	GLN	ASN	conflict	UNP P19491
C	758	LEU	VAL	engineered mutation	UNP P19491
C	827	GLY	-	linker	UNP P19491
C	828	THR	-	linker	UNP P19491
C	875	ASP	ASN	conflict	UNP O88602
C	1036	THR	-	expression tag	UNP O88602
C	1037	GLY	-	expression tag	UNP O88602

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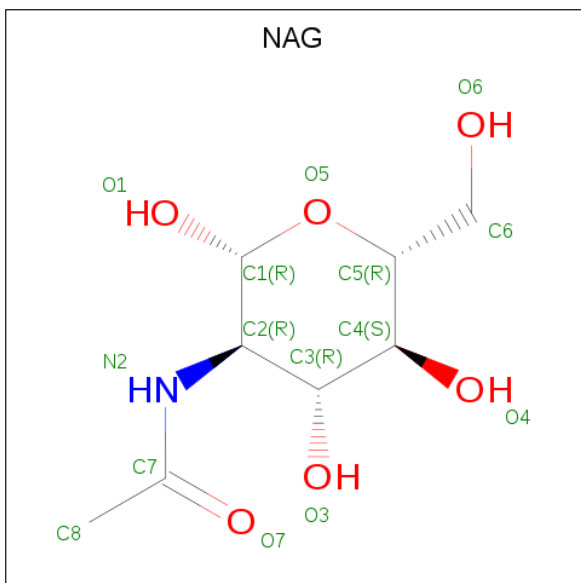
Chain	Residue	Modelled	Actual	Comment	Reference
C	1038	GLY	-	expression tag	UNP O88602
C	1039	LEU	-	expression tag	UNP O88602
C	1040	VAL	-	expression tag	UNP O88602
C	1041	PRO	-	expression tag	UNP O88602
C	1042	ARG	-	expression tag	UNP O88602
C	1043	GLY	-	expression tag	UNP O88602
D	241	GLU	ASN	engineered mutation	UNP P19491
D	382	LEU	VAL	engineered mutation	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	THR	deletion	UNP P19491
D	?	-	GLU	deletion	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	PRO	deletion	UNP P19491
D	?	-	SER	deletion	UNP P19491
D	384	GLU	GLY	engineered mutation	UNP P19491
D	385	ASP	ASN	engineered mutation	UNP P19491
D	392	GLN	ASN	conflict	UNP P19491
D	758	LEU	VAL	engineered mutation	UNP P19491
D	827	GLY	-	linker	UNP P19491
D	828	THR	-	linker	UNP P19491
D	875	ASP	ASN	conflict	UNP O88602
D	1036	THR	-	expression tag	UNP O88602
D	1037	GLY	-	expression tag	UNP O88602
D	1038	GLY	-	expression tag	UNP O88602
D	1039	LEU	-	expression tag	UNP O88602
D	1040	VAL	-	expression tag	UNP O88602
D	1041	PRO	-	expression tag	UNP O88602
D	1042	ARG	-	expression tag	UNP O88602
D	1043	GLY	-	expression tag	UNP O88602

- Molecule 2 is {[7-morpholin-4-yl-2,3-dioxo-6-(trifluoromethyl)-3,4-dihydroquinoxalin-1(2H)-yl]methyl}phosphonic acid (three-letter code: ZK1) (formula: C₁₄H₁₅F₃N₃O₆P).

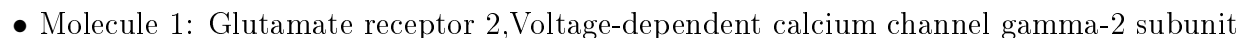


Mol	Chain	Residues	Atoms						AltConf
2	A	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
2	B	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
2	C	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
2	D	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	

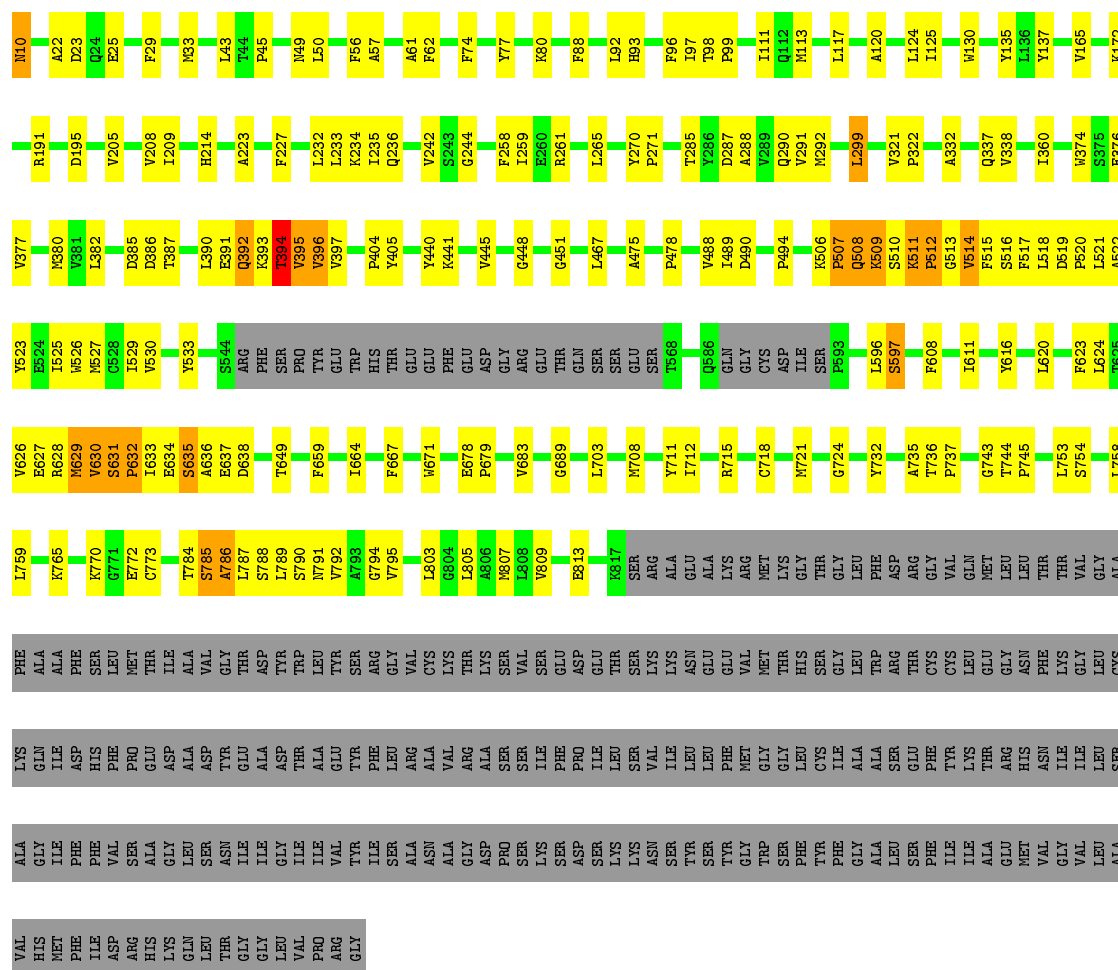
- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	



Chain D:  57% 17% . 25%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	7993	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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: NAG, ZK1

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 >2	RMSZ	# Z >2
1	A	0.25	1/5747 (0.0%)	0.53	5/7870 (0.1%)
1	B	0.24	0/5768	0.37	2/7888 (0.0%)
1	C	0.24	0/5721	0.43	6/7837 (0.1%)
1	D	0.24	0/5721	0.37	1/7837 (0.0%)
All	All	0.24	1/22957 (0.0%)	0.43	14/31432 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	787	LEU	C-N	-5.18	1.22	1.34

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	787	LEU	O-C-N	-28.18	77.62	122.70
1	C	628	ARG	NE-CZ-NH1	-13.77	113.42	120.30
1	A	628	ARG	NE-CZ-NH2	-12.47	114.06	120.30
1	C	628	ARG	NE-CZ-NH2	11.86	126.23	120.30
1	A	628	ARG	NE-CZ-NH1	11.01	125.80	120.30
1	A	628	ARG	CD-NE-CZ	5.76	131.67	123.60
1	C	628	ARG	CD-NE-CZ	5.32	131.05	123.60
1	D	511	LYS	C-N-CD	5.10	139.10	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	511	LYS	C-N-CD	5.07	139.05	128.40
1	B	511	LYS	C-N-CD	5.07	139.04	128.40
1	C	631	SER	C-N-CD	5.07	139.04	128.40
1	B	631	SER	C-N-CD	5.06	139.02	128.40
1	A	511	LYS	C-N-CD	5.05	139.01	128.40
1	C	506	LYS	C-N-CD	5.05	139.01	128.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	787	LEU	Mainchain

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	5626	0	5105	206	0
1	B	5647	0	5177	226	0
1	C	5600	0	5073	181	0
1	D	5600	0	5072	212	0
2	A	27	0	13	0	0
2	B	27	0	13	1	0
2	C	27	0	13	0	0
2	D	27	0	13	0	0
3	A	14	0	13	2	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
3	D	14	0	13	2	0
All	All	22637	0	20531	746	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 17.

All (746) 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:C:512:PRO:CB	1:C:790:SER:HB2	1.23	1.59
1:C:512:PRO:HB3	1:C:790:SER:CB	1.19	1.58
1:C:611:ILE:HD12	1:D:517:PHE:CE1	1.36	1.57
1:D:514:VAL:HG22	1:D:794:GLY:CA	1.30	1.55
1:D:512:PRO:HB3	1:D:790:SER:CB	1.43	1.45
1:D:512:PRO:CB	1:D:790:SER:HB2	1.45	1.45
1:A:771:GLY:HA2	1:A:772:GLU:CB	1.45	1.43
1:D:718:CYS:HB3	1:D:773:CYS:SG	1.60	1.42
1:A:623:PHE:HE1	1:B:785:SER:CB	1.33	1.39
1:C:512:PRO:HB3	1:C:790:SER:CA	1.54	1.34
1:C:512:PRO:CA	1:C:790:SER:HB2	1.54	1.33
1:A:771:GLY:CA	1:A:772:GLU:HB2	1.47	1.32
1:C:611:ILE:CD1	1:D:517:PHE:CE1	2.13	1.30
1:C:782:GLU:HA	1:C:783:LYS:CB	1.51	1.29
1:A:809:VAL:HA	1:A:812:ILE:CD1	1.60	1.29
1:B:507:PRO:O	1:B:508:GLN:HG3	1.10	1.26
1:A:519:ASP:O	1:B:787:LEU:HD21	1.35	1.22
1:A:623:PHE:CE1	1:B:785:SER:CB	2.24	1.20
1:D:514:VAL:CG2	1:D:794:GLY:HA2	1.73	1.17
1:C:787:LEU:HD13	1:C:788:SER:H	1.11	1.15
1:B:611:ILE:HD12	1:C:517:PHE:CE1	1.81	1.15
1:D:718:CYS:CB	1:D:773:CYS:SG	2.33	1.15
1:D:514:VAL:CG2	1:D:794:GLY:CA	2.24	1.13
1:B:632:PRO:O	1:B:633:ILE:HG23	1.48	1.12
1:C:394:THR:CG2	1:C:395:VAL:H	1.63	1.12
1:C:394:THR:HG22	1:C:395:VAL:N	1.61	1.12
1:B:611:ILE:HD12	1:C:517:PHE:HE1	0.96	1.12
1:B:611:ILE:CD1	1:C:517:PHE:HE1	1.63	1.11
1:A:810:ALA:O	1:A:814:PHE:CD2	2.04	1.11
1:B:633:ILE:HG21	1:B:723:VAL:HG11	1.30	1.10
1:A:809:VAL:HA	1:A:812:ILE:HD11	1.32	1.10
1:D:509:LYS:CB	1:D:629:MET:SD	2.38	1.10
1:B:394:THR:HG22	1:B:395:VAL:H	1.06	1.10
1:B:507:PRO:HG2	1:B:631:SER:HB3	1.33	1.09
1:B:507:PRO:O	1:B:508:GLN:CG	1.99	1.09
1:A:809:VAL:HA	1:A:812:ILE:CG1	1.81	1.09
1:C:520:PRO:O	1:D:787:LEU:CD2	2.01	1.09
1:B:509:LYS:HG2	1:B:510:SER:H	1.12	1.07
1:A:812:ILE:O	1:A:816:TYR:CD2	2.06	1.07
1:B:508:GLN:HG2	1:B:629:MET:HG3	1.34	1.07
1:B:507:PRO:HG2	1:B:631:SER:CB	1.84	1.06
1:A:809:VAL:O	1:A:813:GLU:HG3	1.56	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:506:LYS:HG2	1:B:719:ASP:HA	1.35	1.05
1:B:630:VAL:HG22	1:B:631:SER:H	1.22	1.04
1:C:517:PHE:CZ	1:C:526:TRP:CH2	2.45	1.03
1:C:611:ILE:CD1	1:D:517:PHE:HE1	1.60	1.02
1:B:506:LYS:HG2	1:B:719:ASP:CA	1.89	1.02
1:B:626:VAL:HB	1:C:628:ARG:HH11	1.24	1.02
1:B:611:ILE:CD1	1:C:517:PHE:CE1	2.40	1.01
1:B:507:PRO:CB	1:B:630:VAL:O	2.10	0.99
1:A:611:ILE:HD12	1:B:517:PHE:CE1	1.97	0.99
1:A:771:GLY:CA	1:A:772:GLU:CB	2.18	0.98
1:A:611:ILE:HD12	1:B:517:PHE:HE1	1.25	0.98
1:C:611:ILE:HD11	1:D:517:PHE:CZ	1.99	0.98
1:A:812:ILE:O	1:A:816:TYR:HD2	1.44	0.98
1:B:507:PRO:HG2	1:B:631:SER:CA	1.94	0.98
1:D:514:VAL:HG22	1:D:794:GLY:HA3	1.39	0.98
1:B:507:PRO:HB2	1:B:630:VAL:O	1.64	0.97
1:C:782:GLU:CA	1:C:783:LYS:CB	2.41	0.97
1:C:611:ILE:CD1	1:D:517:PHE:CZ	2.47	0.97
1:A:519:ASP:O	1:B:787:LEU:CD2	2.11	0.97
1:C:512:PRO:CB	1:C:790:SER:CB	2.01	0.97
1:D:517:PHE:CE2	1:D:526:TRP:CH2	2.53	0.97
1:A:718:CYS:HB3	1:A:776:LYS:CB	1.95	0.97
1:B:394:THR:HG22	1:B:395:VAL:N	1.80	0.96
1:B:394:THR:HG23	1:B:439:LYS:C	1.85	0.96
1:D:631:SER:HB3	1:D:632:PRO:HD2	1.48	0.95
1:D:718:CYS:CB	1:D:773:CYS:HG	1.74	0.95
1:A:511:LYS:H	1:A:512:PRO:HD3	1.30	0.95
1:A:809:VAL:HA	1:A:812:ILE:HG12	1.49	0.95
1:C:512:PRO:CB	1:C:790:SER:CA	2.39	0.95
1:A:787:LEU:HG	1:A:788:SER:H	1.30	0.95
1:A:520:PRO:O	1:B:787:LEU:HG	1.66	0.94
1:C:394:THR:HG22	1:C:395:VAL:H	0.78	0.93
1:D:718:CYS:HB3	1:D:773:CYS:HG	1.19	0.93
1:D:518:LEU:O	1:D:521:LEU:O	1.86	0.92
1:B:394:THR:HG23	1:B:439:LYS:O	1.67	0.92
1:B:508:GLN:HG2	1:B:629:MET:CG	1.99	0.92
1:A:809:VAL:CA	1:A:812:ILE:HG12	1.99	0.92
1:B:633:ILE:HB	1:B:634:GLU:CB	1.99	0.92
1:A:810:ALA:O	1:A:814:PHE:HD2	1.51	0.91
1:A:514:VAL:HG13	1:A:794:GLY:HA3	1.53	0.90
1:C:517:PHE:CE2	1:C:526:TRP:CH2	2.60	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:808:LEU:O	1:A:812:ILE:HG23	1.71	0.89
1:B:394:THR:CG2	1:B:395:VAL:H	1.86	0.89
1:C:521:LEU:HA	1:D:787:LEU:HD23	1.51	0.89
1:D:506:LYS:O	1:D:508:GLN:N	2.06	0.88
1:C:520:PRO:O	1:D:787:LEU:HD22	1.71	0.87
1:B:507:PRO:CG	1:B:631:SER:HA	2.05	0.87
1:D:517:PHE:CZ	1:D:526:TRP:CH2	2.63	0.87
1:A:718:CYS:CB	1:A:776:LYS:CB	2.52	0.86
1:B:632:PRO:O	1:B:633:ILE:CG2	2.23	0.86
1:C:787:LEU:CD1	1:C:788:SER:H	1.88	0.86
1:B:509:LYS:HG2	1:B:510:SER:N	1.91	0.85
1:B:633:ILE:HB	1:B:634:GLU:CA	2.06	0.85
1:C:520:PRO:O	1:D:787:LEU:HD23	1.74	0.85
1:D:517:PHE:CZ	1:D:526:TRP:HH2	1.94	0.84
1:D:632:PRO:C	1:D:633:ILE:HD12	1.96	0.84
1:D:630:VAL:HG23	1:D:631:SER:N	1.91	0.84
1:D:507:PRO:CG	1:D:721:MET:SD	2.66	0.84
1:C:517:PHE:CZ	1:C:526:TRP:HH2	1.93	0.84
1:A:809:VAL:CA	1:A:812:ILE:HD11	2.07	0.84
1:C:518:LEU:O	1:C:521:LEU:O	1.95	0.84
1:B:507:PRO:HG2	1:B:630:VAL:O	1.77	0.83
1:B:509:LYS:CG	1:B:510:SER:H	1.91	0.83
1:B:507:PRO:CG	1:B:630:VAL:O	2.26	0.83
1:C:512:PRO:CA	1:C:790:SER:CB	2.47	0.82
1:A:517:PHE:HE1	1:D:611:ILE:HD12	1.41	0.82
1:A:633:ILE:HG22	1:A:634:GLU:H	1.45	0.82
1:D:631:SER:HB3	1:D:632:PRO:CD	2.09	0.82
1:A:386:ASP:O	1:A:388:SER:N	2.13	0.81
1:B:372:GLY:HA2	1:B:383:THR:HG23	1.61	0.81
1:B:518:LEU:O	1:B:521:LEU:O	1.98	0.81
1:D:514:VAL:HG22	1:D:794:GLY:HA2	0.83	0.81
1:D:518:LEU:HA	1:D:526:TRP:HE1	1.46	0.81
1:B:394:THR:CG2	1:B:439:LYS:O	2.29	0.81
1:C:517:PHE:CE2	1:C:526:TRP:CZ2	2.68	0.80
1:B:507:PRO:CG	1:B:631:SER:HB3	2.10	0.80
1:A:388:SER:O	1:A:390:LEU:N	2.14	0.80
1:C:514:VAL:HG22	1:C:794:GLY:CA	2.12	0.80
1:D:512:PRO:CG	1:D:790:SER:HB2	2.11	0.80
1:B:504:ILE:HD13	1:B:633:ILE:CG2	2.12	0.80
1:B:508:GLN:CG	1:B:629:MET:HG3	2.11	0.79
1:A:633:ILE:HG23	1:A:638:ASP:CB	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:LYS:H	1:A:512:PRO:CD	1.95	0.78
1:A:787:LEU:HG	1:A:788:SER:N	1.96	0.78
1:C:525:ILE:HD11	1:D:788:SER:O	1.83	0.78
1:D:394:THR:HG22	1:D:440:TYR:HA	1.64	0.78
1:B:692:ARG:HG3	1:B:700:TYR:CD2	2.19	0.77
1:B:506:LYS:HG2	1:B:719:ASP:CB	2.15	0.77
1:D:390:LEU:O	1:D:392:GLN:N	2.18	0.77
1:D:635:SER:OG	1:D:638:ASP:CG	2.24	0.76
1:B:507:PRO:HG2	1:B:631:SER:HA	1.66	0.76
1:A:649:THR:HG22	1:A:703:LEU:HB2	1.68	0.76
1:B:649:THR:HG22	1:B:703:LEU:HB2	1.67	0.76
1:C:611:ILE:HD11	1:D:517:PHE:HZ	1.49	0.76
1:C:521:LEU:HA	1:D:787:LEU:CD2	2.16	0.76
1:D:394:THR:HG22	1:D:440:TYR:CA	2.15	0.76
1:A:809:VAL:C	1:A:812:ILE:HG12	2.06	0.76
1:C:771:GLY:C	1:C:772:GLU:HG3	2.05	0.76
1:B:513:GLY:C	1:B:515:PHE:H	1.90	0.75
1:D:649:THR:HG22	1:D:703:LEU:HB2	1.68	0.75
1:D:394:THR:O	1:D:396:VAL:N	2.20	0.75
1:B:786:ALA:C	1:B:787:LEU:HD13	2.07	0.75
1:A:809:VAL:O	1:A:813:GLU:CG	2.35	0.75
1:C:512:PRO:HA	1:C:790:SER:HB2	1.64	0.75
1:D:512:PRO:HB3	1:D:790:SER:CA	2.17	0.75
1:C:649:THR:HG22	1:C:703:LEU:HB2	1.68	0.75
1:C:512:PRO:HB3	1:C:790:SER:HA	1.61	0.75
1:A:809:VAL:CA	1:A:812:ILE:CG1	2.59	0.74
1:A:525:ILE:HG12	1:B:789:LEU:HD13	1.68	0.74
1:D:630:VAL:O	1:D:631:SER:OG	2.06	0.74
1:B:633:ILE:HB	1:B:634:GLU:HA	1.70	0.74
1:B:392:GLN:O	1:B:394:THR:N	2.21	0.74
1:B:508:GLN:HG2	1:B:629:MET:SD	2.26	0.74
1:D:517:PHE:CE2	1:D:526:TRP:CZ2	2.75	0.74
1:B:630:VAL:HG22	1:B:631:SER:N	2.02	0.74
1:D:630:VAL:HG23	1:D:631:SER:H	1.53	0.74
1:B:394:THR:CG2	1:B:439:LYS:C	2.56	0.73
1:C:514:VAL:HG22	1:C:794:GLY:HA3	1.70	0.73
1:C:518:LEU:HA	1:C:526:TRP:HE1	1.54	0.73
1:C:611:ILE:HG21	1:D:795:VAL:HG21	1.70	0.73
1:C:787:LEU:HD13	1:C:788:SER:N	1.95	0.72
1:A:633:ILE:HG23	1:A:638:ASP:HB3	1.70	0.72
1:A:633:ILE:CG2	1:A:638:ASP:HB2	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:PRO:HG3	1:B:631:SER:HA	1.70	0.72
1:B:513:GLY:O	1:B:515:PHE:N	2.24	0.71
1:B:633:ILE:N	1:B:633:ILE:HD13	2.04	0.71
1:C:512:PRO:CB	1:C:790:SER:C	2.59	0.71
1:D:718:CYS:SG	1:D:773:CYS:HA	2.31	0.71
1:A:809:VAL:HG12	1:A:813:GLU:OE2	1.91	0.71
1:A:812:ILE:HB	1:A:816:TYR:HE2	1.55	0.71
1:A:813:GLU:OE2	1:D:596:LEU:HB3	1.91	0.70
1:C:611:ILE:HD12	1:D:517:PHE:HE1	0.69	0.70
1:D:518:LEU:HA	1:D:526:TRP:NE1	2.05	0.70
1:A:774:GLY:O	1:A:775:ALA:HB2	1.92	0.70
1:D:394:THR:HG22	1:D:440:TYR:C	2.12	0.69
1:B:611:ILE:HD11	1:C:517:PHE:CE1	2.26	0.69
1:A:628:ARG:NH1	1:D:627:GLU:H	1.91	0.69
1:D:507:PRO:HD3	1:D:721:MET:SD	2.33	0.68
1:D:718:CYS:SG	1:D:773:CYS:CB	2.82	0.68
1:D:517:PHE:HD1	1:D:616:TYR:HH	1.42	0.67
1:D:514:VAL:HG13	1:D:794:GLY:C	2.14	0.67
1:D:514:VAL:HA	1:D:794:GLY:HA3	1.77	0.67
1:A:633:ILE:N	1:A:633:ILE:HD13	2.09	0.66
1:D:635:SER:OG	1:D:638:ASP:OD2	2.11	0.66
1:B:505:LYS:HG2	1:B:506:LYS:H	1.61	0.65
1:D:634:GLU:O	1:D:635:SER:HB3	1.96	0.65
1:B:508:GLN:HA	1:B:629:MET:SD	2.37	0.65
1:C:520:PRO:O	1:D:787:LEU:CB	2.45	0.65
1:C:512:PRO:HB2	1:C:790:SER:C	2.16	0.65
1:B:632:PRO:C	1:B:633:ILE:HD13	2.18	0.64
1:D:514:VAL:CA	1:D:794:GLY:HA3	2.27	0.64
1:C:521:LEU:HD22	1:C:526:TRP:CD2	2.32	0.64
1:C:519:ASP:HB2	1:C:520:PRO:HD3	1.79	0.64
1:D:507:PRO:HG3	1:D:721:MET:SD	2.37	0.64
1:B:632:PRO:C	1:B:633:ILE:HG23	2.17	0.63
1:D:507:PRO:CD	1:D:721:MET:SD	2.86	0.63
1:C:633:ILE:HG23	1:C:638:ASP:HB2	1.80	0.63
1:C:525:ILE:HG12	1:D:789:LEU:HD13	1.81	0.63
1:D:521:LEU:HD23	1:D:525:ILE:HB	1.80	0.63
1:A:521:LEU:HD23	1:A:525:ILE:HB	1.80	0.63
1:B:521:LEU:HD23	1:B:525:ILE:HB	1.80	0.63
1:B:507:PRO:C	1:B:508:GLN:HG3	2.11	0.63
1:A:633:ILE:HG23	1:A:638:ASP:HB2	1.77	0.63
1:A:521:LEU:HD22	1:A:526:TRP:CD2	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:519:ASP:HB2	1:D:520:PRO:HD3	1.80	0.62
1:D:521:LEU:HD22	1:D:526:TRP:CD2	2.34	0.62
1:D:514:VAL:CG2	1:D:794:GLY:HA3	2.10	0.62
1:B:521:LEU:HD22	1:B:526:TRP:CD2	2.35	0.62
1:C:518:LEU:HA	1:C:526:TRP:NE1	2.14	0.62
1:D:50:LEU:HD23	1:D:57:ALA:HB1	1.82	0.62
1:A:522:ALA:HB3	1:A:525:ILE:HG13	1.82	0.62
1:C:394:THR:CG2	1:C:395:VAL:N	2.35	0.62
1:B:507:PRO:CG	1:B:631:SER:CA	2.66	0.61
1:A:619:ASN:OD1	1:B:787:LEU:HD12	1.99	0.61
1:B:786:ALA:O	1:B:787:LEU:HD13	2.00	0.61
1:D:489:ILE:HD12	1:D:735:ALA:HB1	1.83	0.61
1:A:812:ILE:HG13	1:A:813:GLU:N	2.13	0.61
1:C:516:SER:OG	1:C:791:ASN:CG	2.39	0.61
1:C:50:LEU:HD23	1:C:57:ALA:HB1	1.82	0.61
1:A:628:ARG:NH2	1:D:623:PHE:HD1	1.98	0.61
1:B:50:LEU:HD23	1:B:57:ALA:HB1	1.83	0.61
1:B:394:THR:HG22	1:B:440:TYR:HA	1.82	0.61
1:C:390:LEU:O	1:C:392:GLN:N	2.34	0.60
1:D:522:ALA:HB3	1:D:525:ILE:HG13	1.83	0.60
1:B:505:LYS:HD3	1:B:698:GLY:N	2.16	0.60
1:C:521:LEU:HD23	1:C:525:ILE:HB	1.83	0.60
1:D:514:VAL:HG22	1:D:794:GLY:C	2.16	0.60
1:A:50:LEU:HD23	1:A:57:ALA:HB1	1.82	0.60
1:A:809:VAL:HG12	1:A:813:GLU:CD	2.22	0.60
1:A:519:ASP:HB2	1:A:520:PRO:HD3	1.82	0.60
1:B:522:ALA:HB3	1:B:525:ILE:HG13	1.82	0.60
1:C:765:LYS:O	1:C:770:LYS:HB2	2.01	0.60
1:D:514:VAL:CB	1:D:794:GLY:HA3	2.30	0.60
1:A:475:ALA:HB3	1:A:735:ALA:HB3	1.82	0.60
1:B:508:GLN:O	1:B:509:LYS:HB2	2.01	0.60
1:C:522:ALA:HB3	1:C:525:ILE:HG13	1.83	0.60
1:C:514:VAL:HG22	1:C:794:GLY:HA2	1.84	0.59
1:A:628:ARG:HH12	1:D:627:GLU:H	1.50	0.59
1:A:611:ILE:CD1	1:B:517:PHE:CE1	2.78	0.59
1:C:475:ALA:HB3	1:C:735:ALA:HB3	1.84	0.59
1:A:810:ALA:C	1:A:814:PHE:CD2	2.76	0.59
1:C:520:PRO:HA	1:C:623:PHE:HE2	1.67	0.59
1:B:626:VAL:CB	1:C:628:ARG:HH11	2.08	0.59
1:B:505:LYS:HE3	1:B:506:LYS:HE3	1.83	0.59
1:C:394:THR:HG23	1:C:439:LYS:C	2.23	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:517:PHE:CE1	1:D:611:ILE:HD12	2.32	0.59
1:A:795:VAL:HG21	1:D:611:ILE:HG21	1.84	0.59
1:A:808:LEU:O	1:A:812:ILE:HG12	2.03	0.58
1:A:10:ASN:N	1:A:10:ASN:HD22	2.01	0.58
1:D:631:SER:CB	1:D:632:PRO:HD2	2.30	0.58
1:A:611:ILE:CD1	1:B:517:PHE:CZ	2.87	0.58
1:B:513:GLY:C	1:B:515:PHE:N	2.55	0.58
1:B:235:ILE:HD13	1:B:242:VAL:HG21	1.85	0.58
1:B:514:VAL:HG22	1:B:794:GLY:CA	2.33	0.58
1:C:394:THR:HG23	1:C:439:LYS:O	2.03	0.57
1:C:512:PRO:N	1:C:790:SER:HB2	2.16	0.57
1:B:597:SER:OG	1:C:810:ALA:HB2	2.04	0.57
1:A:812:ILE:C	1:A:816:TYR:CD2	2.78	0.57
1:B:10:ASN:N	1:B:10:ASN:HD22	2.01	0.57
1:D:235:ILE:HD13	1:D:242:VAL:HG21	1.86	0.57
1:A:235:ILE:HD13	1:A:242:VAL:HG21	1.85	0.57
1:C:235:ILE:HD13	1:C:242:VAL:HG21	1.85	0.57
1:A:809:VAL:CB	1:A:812:ILE:HD11	2.35	0.57
1:C:10:ASN:HD22	1:C:10:ASN:N	2.02	0.57
1:C:389:GLY:C	1:C:391:GLU:H	2.08	0.57
1:A:93:HIS:ND1	1:A:322:PRO:HB3	2.19	0.57
1:A:513:GLY:O	1:A:515:PHE:N	2.37	0.57
1:A:809:VAL:O	1:A:812:ILE:CG1	2.53	0.57
1:C:517:PHE:CZ	1:C:526:TRP:CZ2	2.92	0.57
1:D:10:ASN:N	1:D:10:ASN:HD22	2.02	0.57
1:D:99:PRO:HA	1:D:113:MET:HB2	1.87	0.57
1:D:512:PRO:CB	1:D:790:SER:C	2.74	0.57
1:A:513:GLY:C	1:A:515:PHE:H	2.07	0.57
1:B:489:ILE:HD12	1:B:735:ALA:HB1	1.87	0.57
1:D:633:ILE:HD12	1:D:633:ILE:N	2.20	0.57
1:C:99:PRO:HA	1:C:113:MET:HB2	1.87	0.56
1:C:77:TYR:CE2	1:C:98:THR:HG21	2.40	0.56
1:D:77:TYR:CE2	1:D:98:THR:HG21	2.40	0.56
1:B:394:THR:CG2	1:B:440:TYR:HA	2.34	0.56
1:A:99:PRO:HA	1:A:113:MET:HB2	1.87	0.56
1:B:504:ILE:CD1	1:B:633:ILE:CG2	2.81	0.56
1:D:785:SER:O	1:D:786:ALA:HB2	2.05	0.56
1:D:512:PRO:HB2	1:D:790:SER:C	2.26	0.56
1:B:514:VAL:HG22	1:B:794:GLY:HA3	1.85	0.56
1:B:633:ILE:HG21	1:B:723:VAL:CG1	2.21	0.56
1:D:521:LEU:HD22	1:D:526:TRP:CG	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:TYR:CE2	1:A:98:THR:HG21	2.40	0.56
1:B:99:PRO:HA	1:B:113:MET:HB2	1.87	0.56
1:A:209:ILE:HA	1:A:214:HIS:CD2	2.41	0.56
1:C:521:LEU:HD22	1:C:526:TRP:CG	2.40	0.56
1:D:512:PRO:HB3	1:D:790:SER:HB2	0.65	0.56
1:C:376:GLU:HG3	1:C:377:VAL:HG13	1.88	0.56
1:A:769:ASP:C	1:A:771:GLY:H	2.09	0.56
1:B:521:LEU:HD22	1:B:526:TRP:CG	2.41	0.56
1:C:227:PHE:CD1	1:C:244:GLY:HA3	2.41	0.56
1:B:695:LYS:O	1:B:695:LYS:HG2	2.04	0.56
1:A:376:GLU:HG3	1:A:377:VAL:HG13	1.88	0.55
1:D:227:PHE:CD1	1:D:244:GLY:HA3	2.41	0.55
1:D:376:GLU:HG3	1:D:377:VAL:HG13	1.88	0.55
1:A:227:PHE:CD1	1:A:244:GLY:HA3	2.41	0.55
1:A:521:LEU:HD22	1:A:526:TRP:CG	2.41	0.55
1:A:769:ASP:O	1:A:771:GLY:N	2.39	0.55
1:C:209:ILE:HA	1:C:214:HIS:CD2	2.41	0.55
1:D:209:ILE:HA	1:D:214:HIS:CD2	2.41	0.55
1:B:227:PHE:CD1	1:B:244:GLY:HA3	2.41	0.55
1:C:512:PRO:HB2	1:C:790:SER:O	2.06	0.55
1:D:516:SER:OG	1:D:791:ASN:CG	2.45	0.55
1:B:209:ILE:HA	1:B:214:HIS:CD2	2.41	0.55
1:B:506:LYS:HG2	1:B:719:ASP:HB2	1.88	0.55
1:A:808:LEU:O	1:A:812:ILE:CG2	2.51	0.55
1:B:376:GLU:HG3	1:B:377:VAL:HG13	1.88	0.55
1:D:718:CYS:SG	1:D:773:CYS:CA	2.95	0.55
1:B:77:TYR:CE2	1:B:98:THR:HG21	2.41	0.55
1:D:753:LEU:HD22	1:D:758:LEU:HD13	1.89	0.55
1:C:753:LEU:HD22	1:C:758:LEU:HD13	1.89	0.55
1:A:391:GLU:C	1:A:393:LYS:H	2.10	0.55
1:B:788:SER:OG	1:B:790:SER:OG	2.12	0.55
1:C:771:GLY:O	1:C:772:GLU:HG3	2.06	0.54
1:B:62:PHE:HE2	1:B:92:LEU:HD12	1.72	0.54
1:C:91:THR:HG21	1:D:56:PHE:CE2	2.42	0.54
1:A:62:PHE:HE2	1:A:92:LEU:HD12	1.73	0.54
1:B:299:LEU:HD11	1:B:332:ALA:HB2	1.88	0.54
1:B:635:SER:O	1:B:636:ALA:C	2.44	0.54
1:B:519:ASP:HB2	1:B:520:PRO:HD3	1.90	0.54
1:B:506:LYS:CG	1:B:719:ASP:HA	2.25	0.54
1:C:489:ILE:HD12	1:C:735:ALA:HB1	1.88	0.54
1:C:62:PHE:HE2	1:C:92:LEU:HD12	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:692:ARG:CG	1:B:700:TYR:CD2	2.89	0.54
1:D:394:THR:CG2	1:D:440:TYR:C	2.76	0.54
1:A:753:LEU:HD22	1:A:758:LEU:HD13	1.89	0.54
1:A:754:SER:HB3	1:A:759:LEU:HD12	1.90	0.54
1:D:635:SER:O	1:D:638:ASP:N	2.25	0.54
1:D:765:LYS:O	1:D:770:LYS:HB2	2.08	0.54
1:B:753:LEU:HD22	1:B:758:LEU:HD13	1.89	0.53
1:C:754:SER:HB3	1:C:759:LEU:HD12	1.90	0.53
1:A:812:ILE:C	1:A:816:TYR:HD2	2.08	0.53
1:D:475:ALA:HB3	1:D:735:ALA:HB3	1.90	0.53
1:B:636:ALA:O	1:B:639:LEU:N	2.37	0.53
1:A:774:GLY:O	1:A:775:ALA:CB	2.57	0.53
1:D:62:PHE:HE2	1:D:92:LEU:HD12	1.73	0.53
1:D:337:GLN:HE22	3:D:1102:NAG:H2	1.74	0.53
1:D:754:SER:HB3	1:D:759:LEU:HD12	1.91	0.53
1:A:809:VAL:HG13	1:A:812:ILE:HD11	1.90	0.53
1:B:506:LYS:CG	1:B:719:ASP:HB2	2.39	0.53
1:C:521:LEU:CA	1:D:787:LEU:HD23	2.31	0.53
1:B:626:VAL:HB	1:C:628:ARG:NH1	2.08	0.53
1:A:809:VAL:O	1:A:812:ILE:HG13	2.07	0.52
1:D:405:TYR:CG	1:D:478:PRO:HG3	2.44	0.52
1:A:523:TYR:O	1:A:527:MET:HG2	2.09	0.52
1:D:205:VAL:O	1:D:209:ILE:HG13	2.09	0.52
1:C:512:PRO:HA	1:C:790:SER:CB	2.30	0.52
1:A:628:ARG:HH11	1:D:626:VAL:HB	1.74	0.52
1:C:205:VAL:O	1:C:209:ILE:HG13	2.09	0.52
1:A:513:GLY:C	1:A:515:PHE:N	2.63	0.52
1:A:809:VAL:CG1	1:A:813:GLU:OE2	2.58	0.52
1:C:216:LYS:NZ	1:C:473:ASP:OD2	2.43	0.52
1:D:630:VAL:CG2	1:D:631:SER:H	2.17	0.52
1:C:523:TYR:O	1:C:527:MET:HG2	2.10	0.52
1:C:405:TYR:CG	1:C:478:PRO:HG3	2.44	0.52
1:A:405:TYR:CG	1:A:478:PRO:HG3	2.45	0.52
1:B:754:SER:HB3	1:B:759:LEU:HD12	1.90	0.52
1:D:512:PRO:CB	1:D:790:SER:CB	2.34	0.52
1:A:337:GLN:NE2	3:A:1102:NAG:H2	2.25	0.52
1:A:405:TYR:CD1	1:A:478:PRO:HG3	2.45	0.52
1:A:769:ASP:C	1:A:771:GLY:N	2.64	0.52
1:B:405:TYR:CG	1:B:478:PRO:HG3	2.45	0.52
1:C:83:ASN:ND2	1:D:80:LYS:HA	2.26	0.51
1:D:631:SER:CB	1:D:632:PRO:CD	2.85	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:809:VAL:C	1:A:812:ILE:CG1	2.77	0.51
1:D:512:PRO:CB	1:D:790:SER:CA	2.82	0.51
1:A:517:PHE:HE1	1:D:611:ILE:CD1	2.17	0.51
1:B:523:TYR:O	1:B:527:MET:HG2	2.10	0.51
1:B:630:VAL:CG2	1:B:631:SER:H	2.05	0.51
1:C:517:PHE:HZ	1:C:526:TRP:CH2	2.21	0.51
1:C:520:PRO:O	1:D:787:LEU:HB3	2.10	0.51
1:A:810:ALA:C	1:A:814:PHE:HD2	2.12	0.51
1:B:205:VAL:O	1:B:209:ILE:HG13	2.10	0.51
1:D:523:TYR:O	1:D:527:MET:HG2	2.10	0.51
1:A:337:GLN:HE22	3:A:1102:NAG:H2	1.74	0.51
1:A:771:GLY:CA	1:A:772:GLU:HB3	2.28	0.51
1:B:405:TYR:CD1	1:B:478:PRO:HG3	2.46	0.51
1:D:405:TYR:CD1	1:D:478:PRO:HG3	2.45	0.51
1:B:475:ALA:HB3	1:B:735:ALA:HB3	1.93	0.51
1:B:494:PRO:HA	1:B:732:TYR:O	2.10	0.51
1:B:515:PHE:HD1	1:B:518:LEU:HD12	1.76	0.51
1:C:74:PHE:CZ	1:C:285:THR:HG23	2.46	0.51
1:D:290:GLN:HG2	1:D:338:VAL:HG21	1.93	0.51
1:C:515:PHE:HD1	1:C:518:LEU:HD12	1.76	0.51
1:A:205:VAL:O	1:A:209:ILE:HG13	2.10	0.51
1:A:515:PHE:HD1	1:A:518:LEU:HD12	1.76	0.51
1:B:611:ILE:HG21	1:C:795:VAL:HG21	1.93	0.51
1:D:74:PHE:CZ	1:D:285:THR:HG23	2.46	0.51
1:B:74:PHE:CZ	1:B:285:THR:HG23	2.46	0.50
1:B:43:LEU:O	1:B:45:PRO:HD3	2.11	0.50
1:B:611:ILE:HD11	1:C:517:PHE:CZ	2.45	0.50
1:A:611:ILE:HG21	1:B:795:VAL:HG21	1.92	0.50
1:D:633:ILE:HB	1:D:638:ASP:OD1	2.11	0.50
1:D:634:GLU:CB	1:D:724:GLY:N	2.74	0.50
1:B:765:LYS:O	1:B:770:LYS:HB2	2.10	0.50
1:C:405:TYR:CD1	1:C:478:PRO:HG3	2.45	0.50
1:B:769:ASP:C	1:B:771:GLY:H	2.15	0.50
1:D:515:PHE:HD1	1:D:518:LEU:HD12	1.76	0.50
1:D:517:PHE:HD1	1:D:616:TYR:OH	1.93	0.50
1:B:507:PRO:CB	1:B:630:VAL:C	2.80	0.50
1:B:536:VAL:HG22	1:C:803:LEU:HD21	1.94	0.50
1:A:56:PHE:CE2	1:B:91:THR:HG21	2.47	0.50
1:A:80:LYS:HA	1:B:83:ASN:ND2	2.27	0.50
1:A:489:ILE:HD12	1:A:735:ALA:HB1	1.94	0.49
1:D:337:GLN:NE2	3:D:1102:NAG:H2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:LEU:CG	1:A:788:SER:H	2.05	0.49
1:A:525:ILE:HG12	1:B:789:LEU:CD1	2.40	0.49
1:C:494:PRO:HA	1:C:732:TYR:O	2.11	0.49
1:C:659:PHE:HB3	1:C:671:TRP:HB2	1.95	0.49
1:C:445:VAL:HG13	1:C:448:GLY:HA2	1.95	0.49
1:D:526:TRP:O	1:D:529:ILE:HG22	2.13	0.49
1:B:629:MET:HA	1:B:629:MET:CE	2.42	0.49
1:A:633:ILE:HG22	1:A:634:GLU:N	2.22	0.49
1:A:526:TRP:O	1:A:529:ILE:HG22	2.13	0.49
1:A:74:PHE:CZ	1:A:285:THR:HG23	2.47	0.49
1:B:386:ASP:C	1:B:388:SER:H	2.16	0.49
1:D:507:PRO:HG2	1:D:721:MET:SD	2.49	0.49
1:A:494:PRO:HA	1:A:732:TYR:O	2.12	0.49
1:B:526:TRP:O	1:B:529:ILE:HG22	2.12	0.49
1:D:195:ASP:HA	1:D:223:ALA:HB3	1.95	0.49
1:A:608:PHE:HZ	1:B:796:PHE:CZ	2.30	0.49
1:B:659:PHE:HB3	1:B:671:TRP:HB2	1.95	0.49
1:C:43:LEU:O	1:C:45:PRO:HD3	2.12	0.49
1:D:93:HIS:ND1	1:D:322:PRO:HB3	2.28	0.49
1:D:50:LEU:HD22	1:D:61:ALA:HB2	1.95	0.49
1:A:810:ALA:HB2	1:D:597:SER:OG	2.12	0.49
1:B:50:LEU:HD22	1:B:61:ALA:HB2	1.95	0.49
1:D:395:VAL:O	1:D:397:VAL:HG23	2.13	0.49
1:B:384:GLU:O	1:B:385:ASP:CB	2.60	0.48
1:C:127:TYR:CE2	1:C:382:LEU:HD21	2.47	0.48
1:A:659:PHE:HB3	1:A:671:TRP:HB2	1.94	0.48
1:A:664:ILE:HB	1:A:667:PHE:HD2	1.78	0.48
1:D:393:LYS:O	1:D:395:VAL:N	2.45	0.48
1:D:43:LEU:O	1:D:45:PRO:HD3	2.12	0.48
1:C:619:ASN:HA	1:D:624:LEU:HD13	1.95	0.48
1:A:445:VAL:HG13	1:A:448:GLY:HA2	1.95	0.48
1:A:517:PHE:CZ	1:A:526:TRP:CH2	3.01	0.48
1:B:445:VAL:HG13	1:B:448:GLY:HA2	1.95	0.48
1:D:445:VAL:HG13	1:D:448:GLY:HA2	1.95	0.48
1:D:628:ARG:HG3	1:D:628:ARG:O	2.14	0.48
1:D:659:PHE:HB3	1:D:671:TRP:HB2	1.95	0.48
1:A:43:LEU:O	1:A:45:PRO:HD3	2.12	0.48
1:C:664:ILE:HB	1:C:667:PHE:HD2	1.79	0.48
1:C:783:LYS:N	1:C:784:THR:HA	2.28	0.48
1:C:50:LEU:HD22	1:C:61:ALA:HB2	1.94	0.48
1:B:539:VAL:HG13	1:C:807:MET:SD	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:664:ILE:HB	1:D:667:PHE:HD2	1.79	0.48
1:A:258:PHE:HD2	1:A:259:ILE:HD12	1.79	0.48
1:A:50:LEU:HD22	1:A:61:ALA:HB2	1.95	0.48
1:B:514:VAL:HG13	1:B:794:GLY:HA3	1.96	0.48
1:A:628:ARG:CZ	1:D:623:PHE:HD1	2.27	0.48
1:B:195:ASP:HA	1:B:223:ALA:HB3	1.96	0.48
1:B:509:LYS:CG	1:B:510:SER:N	2.60	0.48
1:C:521:LEU:HD22	1:C:526:TRP:CE2	2.49	0.48
1:C:526:TRP:O	1:C:529:ILE:HG22	2.13	0.48
1:B:97:ILE:HG13	1:B:111:ILE:HB	1.96	0.47
1:D:494:PRO:HA	1:D:732:TYR:O	2.14	0.47
1:B:664:ILE:HB	1:B:667:PHE:HD2	1.79	0.47
1:A:711:TYR:O	1:A:715:ARG:HG2	2.14	0.47
1:B:258:PHE:HD2	1:B:259:ILE:HD12	1.79	0.47
1:A:530:VAL:O	1:A:533:TYR:HB3	2.15	0.47
1:A:634:GLU:O	1:A:724:GLY:HA3	2.15	0.47
1:A:810:ALA:HB1	1:A:814:PHE:HE2	1.79	0.47
1:D:258:PHE:HD2	1:D:259:ILE:HD12	1.79	0.47
1:B:29:PHE:O	1:B:33:MET:HG2	2.14	0.47
1:D:711:TYR:O	1:D:715:ARG:HG2	2.14	0.47
1:B:504:ILE:HD13	1:B:633:ILE:HG22	1.93	0.47
1:B:506:LYS:CG	1:B:719:ASP:CA	2.78	0.47
1:D:29:PHE:O	1:D:33:MET:HG2	2.15	0.47
1:D:512:PRO:HB3	1:D:790:SER:C	2.34	0.47
1:C:29:PHE:O	1:C:33:MET:HG2	2.15	0.47
1:C:530:VAL:O	1:C:533:TYR:HB3	2.15	0.47
1:C:711:TYR:O	1:C:715:ARG:HG2	2.14	0.47
1:D:124:LEU:HD13	1:D:380:MET:HE1	1.96	0.47
1:A:195:ASP:HA	1:A:223:ALA:HB3	1.96	0.47
1:C:135:TYR:CE1	1:C:137:TYR:HB3	2.50	0.47
1:B:519:ASP:N	1:B:520:PRO:CD	2.78	0.47
1:B:530:VAL:O	1:B:533:TYR:HB3	2.15	0.47
1:C:195:ASP:HA	1:C:223:ALA:HB3	1.96	0.47
1:C:299:LEU:HD11	1:C:332:ALA:HB2	1.97	0.47
1:B:711:TYR:O	1:B:715:ARG:HG2	2.14	0.47
1:C:208:VAL:HG12	1:C:214:HIS:HB3	1.97	0.47
1:A:124:LEU:HD13	1:A:380:MET:HE1	1.96	0.46
1:A:521:LEU:CD2	1:A:525:ILE:HB	2.45	0.46
1:B:636:ALA:O	1:B:638:ASP:N	2.48	0.46
1:C:97:ILE:HG13	1:C:111:ILE:HB	1.97	0.46
1:C:258:PHE:HD2	1:C:259:ILE:HD12	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:ALA:HB1	1:C:25:GLU:HB2	1.97	0.46
1:A:135:TYR:CE1	1:A:137:TYR:HB3	2.50	0.46
1:D:208:VAL:HG12	1:D:214:HIS:HB3	1.97	0.46
1:C:783:LYS:H	1:C:784:THR:HA	1.81	0.46
1:D:530:VAL:O	1:D:533:TYR:HB3	2.15	0.46
1:D:514:VAL:CG1	1:D:794:GLY:C	2.84	0.46
1:A:97:ILE:HG13	1:A:111:ILE:HB	1.97	0.46
1:B:536:VAL:HG21	1:B:605:TRP:CE3	2.51	0.46
1:C:23:ASP:HB3	1:C:271:PRO:HB2	1.98	0.46
1:C:520:PRO:HA	1:C:623:PHE:CE2	2.50	0.46
1:D:394:THR:O	1:D:395:VAL:C	2.54	0.46
1:D:394:THR:CG2	1:D:440:TYR:CA	2.92	0.46
1:D:490:ASP:HB2	1:D:736:THR:HG23	1.97	0.46
1:D:517:PHE:CD1	1:D:616:TYR:OH	2.68	0.46
1:C:467:LEU:HD22	1:C:737:PRO:HD3	1.96	0.46
1:D:22:ALA:HB1	1:D:25:GLU:HB2	1.98	0.46
1:D:23:ASP:HB3	1:D:271:PRO:HB2	1.98	0.46
1:A:22:ALA:HB1	1:A:25:GLU:HB2	1.98	0.46
1:A:812:ILE:HG13	1:A:813:GLU:H	1.81	0.46
1:B:117:LEU:HD12	1:B:120:ALA:HB3	1.98	0.46
1:C:62:PHE:CE2	1:C:92:LEU:HD12	2.51	0.46
1:D:117:LEU:HD12	1:D:120:ALA:HB3	1.98	0.46
1:C:619:ASN:CA	1:D:624:LEU:HD13	2.46	0.46
1:A:209:ILE:CD1	1:A:234:LYS:HB2	2.46	0.46
1:A:619:ASN:OD1	1:B:787:LEU:CD1	2.63	0.46
1:A:62:PHE:CE2	1:A:92:LEU:HD12	2.51	0.46
1:B:208:VAL:HG12	1:B:214:HIS:HB3	1.97	0.46
1:B:388:SER:HA	1:B:389:GLY:HA2	1.61	0.46
1:D:135:TYR:CE1	1:D:137:TYR:HB3	2.51	0.46
1:D:62:PHE:CE2	1:D:92:LEU:HD12	2.51	0.46
1:B:23:ASP:HB3	1:B:271:PRO:HB2	1.98	0.45
1:C:209:ILE:CD1	1:C:234:LYS:HB2	2.46	0.45
1:B:601:VAL:HG23	1:C:806:ALA:CB	2.47	0.45
1:D:97:ILE:HG13	1:D:111:ILE:HB	1.97	0.45
1:D:521:LEU:HD22	1:D:526:TRP:CE2	2.52	0.45
1:D:512:PRO:HB2	1:D:790:SER:O	2.16	0.45
1:A:683:VAL:HG11	1:A:689:GLY:HA2	1.99	0.45
1:C:512:PRO:HG2	1:C:513:GLY:H	1.79	0.45
1:C:517:PHE:HZ	1:C:526:TRP:HH2	1.54	0.45
1:A:208:VAL:HG12	1:A:214:HIS:HB3	1.97	0.45
1:A:809:VAL:HG22	1:A:812:ILE:HD11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:774:GLY:O	1:B:778:SER:N	2.47	0.45
1:C:117:LEU:HD12	1:C:120:ALA:HB3	1.97	0.45
1:C:394:THR:O	1:C:395:VAL:HG23	2.16	0.45
1:C:683:VAL:HG11	1:C:689:GLY:HA2	1.98	0.45
1:A:628:ARG:HB2	1:D:626:VAL:HG21	1.98	0.45
1:B:135:TYR:CE1	1:B:137:TYR:HB3	2.50	0.45
1:B:507:PRO:HG2	1:B:630:VAL:C	2.37	0.45
1:D:683:VAL:HG11	1:D:689:GLY:HA2	1.98	0.45
1:A:628:ARG:HH12	1:D:627:GLU:N	2.14	0.45
1:B:683:VAL:HG11	1:B:689:GLY:HA2	1.99	0.45
1:C:387:THR:C	1:C:389:GLY:H	2.19	0.45
1:A:29:PHE:O	1:A:33:MET:HG2	2.15	0.45
1:A:384:GLU:O	1:A:385:ASP:CB	2.64	0.45
1:B:165:VAL:O	1:B:165:VAL:HG22	2.17	0.45
1:B:22:ALA:HB1	1:B:25:GLU:HB2	1.98	0.45
1:B:505:LYS:HG2	1:B:506:LYS:N	2.28	0.45
1:B:521:LEU:HD22	1:B:526:TRP:CE2	2.52	0.45
1:D:514:VAL:CG1	1:D:794:GLY:O	2.64	0.45
1:A:611:ILE:HD12	1:B:517:PHE:CZ	2.42	0.45
1:C:261:ARG:O	1:C:265:LEU:HG	2.17	0.45
1:D:209:ILE:CD1	1:D:234:LYS:HB2	2.47	0.45
1:D:62:PHE:CE2	1:D:88:PHE:HB3	2.52	0.45
1:B:515:PHE:CD1	1:B:518:LEU:HD12	2.52	0.45
1:D:125:ILE:HG23	1:D:130:TRP:HB2	1.99	0.45
1:D:620:LEU:HA	1:D:623:PHE:HD2	1.82	0.45
1:B:505:LYS:HD3	1:B:697:LYS:C	2.37	0.44
1:B:636:ALA:C	1:B:638:ASP:N	2.70	0.44
1:A:521:LEU:HD22	1:A:526:TRP:CE2	2.52	0.44
1:A:809:VAL:O	1:A:812:ILE:HG12	2.15	0.44
1:B:787:LEU:HD13	1:B:787:LEU:N	2.31	0.44
1:C:321:VAL:HA	1:C:322:PRO:HD3	1.86	0.44
1:D:261:ARG:O	1:D:265:LEU:HG	2.17	0.44
1:D:488:VAL:HG23	1:D:489:ILE:HG23	2.00	0.44
1:D:635:SER:O	1:D:636:ALA:C	2.55	0.44
1:A:130:TRP:CE2	1:A:191:ARG:HD3	2.53	0.44
1:B:130:TRP:CH2	1:B:191:ARG:HB3	2.53	0.44
1:B:209:ILE:CD1	1:B:234:LYS:HB2	2.47	0.44
1:B:62:PHE:CE2	1:B:88:PHE:HB3	2.52	0.44
1:C:125:ILE:HG23	1:C:130:TRP:HB2	1.99	0.44
1:A:117:LEU:HD12	1:A:120:ALA:HB3	1.98	0.44
1:B:261:ARG:O	1:B:265:LEU:HG	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:490:ASP:HB2	1:B:736:THR:HG23	1.98	0.44
1:B:62:PHE:CE2	1:B:92:LEU:HD12	2.51	0.44
1:C:521:LEU:CD2	1:C:525:ILE:HB	2.47	0.44
1:C:96:PHE:CE2	1:C:98:THR:HB	2.53	0.44
1:D:635:SER:O	1:D:637:GLU:N	2.51	0.44
1:B:125:ILE:HG23	1:B:130:TRP:HB2	1.99	0.44
1:B:525:ILE:HD13	1:C:792:VAL:HG21	1.99	0.44
1:D:521:LEU:CD2	1:D:525:ILE:HB	2.46	0.44
1:A:23:ASP:HB3	1:A:271:PRO:HB2	1.98	0.44
1:A:49:ASN:C	1:A:50:LEU:HD12	2.38	0.44
1:A:809:VAL:HG12	1:A:813:GLU:CG	2.48	0.44
1:C:93:HIS:ND1	1:C:322:PRO:HB3	2.33	0.44
1:D:287:ASP:O	1:D:291:VAL:HG23	2.18	0.44
1:A:519:ASP:N	1:A:520:PRO:CD	2.81	0.44
1:A:633:ILE:CG2	1:A:638:ASP:CB	2.82	0.44
1:A:809:VAL:CG1	1:A:812:ILE:HD11	2.48	0.44
1:B:96:PHE:CE2	1:B:98:THR:HB	2.53	0.44
1:C:389:GLY:O	1:C:391:GLU:N	2.50	0.44
1:C:521:LEU:HB3	1:C:526:TRP:CE2	2.53	0.44
1:C:62:PHE:CE2	1:C:88:PHE:HB3	2.52	0.44
1:D:130:TRP:CE2	1:D:191:ARG:HD3	2.53	0.44
1:A:125:ILE:HG23	1:A:130:TRP:HB2	1.99	0.44
1:A:261:ARG:O	1:A:265:LEU:HG	2.18	0.44
1:B:394:THR:CG2	1:B:440:TYR:CA	2.96	0.44
1:C:49:ASN:C	1:C:50:LEU:HD12	2.38	0.44
1:C:512:PRO:CB	1:C:790:SER:HA	2.34	0.44
1:D:49:ASN:C	1:D:50:LEU:HD12	2.38	0.44
1:A:809:VAL:HA	1:A:812:ILE:HD13	1.82	0.43
1:A:62:PHE:CE2	1:A:88:PHE:HB3	2.52	0.43
1:B:488:VAL:HG23	1:B:489:ILE:HG23	2.00	0.43
1:B:514:VAL:HG22	1:B:794:GLY:HA2	1.99	0.43
1:A:96:PHE:CE2	1:A:98:THR:HB	2.53	0.43
1:B:519:ASP:N	1:B:520:PRO:HD2	2.33	0.43
1:B:632:PRO:C	1:B:633:ILE:CD1	2.86	0.43
1:C:270:TYR:HA	1:C:271:PRO:HD2	1.87	0.43
1:C:512:PRO:CG	1:C:513:GLY:H	2.31	0.43
1:C:515:PHE:CD1	1:C:518:LEU:HD12	2.52	0.43
1:C:525:ILE:HD13	1:D:792:VAL:HG21	2.00	0.43
1:A:130:TRP:CH2	1:A:191:ARG:HB3	2.53	0.43
1:A:488:VAL:HG23	1:A:489:ILE:HG23	2.00	0.43
1:A:515:PHE:CD1	1:A:518:LEU:HD12	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:TRP:CE2	1:C:191:ARG:HD3	2.53	0.43
1:A:290:GLN:HG2	1:A:338:VAL:HG21	2.00	0.43
1:B:508:GLN:HE21	1:B:629:MET:HG3	1.84	0.43
1:A:810:ALA:O	1:A:814:PHE:CE2	2.65	0.43
1:B:130:TRP:CE2	1:B:191:ARG:HD3	2.54	0.43
1:B:633:ILE:CB	1:B:634:GLU:CB	2.85	0.43
1:C:488:VAL:HG23	1:C:489:ILE:HG23	2.00	0.43
1:D:96:PHE:CE2	1:D:98:THR:HB	2.53	0.43
1:B:518:LEU:HA	1:B:526:TRP:HE1	1.83	0.43
1:C:165:VAL:O	1:C:165:VAL:HG22	2.18	0.43
1:A:165:VAL:HG22	1:A:165:VAL:O	2.18	0.43
1:A:321:VAL:HA	1:A:322:PRO:HD3	1.86	0.43
1:A:97:ILE:N	1:A:97:ILE:HD12	2.34	0.43
1:D:97:ILE:HD12	1:D:97:ILE:N	2.34	0.43
1:B:394:THR:CG2	1:B:395:VAL:N	2.53	0.43
1:C:97:ILE:N	1:C:97:ILE:HD12	2.34	0.43
1:D:165:VAL:HG22	1:D:165:VAL:O	2.18	0.43
1:A:771:GLY:HA2	1:A:772:GLU:HB2	0.57	0.43
1:B:521:LEU:CD2	1:B:525:ILE:HB	2.45	0.43
1:B:97:ILE:N	1:B:97:ILE:HD12	2.34	0.43
1:C:130:TRP:CH2	1:C:191:ARG:HB3	2.53	0.43
1:A:209:ILE:HD11	1:A:235:ILE:HG23	2.01	0.42
1:A:287:ASP:O	1:A:291:VAL:HG23	2.18	0.42
1:A:795:VAL:HG12	1:D:608:PHE:CD1	2.54	0.42
1:B:209:ILE:HD11	1:B:235:ILE:HG23	2.01	0.42
1:B:360:ILE:HD11	1:B:374:TRP:HB2	2.01	0.42
1:C:287:ASP:O	1:C:291:VAL:HG23	2.18	0.42
1:D:382:LEU:N	1:D:382:LEU:HD12	2.34	0.42
1:A:521:LEU:HB3	1:A:526:TRP:CE2	2.54	0.42
1:A:533:TYR:CZ	1:A:583:ALA:HB1	2.55	0.42
1:A:628:ARG:NH1	1:D:623:PHE:HA	2.33	0.42
1:B:506:LYS:H	1:B:506:LYS:HG3	1.74	0.42
1:A:360:ILE:HD11	1:A:374:TRP:HB2	2.01	0.42
1:A:809:VAL:HG12	1:A:813:GLU:HG3	2.02	0.42
1:B:49:ASN:C	1:B:50:LEU:HD12	2.38	0.42
1:D:270:TYR:HA	1:D:271:PRO:HD2	1.87	0.42
1:D:299:LEU:HD11	1:D:332:ALA:HB2	2.01	0.42
1:D:809:VAL:O	1:D:813:GLU:HG3	2.19	0.42
1:A:385:ASP:C	1:A:387:THR:N	2.73	0.42
1:A:514:VAL:HG13	1:A:794:GLY:CA	2.38	0.42
1:B:287:ASP:O	1:B:291:VAL:HG23	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LEU:HD23	1:A:236:GLN:OE1	2.19	0.42
1:A:812:ILE:O	1:A:816:TYR:CE2	2.69	0.42
1:D:519:ASP:N	1:D:520:PRO:CD	2.82	0.42
1:A:517:PHE:CE1	1:D:611:ILE:CD1	2.99	0.42
1:A:628:ARG:NH2	1:D:623:PHE:CD1	2.84	0.42
1:A:795:VAL:HG12	1:D:608:PHE:HD1	1.85	0.42
1:C:519:ASP:N	1:C:520:PRO:CD	2.82	0.42
1:C:708:MET:O	1:C:712:ILE:HG12	2.20	0.42
1:D:130:TRP:CH2	1:D:191:ARG:HB3	2.54	0.42
1:B:233:LEU:HD23	1:B:236:GLN:OE1	2.19	0.42
1:B:512:PRO:HB2	1:B:513:GLY:H	1.72	0.42
1:A:770:LYS:HG3	1:A:770:LYS:O	2.20	0.42
1:A:718:CYS:HB2	1:A:776:LYS:CB	2.45	0.42
1:B:708:MET:O	1:B:712:ILE:HG12	2.19	0.42
1:C:233:LEU:HD23	1:C:236:GLN:OE1	2.20	0.42
1:C:232:LEU:O	1:C:236:GLN:HB2	2.20	0.42
1:C:360:ILE:HD11	1:C:374:TRP:HB2	2.01	0.42
1:C:533:TYR:CZ	1:C:583:ALA:HB1	2.54	0.42
1:D:321:VAL:HA	1:D:322:PRO:HD3	1.86	0.42
1:D:360:ILE:HD11	1:D:374:TRP:HB2	2.01	0.42
1:D:515:PHE:CD1	1:D:518:LEU:HD12	2.52	0.42
1:B:521:LEU:HB3	1:B:526:TRP:CE2	2.55	0.41
1:B:608:PHE:HD1	1:C:795:VAL:HG12	1.85	0.41
1:A:744:THR:HB	1:A:745:PRO:HD3	2.02	0.41
1:B:633:ILE:CB	1:B:634:GLU:HA	2.41	0.41
1:B:608:PHE:HZ	1:C:796:PHE:CZ	2.38	0.41
1:D:233:LEU:HD23	1:D:236:GLN:OE1	2.20	0.41
1:B:394:THR:HG22	1:B:439:LYS:O	2.16	0.41
1:B:809:VAL:O	1:B:813:GLU:HG3	2.19	0.41
1:C:809:VAL:O	1:C:813:GLU:HG3	2.19	0.41
1:D:394:THR:HG22	1:D:441:LYS:N	2.36	0.41
1:D:630:VAL:CG2	1:D:631:SER:N	2.61	0.41
1:D:805:LEU:O	1:D:809:VAL:HG23	2.20	0.41
1:A:391:GLU:C	1:A:393:LYS:N	2.74	0.41
1:B:232:LEU:O	1:B:236:GLN:HB2	2.20	0.41
1:B:805:LEU:O	1:B:809:VAL:HG23	2.20	0.41
1:C:288:ALA:O	1:C:292:MET:HG3	2.21	0.41
1:C:803:LEU:O	1:C:807:MET:HG2	2.21	0.41
1:D:521:LEU:HB3	1:D:526:TRP:CE2	2.55	0.41
1:D:708:MET:O	1:D:712:ILE:HG12	2.20	0.41
1:A:375:SER:HB3	1:A:378:ASP:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:708:MET:O	1:A:712:ILE:HG12	2.20	0.41
2:B:1101:ZK1:HAI	2:B:1101:ZK1:HAOA	1.81	0.41
1:B:288:ALA:O	1:B:292:MET:HG3	2.21	0.41
1:B:633:ILE:CB	1:B:634:GLU:CA	2.83	0.41
1:D:232:LEU:O	1:D:236:GLN:HB2	2.21	0.41
1:D:744:THR:HB	1:D:745:PRO:HD3	2.03	0.41
1:C:209:ILE:HD11	1:C:235:ILE:HG23	2.01	0.41
1:A:107:HIS:HA	1:A:108:PRO:HD3	1.92	0.41
1:A:385:ASP:O	1:A:387:THR:N	2.53	0.41
1:A:403:SER:HA	1:A:404:PRO:HA	1.87	0.41
1:A:678:GLU:HA	1:A:679:PRO:C	2.41	0.41
1:B:127:TYR:CE2	1:B:382:LEU:HD21	2.56	0.41
1:C:744:THR:HB	1:C:745:PRO:HD3	2.02	0.41
1:D:209:ILE:HD11	1:D:235:ILE:HG23	2.01	0.41
1:B:803:LEU:O	1:B:807:MET:HG2	2.20	0.41
1:C:101:PHE:HA	1:C:102:PRO:HD3	1.94	0.41
1:D:467:LEU:HD22	1:D:737:PRO:HD3	2.02	0.41
1:B:758:LEU:HD23	1:B:758:LEU:O	2.21	0.41
1:D:678:GLU:HA	1:D:679:PRO:C	2.41	0.41
1:A:758:LEU:HD23	1:A:758:LEU:O	2.21	0.41
1:B:101:PHE:HA	1:B:102:PRO:HD3	1.94	0.41
1:A:611:ILE:HD11	1:B:517:PHE:HZ	1.86	0.41
1:D:404:PRO:HB3	1:D:711:TYR:CE1	2.56	0.41
1:B:744:THR:HB	1:B:745:PRO:HD3	2.02	0.41
1:C:192:VAL:HB	1:C:220:TYR:CD1	2.56	0.41
1:A:805:LEU:O	1:A:809:VAL:HG23	2.21	0.40
1:B:114:ARG:HA	1:B:115:PRO:HD3	1.92	0.40
1:B:192:VAL:HB	1:B:220:TYR:CD1	2.56	0.40
1:B:505:LYS:HE3	1:B:506:LYS:CE	2.51	0.40
1:C:805:LEU:O	1:C:809:VAL:HG23	2.20	0.40
1:A:192:VAL:HB	1:A:220:TYR:CD1	2.56	0.40
1:A:467:LEU:HD22	1:A:737:PRO:HD3	2.02	0.40
1:A:624:LEU:O	1:A:628:ARG:HG3	2.20	0.40
1:A:792:VAL:HG21	1:D:525:ILE:HD13	2.03	0.40
1:B:231:ASP:HB3	1:B:234:LYS:HE2	2.04	0.40
1:B:477:ALA:HB1	1:B:478:PRO:CD	2.52	0.40
1:B:608:PHE:CD1	1:C:795:VAL:HG12	2.57	0.40
1:A:628:ARG:CZ	1:D:623:PHE:HA	2.52	0.40
1:C:624:LEU:O	1:C:628:ARG:HG3	2.21	0.40
1:D:10:ASN:N	1:D:10:ASN:ND2	2.70	0.40
1:A:511:LYS:N	1:A:512:PRO:CD	2.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:803:LEU:O	1:A:807:MET:HG2	2.21	0.40
1:B:678:GLU:HA	1:B:679:PRO:C	2.41	0.40
1:C:325:GLN:O	1:C:329:ILE:HG13	2.22	0.40
1:C:758:LEU:HD23	1:C:758:LEU:O	2.21	0.40
1:B:266:GLU:HG2	1:B:268:LYS:H	1.86	0.40
1:D:288:ALA:O	1:D:292:MET:HG3	2.21	0.40
1:D:803:LEU:O	1:D:807:MET:HG2	2.21	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 PDB entries followed by that with respect to all EM entries.

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	776/1034 (75%)	701 (90%)	56 (7%)	19 (2%)	7	42
1	B	773/1034 (75%)	699 (90%)	56 (7%)	18 (2%)	7	43
1	C	773/1034 (75%)	700 (91%)	58 (8%)	15 (2%)	9	47
1	D	773/1034 (75%)	692 (90%)	54 (7%)	27 (4%)	4	34
All	All	3095/4136 (75%)	2792 (90%)	224 (7%)	79 (3%)	10	40

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	LYS
1	A	385	ASP
1	A	387	THR
1	A	389	GLY
1	A	511	LYS
1	A	633	ILE
1	A	634	GLU
1	A	772	GLU

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Mol	Chain	Res	Type
1	A	775	ALA
1	A	785	SER
1	B	172	LYS
1	B	385	ASP
1	B	393	LYS
1	B	508	GLN
1	B	514	VAL
1	B	633	ILE
1	B	785	SER
1	C	172	LYS
1	C	391	GLU
1	C	512	PRO
1	D	172	LYS
1	D	385	ASP
1	D	391	GLU
1	D	394	THR
1	D	395	VAL
1	D	514	VAL
1	D	630	VAL
1	D	631	SER
1	D	635	SER
1	A	514	VAL
1	A	770	LYS
1	B	394	THR
1	B	509	LYS
1	B	784	THR
1	C	393	LYS
1	C	783	LYS
1	D	387	THR
1	D	392	GLN
1	D	508	GLN
1	D	510	SER
1	D	512	PRO
1	D	513	GLY
1	D	632	PRO
1	D	784	THR
1	A	388	SER
1	A	787	LEU
1	B	512	PRO
1	C	390	LEU
1	C	508	GLN
1	C	785	SER

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Mol	Chain	Res	Type
1	D	507	PRO
1	D	509	LYS
1	D	785	SER
1	D	786	ALA
1	A	597	SER
1	B	597	SER
1	B	637	GLU
1	C	392	GLN
1	C	597	SER
1	D	386	ASP
1	D	396	VAL
1	D	597	SER
1	A	386	ASP
1	A	508	GLN
1	B	387	THR
1	B	786	ALA
1	C	510	SER
1	C	513	GLY
1	C	784	THR
1	D	511	LYS
1	A	743	GLY
1	B	631	SER
1	B	743	GLY
1	C	743	GLY
1	D	743	GLY
1	A	451	GLY
1	B	451	GLY
1	C	451	GLY
1	D	451	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	537/876 (61%)	532 (99%)	5 (1%)	82	91
1	B	546/876 (62%)	540 (99%)	6 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	534/876 (61%)	529 (99%)	5 (1%)	82	91
1	D	534/876 (61%)	529 (99%)	5 (1%)	82	91
All	All	2151/3504 (61%)	2130 (99%)	21 (1%)	81	90

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	299	LEU
1	A	631	SER
1	A	770	LYS
1	A	773	CYS
1	B	10	ASN
1	B	299	LEU
1	B	506	LYS
1	B	631	SER
1	B	633	ILE
1	B	787	LEU
1	C	10	ASN
1	C	299	LEU
1	C	628	ARG
1	C	772	GLU
1	C	787	LEU
1	D	10	ASN
1	D	299	LEU
1	D	394	THR
1	D	629	MET
1	D	772	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	337	GLN
1	B	83	ASN
1	B	619	ASN
1	C	83	ASN
1	D	337	GLN
1	D	344	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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$
2	ZK1	A	1101	-	28,29,29	3.25	14 (50%)	36,45,45	1.70	5 (13%)
3	NAG	A	1102	1	14,14,15	0.47	0	15,19,21	0.69	0
2	ZK1	B	1101	-	28,29,29	3.24	14 (50%)	36,45,45	1.71	5 (13%)
3	NAG	B	1102	1	14,14,15	0.48	0	15,19,21	0.67	0
2	ZK1	C	1101	-	28,29,29	3.24	14 (50%)	36,45,45	1.71	5 (13%)
3	NAG	C	1102	1	14,14,15	0.47	0	15,19,21	0.92	1 (6%)
2	ZK1	D	1101	-	28,29,29	3.24	14 (50%)	36,45,45	1.71	5 (13%)
3	NAG	D	1102	1	14,14,15	0.50	0	15,19,21	0.65	0

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	ZK1	A	1101	-	-	0/13/23/23	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1102	1	-	0/6/23/26	0/1/1/1
2	ZK1	B	1101	-	-	0/13/23/23	0/3/3/3
3	NAG	B	1102	1	-	0/6/23/26	0/1/1/1
2	ZK1	C	1101	-	-	0/13/23/23	0/3/3/3
3	NAG	C	1102	1	-	0/6/23/26	0/1/1/1
2	ZK1	D	1101	-	-	0/13/23/23	0/3/3/3
3	NAG	D	1102	1	-	0/6/23/26	0/1/1/1

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1101	ZK1	PBA-OAD	-3.55	1.46	1.54
2	D	1101	ZK1	PBA-OAD	-3.50	1.46	1.54
2	A	1101	ZK1	PBA-OAD	-3.49	1.46	1.54
2	B	1101	ZK1	PBA-OAD	-3.47	1.46	1.54
2	B	1101	ZK1	CAN-NAX	2.04	1.49	1.46
2	A	1101	ZK1	CAN-NAX	2.04	1.49	1.46
2	C	1101	ZK1	CAN-NAX	2.04	1.49	1.46
2	D	1101	ZK1	CAN-NAX	2.09	1.49	1.46
2	C	1101	ZK1	PBA-CAO	2.11	1.86	1.81
2	A	1101	ZK1	PBA-CAO	2.12	1.86	1.81
2	B	1101	ZK1	PBA-CAO	2.12	1.86	1.81
2	D	1101	ZK1	PBA-CAO	2.14	1.86	1.81
2	B	1101	ZK1	CAR-NAX	2.15	1.46	1.41
2	D	1101	ZK1	CAR-NAX	2.16	1.46	1.41
2	C	1101	ZK1	CAR-NAX	2.18	1.46	1.41
2	A	1101	ZK1	CAR-NAX	2.18	1.46	1.41
2	B	1101	ZK1	CAM-NAX	2.19	1.50	1.46
2	C	1101	ZK1	CAM-NAX	2.19	1.50	1.46
2	A	1101	ZK1	CAM-NAX	2.22	1.50	1.46
2	D	1101	ZK1	CAM-NAX	2.24	1.50	1.46
2	D	1101	ZK1	CAV-NAP	2.28	1.38	1.35
2	C	1101	ZK1	CAV-NAP	2.29	1.38	1.35
2	B	1101	ZK1	CAV-NAP	2.29	1.38	1.35
2	A	1101	ZK1	CAV-NAP	2.36	1.38	1.35
2	A	1101	ZK1	CAI-CAR	2.64	1.42	1.37
2	D	1101	ZK1	CAI-CAR	2.70	1.42	1.37
2	C	1101	ZK1	CAI-CAR	2.73	1.42	1.37
2	B	1101	ZK1	CAI-CAR	2.77	1.42	1.37
2	C	1101	ZK1	PBA-OAE	4.48	1.65	1.54
2	A	1101	ZK1	PBA-OAE	4.52	1.65	1.54
2	B	1101	ZK1	PBA-OAE	4.55	1.65	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1101	ZK1	PBA-OAE	4.58	1.65	1.54
2	D	1101	ZK1	CAJ-CAS	4.58	1.44	1.37
2	C	1101	ZK1	CAJ-CAS	4.60	1.44	1.37
2	A	1101	ZK1	CAJ-CAS	4.66	1.44	1.37
2	B	1101	ZK1	CAJ-CAS	4.66	1.44	1.37
2	C	1101	ZK1	CAW-NAY	4.77	1.46	1.40
2	D	1101	ZK1	CAW-NAY	4.80	1.46	1.40
2	B	1101	ZK1	CAW-NAY	4.91	1.47	1.40
2	A	1101	ZK1	CAW-NAY	4.91	1.47	1.40
2	B	1101	ZK1	CAT-NAP	6.05	1.44	1.33
2	C	1101	ZK1	CAT-NAP	6.09	1.44	1.33
2	D	1101	ZK1	CAT-NAP	6.15	1.44	1.33
2	A	1101	ZK1	CAT-NAP	6.17	1.44	1.33
2	A	1101	ZK1	OAB-CAU	6.53	1.40	1.24
2	D	1101	ZK1	OAB-CAU	6.56	1.40	1.24
2	B	1101	ZK1	OAB-CAU	6.57	1.40	1.24
2	C	1101	ZK1	OAB-CAU	6.60	1.41	1.24
2	C	1101	ZK1	OAA-CAT	6.61	1.41	1.24
2	B	1101	ZK1	OAA-CAT	6.63	1.41	1.24
2	D	1101	ZK1	OAA-CAT	6.67	1.41	1.24
2	A	1101	ZK1	OAA-CAT	6.69	1.41	1.24
2	B	1101	ZK1	PBA-OAC	6.92	1.65	1.50
2	D	1101	ZK1	PBA-OAC	6.94	1.65	1.50
2	A	1101	ZK1	PBA-OAC	7.01	1.65	1.50
2	C	1101	ZK1	PBA-OAC	7.01	1.65	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	ZK1	CAI-CAR-NAX	-2.71	118.99	122.69
2	B	1101	ZK1	CAI-CAR-NAX	-2.69	119.01	122.69
2	C	1101	ZK1	CAI-CAR-NAX	-2.67	119.04	122.69
2	D	1101	ZK1	CAI-CAR-NAX	-2.64	119.08	122.69
2	C	1101	ZK1	CAO-NAY-CAU	2.10	120.33	117.79
2	D	1101	ZK1	CAO-NAY-CAU	2.10	120.33	117.79
2	B	1101	ZK1	CAO-NAY-CAU	2.11	120.34	117.79
2	A	1101	ZK1	CAO-NAY-CAU	2.12	120.35	117.79
3	C	1102	NAG	C1-O5-C5	2.14	115.12	112.17
2	B	1101	ZK1	CAV-CAW-NAY	3.28	120.09	117.66
2	C	1101	ZK1	CAV-CAW-NAY	3.38	120.17	117.66
2	A	1101	ZK1	CAV-CAW-NAY	3.40	120.18	117.66
2	D	1101	ZK1	CAV-CAW-NAY	3.54	120.29	117.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	ZK1	CAT-NAP-CAV	4.53	119.96	116.42
2	D	1101	ZK1	CAT-NAP-CAV	4.61	120.02	116.42
2	C	1101	ZK1	CAT-NAP-CAV	4.64	120.05	116.42
2	B	1101	ZK1	CAN-NAX-CAM	4.66	121.44	111.57
2	D	1101	ZK1	CAN-NAX-CAM	4.66	121.45	111.57
2	A	1101	ZK1	CAN-NAX-CAM	4.69	121.51	111.57
2	C	1101	ZK1	CAN-NAX-CAM	4.74	121.61	111.57
2	B	1101	ZK1	CAT-NAP-CAV	4.77	120.15	116.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1102	NAG	2	0
2	B	1101	ZK1	1	0
3	D	1102	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.