



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:21 PM UTC

PDB ID : 3N23 / pdb_00003n23
Title : Crystal structure of the high affinity complex between ouabain and the E2P form of the sodium-potassium pump
Authors : Yatime, L.; Laursen, M.; Morth, J.P.; Esmann, M.; Nissen, P.; Fedosova, N.U.
Deposited on : 2010-05-17
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

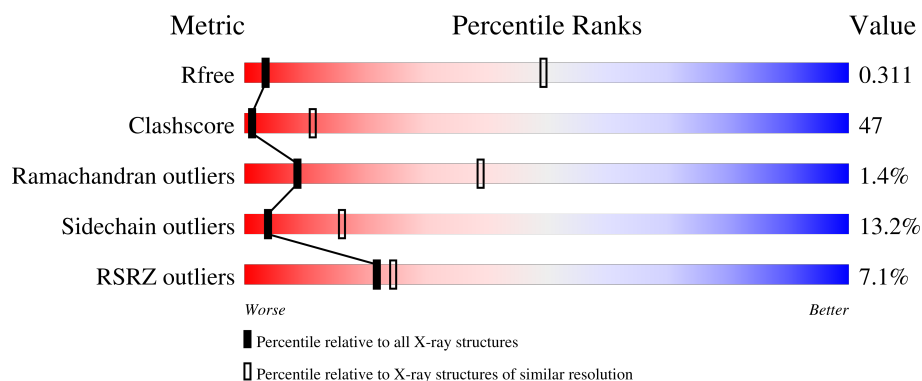
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.60 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	1007 (5.28-3.92)
Clashscore	190562	1022 (5.26-3.94)
Ramachandran outliers	187476	1069 (5.30-3.90)
Sidechain outliers	187428	1051 (5.30-3.90)
RSRZ outliers	180081	1002 (5.28-3.92)

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	992	7% 42% 49% 8%
1	C	992	6% 42% 49% 8%
2	B	277	11% 29% 54% 13% 5%
2	D	277	7% 27% 56% 13% 5%
3	E	31	6% 48% 52%

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Mol	Chain	Length	Quality of chain
3	G	31	

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
1	PHD	A	369	-	-	X	-
4	OBN	A	1	-	-	X	-
4	OBN	C	1	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20272 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 Sodium/potassium-transporting ATPase subunit alpha-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	992	Total	C	N	O	P	S	0	0	0
			7693	4901	1293	1451	1	47			
1	C	992	Total	C	N	O	P	S	0	0	0
			7693	4901	1293	1451	1	47			

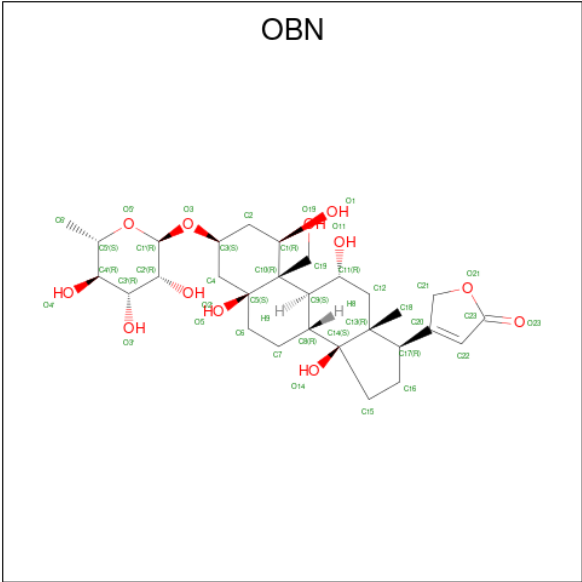
- Molecule 2 is a protein called Sodium/potassium-transporting ATPase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	0	0	0
			2155	1400	352	390	13			
2	D	264	Total	C	N	O	S	0	0	0
			2155	1400	352	390	13			

- Molecule 3 is a protein called Na⁺/K⁺ ATPase gamma subunit transcript variant a.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	31	Total	C	N	O	0	0	0
			246	168	35	43			
3	E	31	Total	C	N	O	0	0	0
			246	168	35	43			

- Molecule 4 is OUABAIN (CCD ID: OBN) (formula: C₂₉H₄₄O₁₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			41	29	12		
4	C	1	Total	C	O	0	0
			41	29	12		

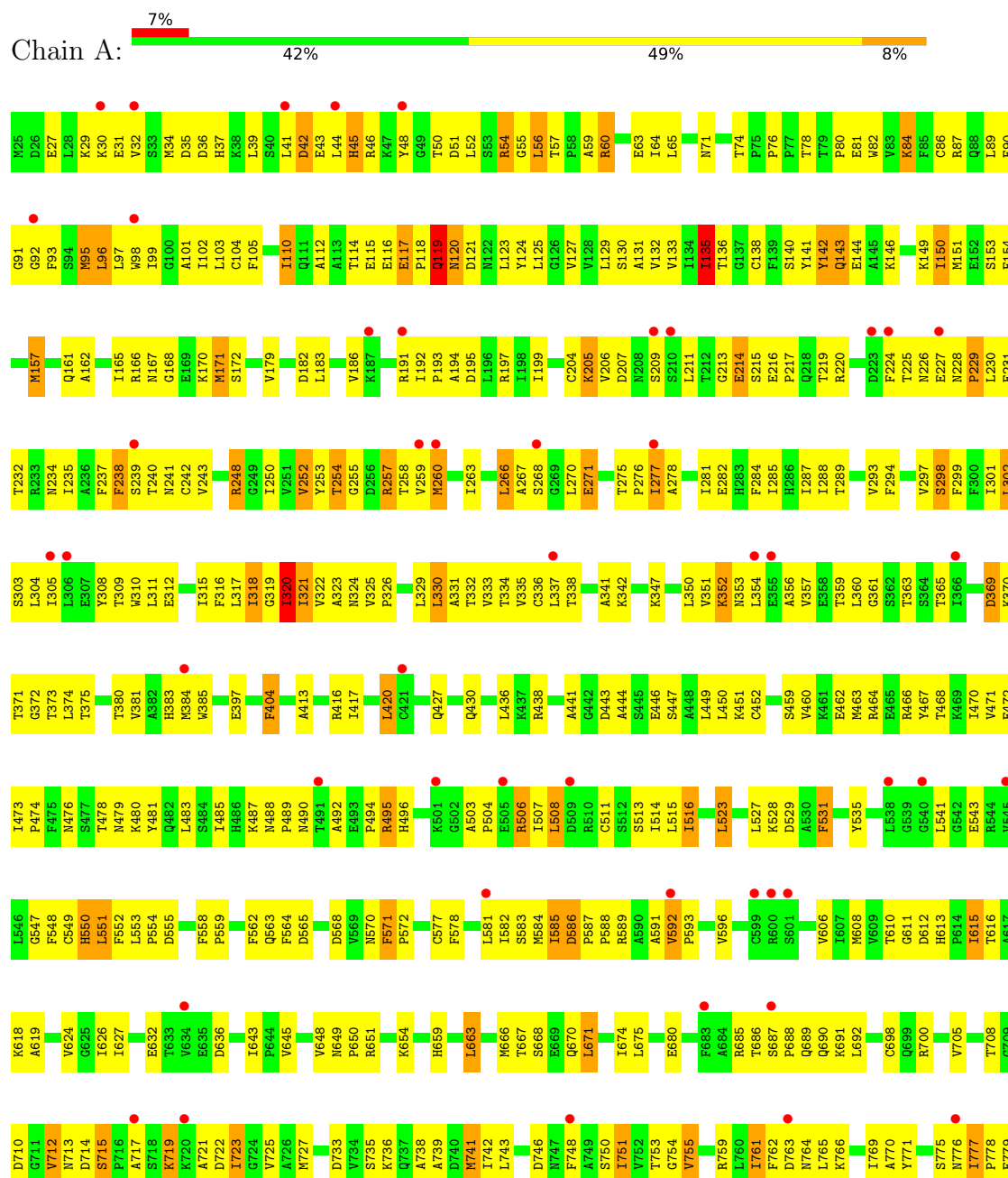
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

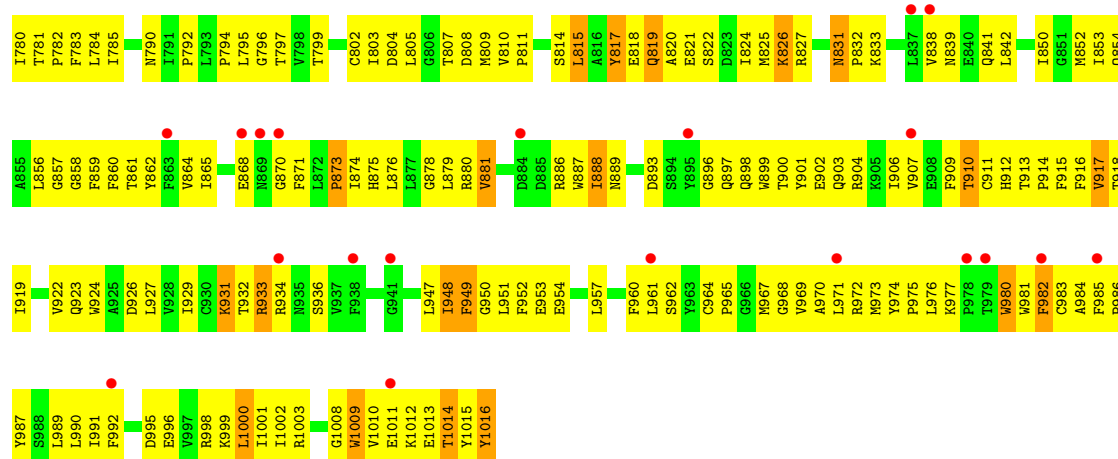
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

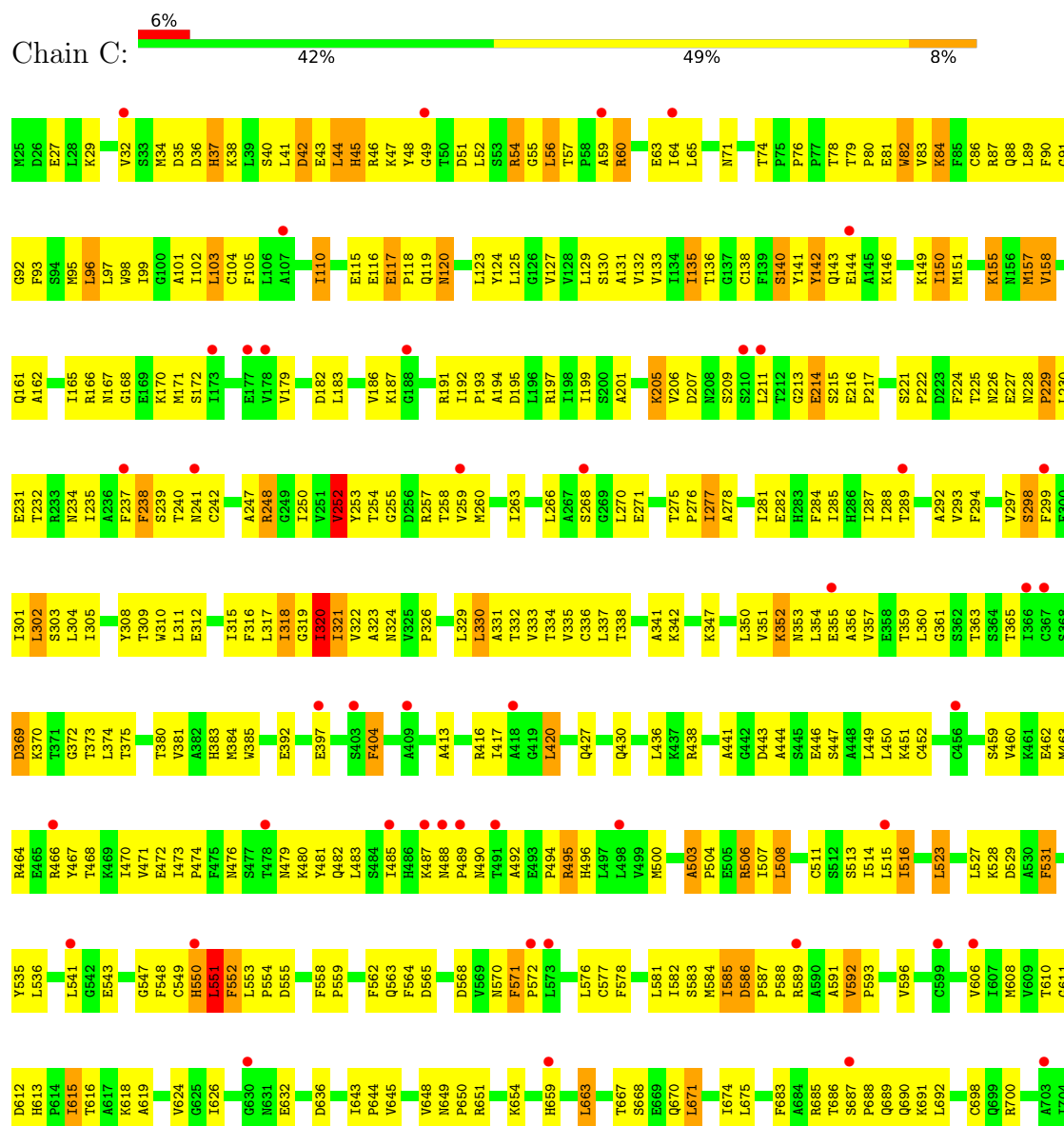
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

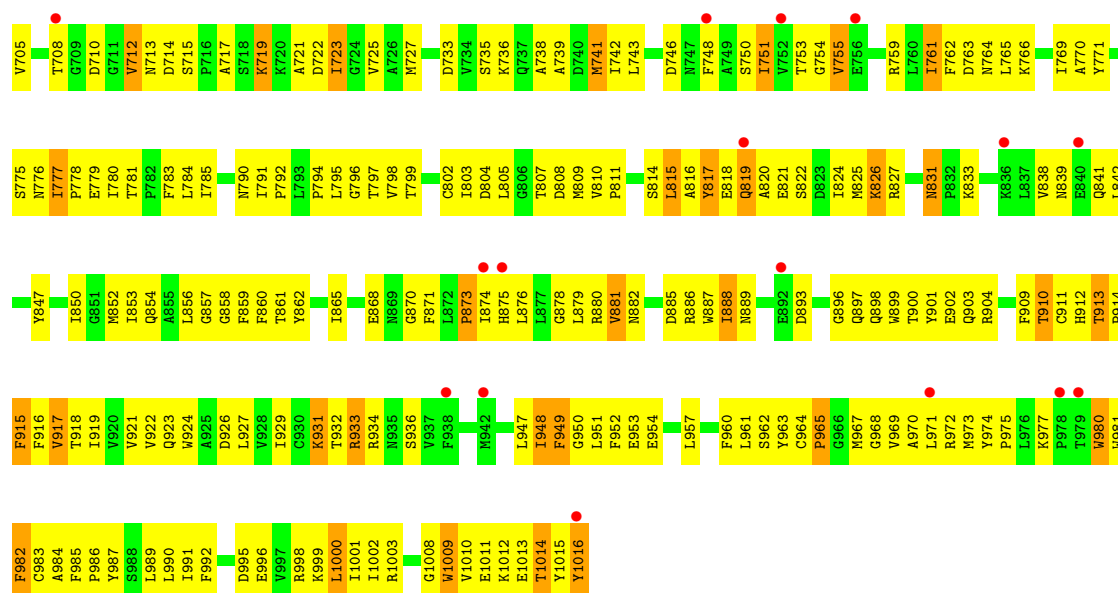
- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1



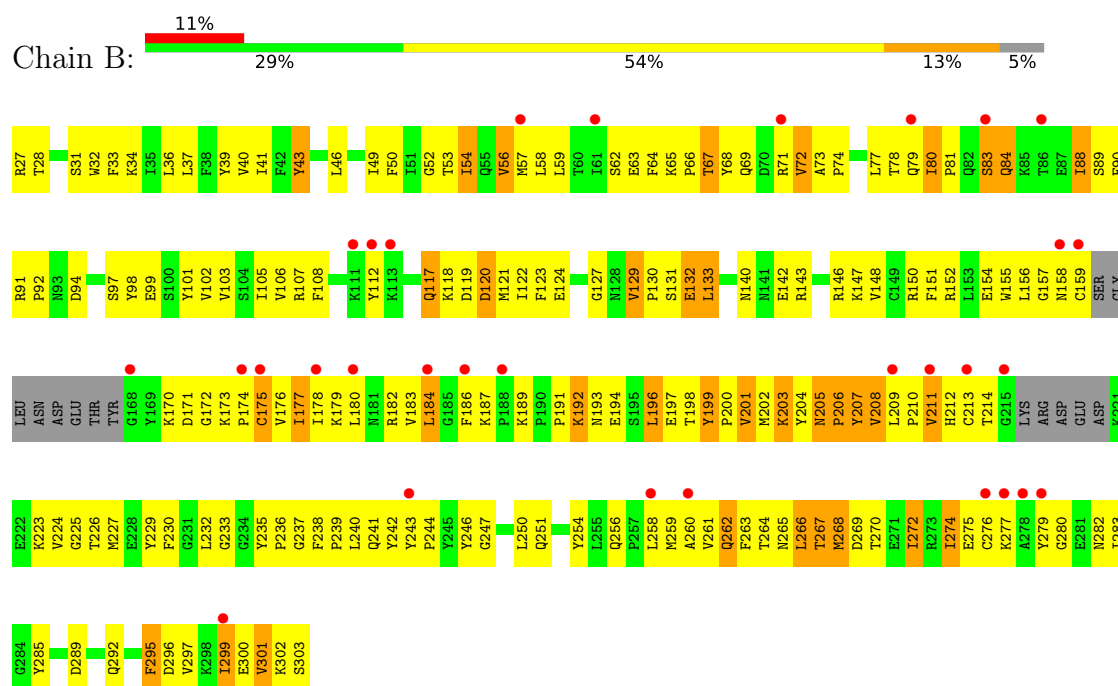


• Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

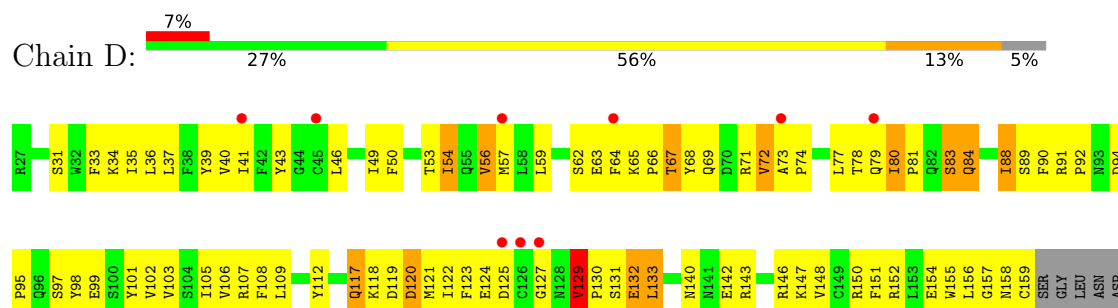


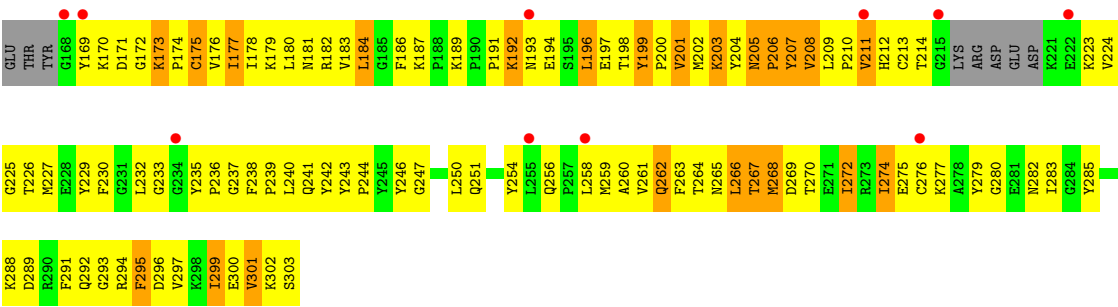


• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1





● Molecule 3: Na⁺/K⁺ ATPase gamma subunit transcript variant a



● Molecule 3: Na⁺/K⁺ ATPase gamma subunit transcript variant a



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.16Å 118.93Å 494.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.55 – 4.60 39.55 – 4.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.55-4.60) 99.7 (39.55-4.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 4.64Å)	Xtriage
Refinement program	CNS, PHENIX 1.6_289	Depositor
R, R_{free}	0.272 , 0.302 0.284 , 0.311	Depositor DCC
R_{free} test set	1977 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	186.0	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 253.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.056 for k,h,-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	20272	wwPDB-VP
Average B, all atoms (Å ²)	277.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: PHD, OBN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.43	1/7830 (0.0%)	0.79	9/10626 (0.1%)
1	C	0.44	1/7830 (0.0%)	0.81	10/10626 (0.1%)
2	B	0.41	0/2211	0.81	3/2981 (0.1%)
2	D	0.40	0/2211	0.79	2/2981 (0.1%)
3	E	0.50	0/252	0.84	1/343 (0.3%)
3	G	0.48	0/252	0.79	1/343 (0.3%)
All	All	0.43	2/20586 (0.0%)	0.80	26/27900 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	551	LEU	CG-CD2	-8.31	1.25	1.52
1	A	551	LEU	CG-CD2	-6.88	1.29	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	45	HIS	N-CA-C	-7.63	103.94	113.55
1	C	252	VAL	CB-CA-C	-6.71	105.16	111.06
1	A	248	ARG	NE-CZ-NH2	6.34	124.90	119.20
2	B	233	GLY	N-CA-C	-6.19	107.72	115.08
1	C	551	LEU	CD1-CG-CD2	-6.19	97.19	110.80
2	D	233	GLY	N-CA-C	-6.15	107.77	115.08
1	C	155	LYS	N-CA-C	6.12	119.72	108.58
1	A	551	LEU	CD1-CG-CD2	-5.97	97.66	110.80
1	A	135	ILE	CB-CA-C	-5.68	104.57	112.02
2	D	63	GLU	N-CA-C	-5.66	105.49	112.90
1	C	551	LEU	CB-CG-CD1	5.64	127.61	110.70
1	A	551	LEU	CB-CG-CD1	5.62	127.55	110.70
1	C	551	LEU	CB-CG-CD2	-5.58	93.97	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	915	PHE	N-CA-C	-5.53	105.25	111.28
1	A	551	LEU	CB-CG-CD2	-5.45	94.36	110.70
3	E	34	ALA	N-CA-C	-5.37	106.72	113.28
2	B	63	GLU	N-CA-C	-5.36	105.88	112.90
1	A	119	GLN	CB-CG-CD	5.26	121.55	112.60
1	C	503	ALA	CA-C-N	5.26	125.07	119.28
1	C	503	ALA	C-N-CA	5.26	125.07	119.28
1	A	503	ALA	CA-C-N	5.21	125.01	119.28
1	A	503	ALA	C-N-CA	5.21	125.01	119.28
1	A	248	ARG	NE-CZ-NH1	-5.18	116.32	121.50
3	G	34	ALA	N-CA-C	-5.16	106.98	113.28
2	B	43	TYR	N-CA-C	-5.05	105.28	111.75
1	C	248	ARG	CD-NE-CZ	5.05	131.47	124.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7693	0	7740	647	1
1	C	7693	0	7741	691	0
2	B	2155	0	2143	305	0
2	D	2155	0	2143	304	1
3	E	246	0	246	13	0
3	G	246	0	246	11	0
4	A	41	0	44	25	0
4	C	41	0	44	24	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
All	All	20272	0	20347	1917	1

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 47.

All (1917) 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)
2:D:204:TYR:C	2:D:206:PRO:HD2	1.60	1.25
1:A:48:TYR:OH	1:A:252:VAL:HG12	1.32	1.25
2:B:130:PRO:HG2	2:B:204:TYR:CZ	1.73	1.24
2:B:204:TYR:C	2:B:206:PRO:HD2	1.65	1.21
2:D:129:VAL:HG22	2:D:130:PRO:CD	1.73	1.19
2:B:80:ILE:HG13	2:B:81:PRO:HD3	1.19	1.15
2:D:133:LEU:HG	2:D:240:LEU:O	1.47	1.14
2:B:129:VAL:HG22	2:B:130:PRO:CD	1.78	1.13
1:A:48:TYR:OH	1:A:252:VAL:CG1	1.95	1.13
2:B:267:THR:HG21	2:B:270:THR:HG22	1.19	1.12
2:B:133:LEU:HG	2:B:240:LEU:O	1.47	1.11
2:B:80:ILE:HG12	2:B:177:ILE:HG12	1.33	1.10
2:B:207:TYR:HB3	2:B:240:LEU:HB2	1.33	1.10
2:D:267:THR:HG21	2:D:270:THR:HG22	1.18	1.10
1:C:807:THR:HB	1:C:954:GLU:HG3	1.29	1.09
1:C:260:MET:HE1	1:C:712:VAL:HG21	1.28	1.09
1:A:807:THR:HB	1:A:954:GLU:HG3	1.27	1.09
2:D:80:ILE:HG13	2:D:81:PRO:HD3	1.18	1.09
1:C:488:ASN:HB3	1:C:494:PRO:HA	1.35	1.08
2:B:173:LYS:HG2	2:B:264:THR:HA	1.23	1.08
2:D:173:LYS:CG	2:D:264:THR:HA	1.82	1.08
1:C:225:THR:HG23	1:C:226:ASN:H	1.10	1.08
2:D:207:TYR:HB3	2:D:240:LEU:HB2	1.34	1.08
2:B:225:GLY:HA2	2:B:266:LEU:HD21	1.35	1.07
2:D:173:LYS:HG2	2:D:264:THR:CA	1.83	1.07
2:D:129:VAL:HG22	2:D:130:PRO:HD3	1.34	1.07
2:D:129:VAL:HG13	2:D:130:PRO:N	1.66	1.06
1:A:225:THR:HG23	1:A:226:ASN:H	1.15	1.06
1:A:585:ILE:HG12	1:A:586:ASP:H	1.21	1.05
2:D:80:ILE:HG12	2:D:177:ILE:HG12	1.10	1.05
1:A:488:ASN:HB3	1:A:494:PRO:HA	1.35	1.05
1:A:260:MET:HE1	1:A:712:VAL:HG11	1.36	1.04
2:B:130:PRO:HG2	2:B:204:TYR:OH	1.57	1.04
1:A:118:PRO:HG2	4:A:1:OBN:H192	1.40	1.04
1:A:118:PRO:CG	4:A:1:OBN:H192	1.88	1.03
2:D:225:GLY:HA2	2:D:266:LEU:HD21	1.35	1.03
1:C:585:ILE:HG12	1:C:586:ASP:H	1.18	1.03
2:D:196:LEU:HD13	2:D:203:LYS:HD2	1.35	1.03
2:D:129:VAL:HG13	2:D:130:PRO:CD	1.89	1.02
2:D:201:VAL:HG22	2:D:202:MET:HA	1.37	1.02
2:D:130:PRO:HG2	2:D:204:TYR:CZ	1.95	1.02
1:C:195:ASP:HB2	1:C:253:TYR:HB2	1.43	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ASN:ND2	1:A:255:GLY:H	1.59	0.99
2:B:265:ASN:O	2:B:266:LEU:HD23	1.63	0.99
2:B:129:VAL:HG22	2:B:130:PRO:HD2	1.40	0.98
2:D:225:GLY:HA2	2:D:266:LEU:CD2	1.94	0.98
1:C:42:ASP:O	1:C:45:HIS:HB3	1.62	0.98
1:C:987:TYR:OH	2:D:50:PHE:HA	1.63	0.98
1:C:239:SER:OG	1:C:260:MET:HG3	1.61	0.97
2:D:129:VAL:HG22	2:D:130:PRO:HD2	1.44	0.97
1:C:585:ILE:HG12	1:C:586:ASP:N	1.76	0.97
2:B:129:VAL:HG22	2:B:130:PRO:HD3	1.47	0.97
1:C:54:ARG:HH11	1:C:54:ARG:HG3	1.27	0.96
1:C:260:MET:HE1	1:C:712:VAL:CG2	1.94	0.96
1:A:71:ASN:HD22	1:A:255:GLY:H	1.03	0.96
2:B:201:VAL:HG22	2:B:202:MET:HA	1.44	0.96
2:D:202:MET:HG3	2:D:203:LYS:H	1.29	0.96
1:C:225:THR:HG22	1:C:232:THR:HA	1.45	0.96
2:D:204:TYR:C	2:D:206:PRO:CD	2.39	0.96
2:B:173:LYS:HG2	2:B:264:THR:CA	1.96	0.95
2:B:225:GLY:HA2	2:B:266:LEU:CD2	1.94	0.95
1:A:117:GLU:CB	1:A:118:PRO:HD3	1.93	0.95
2:D:265:ASN:O	2:D:266:LEU:HD23	1.64	0.95
1:A:120:ASN:O	1:A:124:TYR:HB2	1.67	0.95
2:B:173:LYS:HB3	2:B:263:PHE:O	1.66	0.94
1:A:54:ARG:HH11	1:A:54:ARG:HG3	1.29	0.94
1:C:120:ASN:O	1:C:124:TYR:HB2	1.66	0.94
1:C:495:ARG:HG3	1:C:555:ASP:HB3	1.48	0.94
1:A:585:ILE:HG12	1:A:586:ASP:N	1.79	0.94
2:D:129:VAL:O	2:D:241:GLN:NE2	2.00	0.94
1:A:404:PHE:HD2	1:A:404:PHE:H	1.15	0.94
1:A:977:LYS:H	1:A:980:TRP:CD1	1.86	0.93
2:B:130:PRO:CG	2:B:204:TYR:OH	2.15	0.93
2:D:73:ALA:HB3	2:D:74:PRO:HD3	1.48	0.93
2:D:173:LYS:HE2	2:D:264:THR:O	1.66	0.93
1:C:117:GLU:CB	1:C:118:PRO:HD3	1.95	0.93
1:C:118:PRO:CG	4:C:1:OBN:H192	1.97	0.93
2:B:129:VAL:HG13	2:B:130:PRO:N	1.82	0.93
1:A:80:PRO:O	1:A:81:GLU:HG2	1.69	0.93
2:D:80:ILE:CG1	2:D:177:ILE:HG12	1.99	0.92
1:A:495:ARG:HG3	1:A:555:ASP:HB3	1.47	0.92
2:B:172:GLY:C	2:B:173:LYS:HD2	1.95	0.92
1:C:93:PHE:HB3	1:C:330:LEU:HD11	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:THR:HG23	1:C:226:ASN:N	1.85	0.91
3:E:42:LEU:HD23	3:E:45:ILE:HD11	1.52	0.91
1:A:93:PHE:HB3	1:A:330:LEU:HD11	1.50	0.91
1:C:260:MET:CE	1:C:712:VAL:HG21	2.00	0.91
1:C:101:ALA:HB2	1:C:129:LEU:HB2	1.49	0.91
2:B:73:ALA:HB3	2:B:74:PRO:HD3	1.50	0.91
1:C:977:LYS:H	1:C:980:TRP:CD1	1.89	0.91
1:A:101:ALA:HB2	1:A:129:LEU:HB2	1.53	0.90
2:D:129:VAL:HG13	2:D:130:PRO:HD2	1.53	0.90
2:D:129:VAL:CG2	2:D:130:PRO:CD	2.50	0.90
1:A:225:THR:HG22	1:A:232:THR:HA	1.51	0.90
1:C:276:PRO:HG3	1:C:359:THR:HG23	1.54	0.90
1:C:898:GLN:NE2	2:D:181:ASN:HA	1.85	0.89
2:D:172:GLY:C	2:D:173:LYS:HD2	1.97	0.89
3:G:42:LEU:HD23	3:G:45:ILE:HD11	1.52	0.89
1:A:95:MET:HE2	1:A:95:MET:HA	1.55	0.89
2:D:208:VAL:HA	2:D:238:PHE:O	1.72	0.89
2:B:204:TYR:C	2:B:206:PRO:CD	2.46	0.88
1:C:118:PRO:HG2	4:C:1:OBN:H192	1.55	0.88
1:C:322:VAL:HB	4:C:1:OBN:O23	1.72	0.88
1:A:783:PHE:CE1	4:A:1:OBN:H161	2.08	0.88
2:B:94:ASP:HB2	2:B:97:SER:HB2	1.55	0.88
1:A:52:LEU:HG	1:A:199:ILE:HD12	1.54	0.88
2:D:94:ASP:HB2	2:D:97:SER:HB2	1.55	0.88
1:A:195:ASP:HB2	1:A:253:TYR:HB2	1.55	0.88
2:D:129:VAL:CG2	2:D:130:PRO:HD2	2.04	0.88
2:B:208:VAL:HA	2:B:238:PHE:O	1.72	0.87
2:B:130:PRO:CG	2:B:204:TYR:CZ	2.56	0.87
1:C:404:PHE:H	1:C:404:PHE:HD2	1.15	0.87
2:B:129:VAL:HG13	2:B:130:PRO:CD	2.05	0.86
1:C:278:ALA:O	1:C:281:ILE:HG22	1.76	0.86
1:C:95:MET:HE2	1:C:95:MET:HA	1.55	0.86
2:D:196:LEU:CD1	2:D:203:LYS:HD2	2.04	0.86
1:A:384:MET:HG2	1:A:582:ILE:HG22	1.57	0.86
1:C:341:ALA:HB2	1:C:357:VAL:HG21	1.57	0.86
1:C:52:LEU:HG	1:C:199:ILE:HD12	1.55	0.86
1:A:93:PHE:HB3	1:A:330:LEU:CD1	2.06	0.86
1:C:117:GLU:HB2	1:C:118:PRO:HD3	1.58	0.86
1:C:898:GLN:NE2	2:D:182:ARG:H	1.73	0.86
1:A:260:MET:CE	1:A:712:VAL:HG11	2.05	0.86
1:C:585:ILE:O	1:C:587:PRO:HD3	1.76	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:ILE:HD12	2:B:105:ILE:HG22	1.58	0.85
1:A:238:PHE:CE2	1:A:260:MET:HG2	2.10	0.85
1:A:785:ILE:HD11	1:A:859:PHE:CZ	2.11	0.85
1:A:294:PHE:O	1:A:298:SER:HB2	1.76	0.85
2:D:80:ILE:HD12	2:D:105:ILE:HG22	1.57	0.85
1:C:275:THR:HB	1:C:276:PRO:HD2	1.59	0.84
1:C:225:THR:CG2	1:C:232:THR:HA	2.07	0.84
1:C:898:GLN:HE21	2:D:181:ASN:HA	1.41	0.84
2:D:264:THR:HG23	2:D:265:ASN:H	1.40	0.84
2:B:129:VAL:CG2	2:B:130:PRO:HD2	2.07	0.84
1:C:93:PHE:HB3	1:C:330:LEU:CD1	2.07	0.84
1:A:643:ILE:HD11	1:A:648:VAL:CG2	2.08	0.84
1:C:384:MET:HG2	1:C:582:ILE:HG22	1.58	0.84
2:D:129:VAL:CG1	2:D:130:PRO:N	2.40	0.83
1:A:117:GLU:HB2	1:A:118:PRO:HD3	1.57	0.83
2:B:130:PRO:CB	2:B:204:TYR:CE2	2.61	0.83
1:C:783:PHE:CZ	4:C:1:OBN:H122	2.13	0.83
1:A:278:ALA:O	1:A:281:ILE:HG22	1.77	0.83
1:A:225:THR:HG23	1:A:226:ASN:N	1.89	0.83
2:D:202:MET:HG3	2:D:203:LYS:N	1.92	0.83
1:C:825:MET:HE2	1:C:825:MET:HA	1.60	0.83
1:C:225:THR:CG2	1:C:226:ASN:H	1.91	0.83
2:D:197:GLU:O	2:D:199:TYR:HA	1.79	0.83
2:B:264:THR:HG23	2:B:265:ASN:H	1.42	0.82
1:A:341:ALA:HB2	1:A:357:VAL:HG21	1.59	0.82
2:B:129:VAL:O	2:B:241:GLN:NE2	2.13	0.82
1:A:101:ALA:O	1:A:105:PHE:HB2	1.79	0.82
1:A:260:MET:HE2	1:A:712:VAL:HG21	1.61	0.82
1:C:101:ALA:O	1:C:105:PHE:HB2	1.80	0.82
1:A:825:MET:HE2	1:A:825:MET:HA	1.60	0.82
1:A:589:ARG:HB2	1:A:592:VAL:HG23	1.61	0.81
1:A:671:LEU:O	1:A:675:LEU:HD12	1.80	0.81
2:B:197:GLU:O	2:B:199:TYR:HA	1.79	0.81
2:B:204:TYR:HE1	2:B:235:TYR:CZ	1.97	0.81
1:A:276:PRO:HG3	1:A:359:THR:HG23	1.62	0.81
1:C:589:ARG:HB2	1:C:592:VAL:HG23	1.63	0.81
1:C:785:ILE:HD11	1:C:859:PHE:CZ	2.16	0.81
2:D:129:VAL:CG1	2:D:130:PRO:HD2	2.11	0.81
2:B:173:LYS:CG	2:B:264:THR:HA	2.10	0.81
1:C:516:ILE:O	1:C:516:ILE:HG13	1.81	0.81
2:B:289:ASP:HB3	2:B:292:GLN:HG3	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:880:ARG:HH21	4:C:1:OBN:H6'3	1.46	0.80
2:D:289:ASP:HB3	2:D:292:GLN:HG3	1.63	0.80
2:B:198:THR:HA	2:B:199:TYR:CG	2.17	0.80
1:A:585:ILE:O	1:A:587:PRO:HD3	1.80	0.80
1:A:165:ILE:HG13	1:A:183:LEU:HD23	1.61	0.80
2:D:80:ILE:HG13	2:D:81:PRO:CD	2.08	0.80
2:D:198:THR:HA	2:D:199:TYR:CG	2.16	0.80
2:D:173:LYS:HG2	2:D:264:THR:HA	0.89	0.80
1:C:238:PHE:CD2	1:C:260:MET:HB2	2.16	0.80
2:B:129:VAL:CG2	2:B:130:PRO:CD	2.58	0.80
1:C:238:PHE:HD2	1:C:260:MET:HB2	1.45	0.80
1:A:918:THR:OG1	1:A:984:ALA:HB2	1.83	0.79
2:B:129:VAL:HG13	2:B:130:PRO:HD2	1.64	0.79
2:D:175:CYS:HA	2:D:262:GLN:HB2	1.64	0.79
1:A:260:MET:CE	1:A:712:VAL:HG21	2.12	0.79
1:A:516:ILE:HG13	1:A:516:ILE:O	1.81	0.79
1:C:294:PHE:O	1:C:298:SER:HB2	1.82	0.79
1:C:449:LEU:HD21	1:C:584:MET:HE1	1.64	0.79
1:A:312:GLU:HA	1:A:315:ILE:HG22	1.63	0.79
1:A:1016:TYR:H	1:A:1016:TYR:HD1	1.31	0.79
1:C:165:ILE:HG13	1:C:183:LEU:HD23	1.64	0.79
1:A:260:MET:HE1	1:A:712:VAL:CG1	2.13	0.79
1:C:312:GLU:HA	1:C:315:ILE:HG22	1.64	0.79
1:C:918:THR:OG1	1:C:984:ALA:HB2	1.83	0.79
2:D:129:VAL:CG1	2:D:130:PRO:CD	2.61	0.79
2:D:130:PRO:HB2	2:D:204:TYR:CE2	2.18	0.79
1:A:225:THR:CG2	1:A:232:THR:HA	2.13	0.79
1:A:71:ASN:HD22	1:A:255:GLY:N	1.81	0.78
1:C:853:ILE:HG12	2:D:46:LEU:HD21	1.66	0.78
1:C:93:PHE:HE1	1:C:285:ILE:HG13	1.48	0.78
1:C:880:ARG:NH2	4:C:1:OBN:H6'3	1.98	0.78
3:E:36:LEU:O	3:E:40:VAL:HG23	1.83	0.78
1:C:643:ILE:HD11	1:C:648:VAL:CG2	2.12	0.78
3:G:41:GLY:O	3:G:45:ILE:HG12	1.84	0.78
2:D:201:VAL:CG2	2:D:202:MET:HA	2.14	0.78
1:A:238:PHE:CD2	1:A:260:MET:HG2	2.19	0.78
2:B:239:PRO:HB2	2:B:241:GLN:HG2	1.66	0.78
1:A:225:THR:CG2	1:A:226:ASN:H	1.96	0.77
2:B:197:GLU:O	2:B:200:PRO:HD2	1.85	0.77
1:C:56:LEU:HD11	1:C:182:ASP:HB3	1.66	0.77
1:A:118:PRO:HG2	4:A:1:OBN:C19	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:459:SER:HB3	1:C:462:GLU:HG3	1.65	0.77
1:A:275:THR:HB	1:A:276:PRO:HD2	1.64	0.77
2:B:80:ILE:HG13	2:B:81:PRO:CD	2.09	0.77
1:A:56:LEU:HD11	1:A:182:ASP:HB3	1.67	0.77
1:A:785:ILE:HD11	1:A:859:PHE:CE2	2.18	0.77
1:A:48:TYR:CZ	1:A:252:VAL:HG12	2.19	0.77
3:E:41:GLY:O	3:E:45:ILE:HG12	1.85	0.77
2:D:239:PRO:HB2	2:D:241:GLN:HG2	1.66	0.77
3:G:36:LEU:O	3:G:40:VAL:HG23	1.85	0.76
1:A:93:PHE:HE1	1:A:285:ILE:HG13	1.51	0.76
2:B:178:ILE:CD1	2:B:211:VAL:HG11	2.16	0.76
2:B:130:PRO:HB2	2:B:204:TYR:CE2	2.20	0.76
2:D:224:VAL:O	2:D:266:LEU:HD22	1.86	0.76
1:A:459:SER:HB3	1:A:462:GLU:HG3	1.66	0.76
1:C:93:PHE:CE1	1:C:285:ILE:HG13	2.21	0.75
1:C:1016:TYR:H	1:C:1016:TYR:HD1	1.32	0.75
1:A:559:PRO:HD2	1:A:562:PHE:CD1	2.21	0.75
1:A:783:PHE:CD1	4:A:1:OBN:H161	2.22	0.75
2:D:264:THR:HG23	2:D:265:ASN:N	2.02	0.75
1:C:853:ILE:HD13	1:C:990:LEU:CD2	2.16	0.75
2:D:130:PRO:CB	2:D:204:TYR:CE2	2.69	0.75
2:D:133:LEU:CG	2:D:240:LEU:O	2.33	0.75
1:A:420:LEU:HD11	1:A:463:MET:HB3	1.69	0.75
1:A:853:ILE:HD13	1:A:990:LEU:CD2	2.17	0.75
1:C:559:PRO:HD2	1:C:562:PHE:CD1	2.22	0.75
2:D:197:GLU:O	2:D:200:PRO:HD2	1.85	0.75
1:C:785:ILE:HD11	1:C:859:PHE:CE2	2.22	0.74
2:D:78:THR:C	2:D:295:PHE:HE2	1.95	0.74
1:A:213:GLY:HA3	1:A:369:PHD:OP1	1.87	0.74
1:A:449:LEU:HD21	1:A:584:MET:HE1	1.68	0.74
1:C:476:ASN:HB2	1:C:479:ASN:HB2	1.70	0.74
2:B:80:ILE:CG1	2:B:81:PRO:HD3	2.10	0.74
1:C:420:LEU:HD11	1:C:463:MET:HB3	1.70	0.74
2:B:78:THR:C	2:B:295:PHE:HE2	1.94	0.74
2:B:133:LEU:CG	2:B:240:LEU:O	2.34	0.74
2:D:90:PHE:CZ	2:D:174:PRO:CG	2.71	0.74
2:B:205:ASN:N	2:B:206:PRO:CD	2.51	0.74
2:D:173:LYS:HB3	2:D:263:PHE:O	1.86	0.74
1:A:157:MET:HE2	1:A:191:ARG:HH22	1.52	0.74
2:B:131:SER:OG	2:B:241:GLN:HB3	1.88	0.74
1:C:119:GLN:O	1:C:123:LEU:HB3	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:858:GLY:O	1:A:861:THR:HG22	1.88	0.73
1:C:858:GLY:O	1:C:861:THR:HG22	1.88	0.73
1:A:797:THR:OG1	4:A:1:OBN:H152	1.88	0.73
1:A:987:TYR:OH	2:B:50:PHE:HA	1.89	0.73
2:B:224:VAL:O	2:B:266:LEU:HD22	1.85	0.73
2:D:98:TYR:O	2:D:102:VAL:HG23	1.88	0.73
1:A:93:PHE:CE1	1:A:285:ILE:HG13	2.23	0.73
1:C:797:THR:OG1	4:C:1:OBN:H152	1.88	0.73
2:D:276:CYS:HB2	2:D:295:PHE:HD1	1.53	0.73
1:A:48:TYR:CZ	1:A:252:VAL:CG1	2.71	0.73
1:A:490:ASN:O	1:A:494:PRO:HB3	1.89	0.73
1:C:480:LYS:HG2	1:C:506:ARG:NH1	2.02	0.73
1:C:853:ILE:HG13	2:D:46:LEU:HD11	1.71	0.73
1:C:506:ARG:HH11	1:C:506:ARG:HG3	1.54	0.73
2:B:202:MET:HG3	2:B:203:LYS:H	1.53	0.73
2:D:175:CYS:SG	2:D:262:GLN:NE2	2.62	0.73
2:B:175:CYS:HA	2:B:262:GLN:HB2	1.70	0.72
1:A:852:MET:HG2	2:B:43:TYR:CE2	2.25	0.72
2:B:214:THR:O	2:B:275:GLU:N	2.20	0.72
2:B:98:TYR:O	2:B:102:VAL:HG23	1.90	0.72
1:C:54:ARG:HH11	1:C:54:ARG:CG	2.02	0.72
1:C:490:ASN:O	1:C:494:PRO:HB3	1.89	0.72
2:D:90:PHE:CZ	2:D:174:PRO:HG3	2.24	0.72
2:D:178:ILE:CD1	2:D:211:VAL:HG11	2.20	0.72
2:D:204:TYR:HE1	2:D:235:TYR:CZ	2.07	0.72
1:A:96:LEU:HA	1:A:99:ILE:HG22	1.70	0.72
1:A:929:ILE:HB	1:A:995:ASP:OD2	1.90	0.72
2:B:264:THR:HG23	2:B:265:ASN:N	2.03	0.72
2:D:175:CYS:SG	2:D:262:GLN:HB3	2.30	0.72
1:A:476:ASN:HB2	1:A:479:ASN:HB2	1.70	0.72
1:A:481:TYR:HE1	1:A:483:LEU:HD23	1.54	0.72
1:A:643:ILE:HD11	1:A:648:VAL:HG22	1.72	0.72
1:C:93:PHE:CZ	1:C:284:PHE:CD2	2.78	0.72
1:A:93:PHE:CZ	1:A:284:PHE:CD2	2.78	0.71
1:A:870:GLY:O	1:A:893:ASP:HB2	1.90	0.71
1:A:897:GLN:HE21	2:B:184:LEU:H	1.36	0.71
1:C:297:VAL:HG12	1:C:317:LEU:HD11	1.72	0.71
1:C:783:PHE:CE1	4:C:1:OBN:H161	2.24	0.71
1:A:119:GLN:O	1:A:123:LEU:HB3	1.90	0.71
1:C:870:GLY:O	1:C:893:ASP:HB2	1.90	0.71
1:A:48:TYR:CE2	1:A:252:VAL:HG13	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:PHE:HD1	1:A:285:ILE:HD11	1.55	0.71
2:D:205:ASN:N	2:D:206:PRO:CD	2.50	0.71
2:B:170:LYS:HD3	2:B:173:LYS:H	1.55	0.71
1:C:93:PHE:HD1	1:C:285:ILE:HD11	1.54	0.71
2:D:225:GLY:CA	2:D:266:LEU:HD21	2.18	0.71
1:A:495:ARG:HB3	1:A:495:ARG:CZ	2.21	0.71
1:A:915:PHE:O	1:A:918:THR:HG22	1.91	0.71
1:C:506:ARG:HH11	1:C:506:ARG:CG	2.03	0.71
1:C:929:ILE:HB	1:C:995:ASP:OD2	1.91	0.71
2:D:130:PRO:HG2	2:D:204:TYR:OH	1.89	0.71
1:A:1009:TRP:CE3	1:A:1013:GLU:HG3	2.26	0.71
2:B:276:CYS:HB2	2:B:295:PHE:HD1	1.54	0.71
1:A:93:PHE:CD2	1:A:330:LEU:CD2	2.73	0.71
2:B:225:GLY:CA	2:B:266:LEU:HD21	2.18	0.71
1:C:1009:TRP:CE3	1:C:1013:GLU:HG3	2.25	0.71
1:C:206:VAL:HG23	1:C:242:CYS:HA	1.73	0.70
1:A:297:VAL:HG12	1:A:317:LEU:HD11	1.72	0.70
1:C:118:PRO:HG2	4:C:1:OBN:C19	2.19	0.70
2:D:183:VAL:HB	2:D:186:PHE:HB2	1.73	0.70
1:A:977:LYS:N	1:A:980:TRP:CD1	2.59	0.70
2:B:204:TYR:CD2	2:B:208:VAL:HB	2.26	0.70
1:C:654:LYS:HE2	1:C:654:LYS:HA	1.73	0.70
1:C:803:ILE:O	1:C:808:ASP:HB2	1.90	0.70
1:C:852:MET:HG2	2:D:43:TYR:CE2	2.26	0.70
1:C:1001:ILE:HG22	1:C:1010:VAL:HG11	1.74	0.70
1:A:157:MET:HE2	1:A:191:ARG:NH2	2.05	0.70
1:C:910:THR:OG1	1:C:974:TYR:HB2	1.92	0.70
2:B:130:PRO:HB2	2:B:204:TYR:HE2	1.55	0.70
1:C:915:PHE:O	1:C:918:THR:HG22	1.91	0.70
1:A:783:PHE:CZ	4:A:1:OBN:H122	2.25	0.70
1:C:481:TYR:HE1	1:C:483:LEU:HD23	1.55	0.70
2:D:129:VAL:CB	2:D:130:PRO:CD	2.70	0.70
1:C:43:GLU:C	1:C:45:HIS:H	1.98	0.70
1:C:96:LEU:HA	1:C:99:ILE:HG22	1.72	0.70
1:C:360:LEU:HD13	1:C:723:ILE:HD13	1.73	0.70
1:C:1011:GLU:O	1:C:1015:TYR:HB3	1.92	0.70
1:A:654:LYS:HA	1:A:654:LYS:HE2	1.72	0.70
1:A:803:ILE:O	1:A:808:ASP:HB2	1.91	0.70
1:C:195:ASP:CB	1:C:253:TYR:HB2	2.19	0.70
2:D:92:PRO:HD2	2:D:303:SER:HB2	1.74	0.70
1:A:404:PHE:CD2	1:A:404:PHE:N	2.58	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:131:SER:OG	2:D:241:GLN:HB3	1.92	0.70
1:A:205:LYS:HG2	1:A:217:PRO:HB2	1.74	0.69
2:B:129:VAL:CG1	2:B:130:PRO:N	2.54	0.69
3:G:22:ASP:O	3:G:25:THR:HG22	1.92	0.69
1:A:910:THR:OG1	1:A:974:TYR:HB2	1.92	0.69
2:B:102:VAL:HA	2:B:105:ILE:HD11	1.73	0.69
1:C:51:ASP:CG	1:C:54:ARG:HB2	2.18	0.69
1:C:205:LYS:HG2	1:C:217:PRO:HB2	1.74	0.69
1:A:473:ILE:HD12	1:A:483:LEU:HD21	1.74	0.69
1:A:898:GLN:HE21	2:B:182:ARG:H	1.38	0.69
1:A:1011:GLU:O	1:A:1015:TYR:HB3	1.92	0.69
1:C:191:ARG:HA	1:C:241:ASN:HA	1.75	0.69
1:A:506:ARG:HH11	1:A:506:ARG:CG	2.05	0.69
1:A:708:THR:HG22	1:A:725:VAL:HB	1.75	0.69
1:A:226:ASN:HB3	1:A:231:GLU:HB2	1.74	0.69
2:D:267:THR:HG21	2:D:270:THR:CG2	2.11	0.69
1:C:42:ASP:O	1:C:45:HIS:CB	2.40	0.69
1:C:495:ARG:HB3	1:C:495:ARG:CZ	2.22	0.69
1:A:54:ARG:HH11	1:A:54:ARG:CG	2.03	0.69
1:C:910:THR:O	1:C:914:PRO:HD3	1.93	0.69
1:A:365:THR:HB	1:A:705:VAL:HG12	1.75	0.69
1:A:804:ASP:C	1:A:805:LEU:HD12	2.18	0.69
2:D:80:ILE:HD11	2:D:177:ILE:HG23	1.74	0.69
2:D:130:PRO:HB2	2:D:204:TYR:HE2	1.55	0.69
1:C:260:MET:HE1	1:C:712:VAL:HG11	1.73	0.69
1:C:293:VAL:O	1:C:297:VAL:HG22	1.92	0.69
1:C:473:ILE:HD12	1:C:483:LEU:HD21	1.73	0.69
2:D:102:VAL:HA	2:D:105:ILE:HD11	1.74	0.69
2:B:173:LYS:HE2	2:B:264:THR:O	1.93	0.68
1:C:449:LEU:CD2	1:C:584:MET:HE1	2.23	0.68
1:C:778:PRO:HB2	1:C:919:ILE:HD11	1.75	0.68
2:B:183:VAL:HB	2:B:186:PHE:HB2	1.74	0.68
1:C:667:THR:HG22	1:C:670:GLN:CD	2.18	0.68
1:A:880:ARG:HH21	4:A:1:OBN:H6'3	1.58	0.68
1:C:1002:ILE:HG13	1:C:1010:VAL:HG12	1.74	0.68
1:A:564:PHE:HA	1:A:570:ASN:HD22	1.58	0.68
1:A:643:ILE:HD11	1:A:648:VAL:HG23	1.75	0.68
1:C:93:PHE:HZ	1:C:284:PHE:CD2	2.11	0.68
1:C:369:PHD:OP3	1:C:610:THR:HA	1.93	0.68
3:G:39:ILE:O	3:G:43:ILE:HG12	1.93	0.68
1:C:564:PHE:HA	1:C:570:ASN:HD22	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:HIS:H	1:A:37:HIS:CD2	2.12	0.68
1:A:360:LEU:HD13	1:A:723:ILE:HD13	1.74	0.68
2:B:103:VAL:O	2:B:106:VAL:HB	1.94	0.68
1:C:504:PRO:HG2	1:C:535:TYR:CE1	2.29	0.68
2:D:204:TYR:O	2:D:206:PRO:HD2	1.92	0.68
1:C:54:ARG:HD2	1:C:168:GLY:N	2.09	0.68
2:D:130:PRO:CG	2:D:204:TYR:CZ	2.76	0.68
1:C:120:ASN:OD1	1:C:120:ASN:N	2.27	0.68
1:C:860:PHE:HD1	2:D:54:ILE:HD12	1.59	0.68
2:B:124:GLU:HG3	2:B:147:LYS:HD2	1.75	0.67
1:C:89:LEU:O	1:C:95:MET:HE3	1.94	0.67
1:A:89:LEU:O	1:A:95:MET:HE3	1.94	0.67
1:A:93:PHE:HZ	1:A:284:PHE:CD2	2.11	0.67
1:A:369:PHD:OP3	1:A:610:THR:HA	1.94	0.67
1:A:853:ILE:HG21	1:A:990:LEU:HD22	1.76	0.67
1:A:1002:ILE:HG13	1:A:1010:VAL:HG12	1.77	0.67
1:C:213:GLY:HA3	1:C:369:PHD:OP1	1.95	0.67
1:A:51:ASP:CG	1:A:54:ARG:HB2	2.19	0.67
1:A:206:VAL:HG23	1:A:242:CYS:HA	1.76	0.67
1:C:226:ASN:HB3	1:C:231:GLU:HB2	1.76	0.67
1:C:853:ILE:HG12	2:D:46:LEU:CD2	2.23	0.67
3:E:39:ILE:O	3:E:43:ILE:HG12	1.94	0.67
1:C:853:ILE:CG1	2:D:46:LEU:HD11	2.25	0.67
1:A:449:LEU:CD2	1:A:584:MET:HE1	2.24	0.67
2:B:129:VAL:CG1	2:B:130:PRO:HD2	2.24	0.67
2:B:130:PRO:CB	2:B:204:TYR:HE2	2.07	0.67
3:E:22:ASP:O	3:E:25:THR:HG22	1.93	0.67
1:A:504:PRO:HG2	1:A:535:TYR:CE1	2.30	0.67
1:A:778:PRO:HB2	1:A:919:ILE:HD11	1.77	0.67
1:C:195:ASP:HB2	1:C:253:TYR:CB	2.22	0.67
1:A:293:VAL:O	1:A:297:VAL:HG22	1.93	0.67
2:B:239:PRO:HG2	2:B:242:TYR:CD1	2.29	0.67
2:D:90:PHE:CE1	2:D:174:PRO:HG2	2.29	0.67
1:C:37:HIS:H	1:C:37:HIS:CD2	2.11	0.67
1:A:1009:TRP:HE3	1:A:1013:GLU:HG3	1.61	0.66
1:C:365:THR:HB	1:C:705:VAL:HG12	1.76	0.66
1:C:977:LYS:N	1:C:980:TRP:CD1	2.62	0.66
1:A:571:PHE:HB2	1:A:572:PRO:HD2	1.77	0.66
1:A:585:ILE:CG1	1:A:586:ASP:H	2.04	0.66
2:B:205:ASN:N	2:B:206:PRO:HD2	2.10	0.66
1:A:667:THR:HG22	1:A:670:GLN:CD	2.20	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:893:ASP:OD1	1:A:897:GLN:HB2	1.95	0.66
1:A:898:GLN:NE2	2:B:182:ARG:H	1.94	0.66
2:B:92:PRO:HD2	2:B:303:SER:HB2	1.76	0.66
1:C:783:PHE:CD1	4:C:1:OBN:H161	2.29	0.66
1:A:54:ARG:HD2	1:A:167:ASN:C	2.20	0.66
1:A:1001:ILE:HG22	1:A:1010:VAL:HG11	1.75	0.66
2:D:184:LEU:HD21	2:D:247:GLY:HA2	1.77	0.66
1:A:982:PHE:N	1:A:982:PHE:HD1	1.94	0.66
1:C:78:THR:C	1:C:80:PRO:HD3	2.21	0.66
1:C:488:ASN:HB3	1:C:494:PRO:CA	2.20	0.66
1:C:643:ILE:HD11	1:C:648:VAL:HG23	1.77	0.66
1:C:853:ILE:HG21	1:C:990:LEU:HD22	1.76	0.66
2:D:103:VAL:O	2:D:106:VAL:HB	1.95	0.66
2:D:129:VAL:CG2	2:D:130:PRO:HD3	2.18	0.66
1:A:191:ARG:HA	1:A:241:ASN:HA	1.77	0.66
1:A:668:SER:HB2	1:A:700:ARG:NH2	2.11	0.66
1:C:480:LYS:CG	1:C:506:ARG:NH1	2.58	0.66
1:A:998:ARG:HE	1:A:1014:THR:HB	1.60	0.66
1:C:804:ASP:C	1:C:805:LEU:HD12	2.20	0.66
1:C:982:PHE:CD1	1:C:982:PHE:N	2.64	0.66
2:B:201:VAL:CG2	2:B:202:MET:HA	2.25	0.65
2:D:140:ASN:HB3	2:D:142:GLU:HG3	1.78	0.65
2:D:239:PRO:HG2	2:D:242:TYR:CD1	2.31	0.65
2:B:274:ILE:HD13	2:B:274:ILE:H	1.61	0.65
1:C:990:LEU:HD23	1:C:990:LEU:C	2.21	0.65
1:A:514:ILE:O	1:A:516:ILE:HG23	1.96	0.65
2:B:99:GLU:O	2:B:103:VAL:HG23	1.96	0.65
1:C:41:LEU:H	1:C:41:LEU:HD12	1.61	0.65
1:A:93:PHE:CD2	1:A:330:LEU:HD21	2.31	0.65
1:A:1015:TYR:O	1:A:1016:TYR:OXT	2.13	0.65
2:B:184:LEU:HD21	2:B:247:GLY:HA2	1.77	0.65
2:B:264:THR:CG2	2:B:265:ASN:H	2.10	0.65
1:C:1009:TRP:HE3	1:C:1013:GLU:HG3	1.59	0.65
2:D:214:THR:O	2:D:275:GLU:N	2.29	0.65
1:C:893:ASP:OD1	1:C:897:GLN:HB2	1.97	0.65
1:C:982:PHE:N	1:C:982:PHE:HD1	1.93	0.65
1:A:226:ASN:OD1	1:A:227:GLU:N	2.30	0.65
1:C:157:MET:C	1:C:158:VAL:CG2	2.69	0.65
1:C:260:MET:HE1	1:C:712:VAL:CG1	2.26	0.65
1:A:854:GLN:HG2	1:A:922:VAL:HB	1.79	0.65
1:C:101:ALA:HB2	1:C:129:LEU:CB	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:708:THR:HG22	1:C:725:VAL:HB	1.77	0.65
2:D:99:GLU:O	2:D:103:VAL:HG23	1.97	0.65
2:D:266:LEU:HD13	2:D:272:ILE:HD12	1.78	0.65
1:C:369:PHD:OP2	1:C:370:LYS:N	2.25	0.65
1:C:854:GLN:HG2	1:C:922:VAL:HB	1.77	0.65
2:B:80:ILE:HD11	2:B:177:ILE:HG23	1.79	0.65
1:C:226:ASN:OD1	1:C:227:GLU:N	2.30	0.65
1:C:571:PHE:HB2	1:C:572:PRO:HD2	1.79	0.65
1:C:643:ILE:HD11	1:C:648:VAL:HG22	1.77	0.65
2:D:124:GLU:HG3	2:D:147:LYS:HD2	1.79	0.65
1:A:117:GLU:CB	1:A:118:PRO:CD	2.73	0.64
1:A:982:PHE:N	1:A:982:PHE:CD1	2.64	0.64
1:C:1015:TYR:O	1:C:1016:TYR:OXT	2.15	0.64
1:A:229:PRO:O	1:A:237:PHE:HZ	1.80	0.64
1:C:98:TRP:HE1	1:C:133:VAL:HG11	1.63	0.64
1:C:898:GLN:HE21	2:D:182:ARG:H	1.46	0.64
1:A:416:ARG:HD2	1:A:467:TYR:CE2	2.32	0.64
2:D:208:VAL:N	2:D:240:LEU:HD13	2.12	0.64
2:D:274:ILE:HD13	2:D:274:ILE:H	1.61	0.64
2:D:80:ILE:CG1	2:D:81:PRO:HD3	2.11	0.64
2:B:193:ASN:OD1	2:B:203:LYS:HD3	1.98	0.64
1:C:54:ARG:HD2	1:C:167:ASN:C	2.22	0.64
1:C:559:PRO:HD2	1:C:562:PHE:HB2	1.79	0.64
1:A:373:THR:HG21	1:A:708:THR:O	1.98	0.64
1:A:796:GLY:HA3	1:A:912:HIS:CE1	2.33	0.64
1:A:842:LEU:HD12	1:A:1016:TYR:HD2	1.62	0.64
2:B:151:PHE:CE1	2:B:232:LEU:HD23	2.33	0.64
1:C:46:ARG:HG2	1:C:46:ARG:O	1.97	0.64
1:C:98:TRP:NE1	1:C:133:VAL:HG11	2.13	0.64
1:C:514:ILE:O	1:C:516:ILE:HG23	1.97	0.64
1:A:98:TRP:HE1	1:A:133:VAL:HG11	1.62	0.64
1:A:98:TRP:NE1	1:A:133:VAL:HG11	2.13	0.64
2:D:264:THR:CG2	2:D:265:ASN:H	2.09	0.64
1:A:559:PRO:HD2	1:A:562:PHE:HB2	1.79	0.64
1:C:239:SER:HG	1:C:260:MET:HG3	1.62	0.64
1:A:799:THR:CG2	1:A:916:PHE:HB2	2.28	0.63
1:A:910:THR:O	1:A:914:PRO:HD3	1.97	0.63
1:C:668:SER:HB2	1:C:700:ARG:NH2	2.13	0.63
1:C:585:ILE:CG1	1:C:586:ASP:H	2.01	0.63
3:E:21:TYR:HB3	3:E:23:TYR:CD1	2.33	0.63
1:A:211:LEU:HD21	1:A:237:PHE:CG	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:852:MET:HG2	2:B:43:TYR:HE2	1.63	0.63
1:C:93:PHE:CD2	1:C:330:LEU:CD2	2.81	0.63
1:C:117:GLU:CB	1:C:118:PRO:CD	2.74	0.63
1:C:157:MET:C	1:C:158:VAL:HG22	2.23	0.63
1:C:719:LYS:HB2	1:C:738:ALA:HB1	1.80	0.63
2:D:173:LYS:HD2	2:D:173:LYS:N	2.12	0.63
2:D:226:THR:HG21	2:D:265:ASN:H	1.64	0.63
1:A:719:LYS:HB2	1:A:738:ALA:HB1	1.80	0.63
1:C:987:TYR:HH	2:D:50:PHE:HA	1.64	0.63
1:A:347:LYS:HD2	1:A:753:THR:HG21	1.80	0.63
2:B:226:THR:HG21	2:B:265:ASN:H	1.63	0.63
1:C:211:LEU:HD21	1:C:237:PHE:CG	2.34	0.63
1:A:191:ARG:O	1:A:193:PRO:HD3	1.99	0.63
1:A:589:ARG:HB2	1:A:592:VAL:CG2	2.28	0.63
1:A:853:ILE:HG12	2:B:46:LEU:HD21	1.81	0.63
1:A:990:LEU:HD23	1:A:990:LEU:C	2.24	0.63
1:C:347:LYS:HD2	1:C:753:THR:HG21	1.79	0.63
1:C:799:THR:CG2	1:C:916:PHE:HB2	2.29	0.63
2:D:277:LYS:HD2	2:D:279:TYR:CZ	2.34	0.63
1:A:131:ALA:O	1:A:135:ILE:HG12	1.98	0.63
1:C:495:ARG:HB3	1:C:495:ARG:NH1	2.14	0.63
2:D:230:PHE:HB2	2:D:260:ALA:HB3	1.81	0.63
2:B:230:PHE:HB2	2:B:260:ALA:HB3	1.80	0.62
1:A:430:GLN:NE2	1:A:438:ARG:HB2	2.14	0.62
1:A:488:ASN:HB3	1:A:494:PRO:CA	2.20	0.62
1:A:886:ARG:HA	1:A:901:TYR:CD1	2.34	0.62
2:B:267:THR:HG21	2:B:270:THR:CG2	2.13	0.62
1:C:312:GLU:O	1:C:315:ILE:HG22	1.99	0.62
1:C:865:ILE:HD12	1:C:980:TRP:CE2	2.34	0.62
2:D:80:ILE:HG21	2:D:177:ILE:HD11	1.81	0.62
2:D:204:TYR:CA	2:D:206:PRO:HD2	2.27	0.62
1:A:228:ASN:C	1:A:230:LEU:H	2.08	0.62
1:A:495:ARG:CG	1:A:555:ASP:HB3	2.27	0.62
2:B:277:LYS:HD2	2:B:279:TYR:CZ	2.34	0.62
1:A:876:LEU:HD23	1:A:879:LEU:HD12	1.81	0.62
1:A:312:GLU:O	1:A:315:ILE:HG22	1.99	0.62
1:A:624:VAL:HG23	1:A:626:ILE:HG13	1.82	0.62
1:A:868:GLU:O	2:B:67:THR:HG23	2.00	0.62
2:B:266:LEU:HD13	2:B:272:ILE:HD12	1.82	0.62
1:C:151:MET:HE1	1:C:352:LYS:HD2	1.80	0.62
1:C:430:GLN:NE2	1:C:438:ARG:HB2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:151:PHE:CE1	2:D:232:LEU:HD23	2.35	0.62
1:A:495:ARG:HB3	1:A:495:ARG:NH1	2.13	0.62
2:B:140:ASN:HB3	2:B:142:GLU:HG3	1.80	0.62
1:C:322:VAL:HB	4:C:1:OBN:C23	2.30	0.62
1:C:589:ARG:HB2	1:C:592:VAL:CG2	2.29	0.62
1:C:886:ARG:HA	1:C:901:TYR:CD1	2.35	0.62
1:C:338:THR:O	1:C:342:LYS:HG2	2.00	0.62
1:C:416:ARG:HD2	1:C:467:TYR:CE2	2.34	0.62
1:C:56:LEU:N	1:C:56:LEU:HD12	2.15	0.62
2:B:274:ILE:HD13	2:B:297:VAL:O	1.99	0.62
1:C:228:ASN:C	1:C:230:LEU:H	2.08	0.62
2:B:129:VAL:CG1	2:B:130:PRO:CD	2.77	0.61
1:C:191:ARG:O	1:C:193:PRO:HD3	2.00	0.61
1:C:796:GLY:HA3	1:C:912:HIS:CE1	2.35	0.61
1:A:93:PHE:CG	1:A:330:LEU:HD21	2.35	0.61
1:A:120:ASN:N	1:A:120:ASN:OD1	2.33	0.61
2:B:204:TYR:HE1	2:B:235:TYR:CE1	2.16	0.61
1:C:369:PHD:HB2	1:C:373:THR:OG1	1.99	0.61
1:C:898:GLN:HE21	2:D:181:ASN:CA	2.13	0.61
4:A:1:OBN:H212	4:A:1:OBN:H181	1.82	0.61
2:B:272:ILE:HG13	2:B:299:ILE:HG13	1.80	0.61
1:C:481:TYR:CE1	1:C:483:LEU:HD23	2.35	0.61
1:C:842:LEU:HD12	1:C:1016:TYR:HD2	1.65	0.61
1:C:859:PHE:O	1:C:862:TYR:HB3	1.99	0.61
2:D:130:PRO:CG	2:D:204:TYR:OH	2.48	0.61
1:A:117:GLU:HB3	1:A:118:PRO:HD3	1.80	0.61
1:A:254:THR:O	1:A:257:ARG:HB2	2.01	0.61
2:B:207:TYR:C	2:B:240:LEU:HD13	2.26	0.61
2:B:277:LYS:HD2	2:B:279:TYR:OH	2.00	0.61
2:D:88:ILE:HG23	2:D:101:TYR:CE2	2.35	0.61
2:D:274:ILE:HD13	2:D:297:VAL:O	2.00	0.61
1:A:56:LEU:HD12	1:A:56:LEU:N	2.15	0.61
1:A:611:GLY:HA2	1:A:686:THR:N	2.16	0.61
1:C:810:VAL:HB	1:C:811:PRO:HD3	1.82	0.61
2:D:90:PHE:HZ	2:D:174:PRO:CG	2.13	0.61
1:A:54:ARG:HD3	1:A:168:GLY:CA	2.30	0.61
2:B:202:MET:HG3	2:B:203:LYS:N	2.15	0.61
2:D:193:ASN:HA	2:D:203:LYS:NZ	2.16	0.61
1:A:352:LYS:HE2	1:A:739:ALA:O	2.01	0.61
2:B:94:ASP:CB	2:B:97:SER:HB2	2.29	0.61
1:C:373:THR:HG21	1:C:708:THR:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:ASN:C	2:B:283:ILE:HD12	2.26	0.61
1:C:675:LEU:N	1:C:675:LEU:HD12	2.15	0.61
2:D:282:ASN:C	2:D:283:ILE:HD12	2.26	0.61
2:B:157:GLY:O	2:B:159:CYS:N	2.34	0.61
2:B:208:VAL:N	2:B:240:LEU:HD13	2.15	0.61
1:A:810:VAL:HB	1:A:811:PRO:HD3	1.82	0.61
1:A:54:ARG:HD2	1:A:168:GLY:N	2.16	0.60
1:A:93:PHE:C	1:A:330:LEU:HD11	2.25	0.60
1:C:811:PRO:HB3	1:C:927:LEU:HD22	1.82	0.60
1:A:481:TYR:CE1	1:A:483:LEU:HD23	2.34	0.60
1:C:964:CYS:HB3	1:C:967:MET:CG	2.31	0.60
1:A:859:PHE:O	1:A:862:TYR:HB3	2.01	0.60
2:B:88:ILE:HG23	2:B:101:TYR:CE2	2.36	0.60
3:G:21:TYR:HB3	3:G:23:TYR:CD1	2.36	0.60
1:C:117:GLU:HB3	1:C:118:PRO:HD3	1.81	0.60
1:C:783:PHE:HZ	4:C:1:OBN:H122	1.63	0.60
1:C:899:TRP:CE3	2:D:72:VAL:HG13	2.36	0.60
1:C:902:GLU:HG3	2:D:288:LYS:HG3	1.83	0.60
1:A:98:TRP:CD1	1:A:133:VAL:HG11	2.37	0.60
1:C:375:THR:HA	1:C:588:PRO:HA	1.84	0.60
1:C:998:ARG:HE	1:C:1014:THR:HB	1.65	0.60
2:D:36:LEU:O	2:D:40:VAL:HG23	2.00	0.60
2:D:277:LYS:HD2	2:D:279:TYR:OH	2.01	0.60
1:A:811:PRO:HB3	1:A:927:LEU:HD22	1.82	0.60
2:B:178:ILE:HD11	2:B:211:VAL:HG11	1.81	0.60
1:C:93:PHE:C	1:C:330:LEU:HD11	2.27	0.60
1:C:467:TYR:CZ	1:C:489:PRO:HG3	2.37	0.60
1:A:211:LEU:N	1:A:211:LEU:HD12	2.17	0.60
1:C:229:PRO:O	1:C:237:PHE:HZ	1.84	0.60
1:A:687:SER:OG	1:A:690:GLN:HG3	2.02	0.60
1:C:480:LYS:CG	1:C:506:ARG:HH12	2.15	0.60
1:C:624:VAL:HG23	1:C:626:ILE:HG13	1.83	0.60
2:D:94:ASP:CB	2:D:97:SER:HB2	2.29	0.60
2:D:177:ILE:HD12	2:D:258:LEU:HD22	1.83	0.60
2:D:207:TYR:C	2:D:240:LEU:HD13	2.27	0.60
1:C:98:TRP:CD1	1:C:133:VAL:HG11	2.36	0.60
1:C:321:ILE:HD12	1:C:322:VAL:N	2.16	0.60
1:C:585:ILE:CG1	1:C:586:ASP:N	2.58	0.60
1:C:860:PHE:CZ	2:D:57:MET:HG3	2.37	0.60
2:D:236:PRO:HA	2:D:259:MET:HE1	1.83	0.60
2:D:272:ILE:HG13	2:D:299:ILE:HG13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:PHE:CD2	1:A:330:LEU:HD22	2.37	0.59
1:A:338:THR:O	1:A:342:LYS:HG2	2.01	0.59
1:A:101:ALA:HB2	1:A:129:LEU:CB	2.30	0.59
1:A:229:PRO:O	1:A:237:PHE:CZ	2.55	0.59
2:B:129:VAL:CB	2:B:130:PRO:CD	2.80	0.59
2:D:94:ASP:HB2	2:D:97:SER:CB	2.31	0.59
1:C:687:SER:OG	1:C:690:GLN:HG3	2.02	0.59
2:D:90:PHE:HZ	2:D:174:PRO:HG3	1.65	0.59
1:A:842:LEU:HD12	1:A:1016:TYR:CD2	2.37	0.59
2:D:227:MET:HG2	2:D:263:PHE:CE2	2.37	0.59
1:A:467:TYR:CZ	1:A:489:PRO:HG3	2.38	0.59
1:A:964:CYS:HB3	1:A:967:MET:CG	2.32	0.59
1:A:470:ILE:HG12	1:A:485:ILE:O	2.02	0.59
1:C:101:ALA:CB	1:C:129:LEU:HB2	2.28	0.59
1:C:352:LYS:HE2	1:C:739:ALA:O	2.02	0.59
1:C:821:GLU:CD	1:C:933:ARG:H	2.11	0.59
1:C:899:TRP:HZ3	2:D:71:ARG:HB3	1.68	0.59
1:A:55:GLY:HA3	1:A:165:ILE:O	2.01	0.59
1:A:797:THR:OG1	4:A:1:OBN:O14	2.21	0.59
4:C:1:OBN:H181	4:C:1:OBN:H212	1.85	0.59
2:D:90:PHE:CZ	2:D:174:PRO:HG2	2.38	0.59
2:D:210:PRO:HG2	2:D:279:TYR:HB2	1.84	0.59
1:A:790:ASN:HB2	1:A:878:GLY:HA2	1.85	0.59
1:C:101:ALA:HA	1:C:104:CYS:SG	2.43	0.59
2:D:102:VAL:O	2:D:105:ILE:HG12	2.03	0.59
2:B:173:LYS:CB	2:B:263:PHE:O	2.45	0.59
1:C:211:LEU:HD12	1:C:211:LEU:N	2.17	0.59
2:D:80:ILE:HG22	2:D:108:PHE:CG	2.37	0.59
2:B:227:MET:HG2	2:B:263:PHE:CE2	2.38	0.58
1:C:54:ARG:HD3	1:C:168:GLY:CA	2.33	0.58
1:C:842:LEU:HD12	1:C:1016:TYR:CD2	2.38	0.58
1:C:917:VAL:HG12	1:C:918:THR:N	2.17	0.58
1:A:506:ARG:HH11	1:A:506:ARG:HG3	1.68	0.58
1:A:989:LEU:HD23	1:A:989:LEU:C	2.28	0.58
1:A:1000:LEU:HD13	1:A:1000:LEU:C	2.29	0.58
2:B:246:TYR:HB2	2:B:251:GLN:CD	2.28	0.58
1:C:93:PHE:CD2	1:C:330:LEU:HD21	2.38	0.58
1:C:155:LYS:HG2	1:C:155:LYS:O	2.04	0.58
1:C:748:PHE:O	1:C:751:ILE:HG12	2.03	0.58
1:C:889:ASN:CG	2:D:291:PHE:CG	2.81	0.58
1:A:375:THR:HA	1:A:588:PRO:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:236:PRO:HA	2:B:259:MET:HE1	1.85	0.58
1:C:157:MET:N	1:C:157:MET:SD	2.75	0.58
2:D:173:LYS:CE	2:D:264:THR:O	2.44	0.58
1:A:931:LYS:HG2	1:A:932:THR:HG23	1.85	0.58
1:C:480:LYS:HG2	1:C:506:ARG:HH12	1.65	0.58
1:C:632:GLU:HB3	1:C:636:ASP:HB2	1.86	0.58
1:C:790:ASN:HB2	1:C:878:GLY:HA2	1.84	0.58
2:D:112:TYR:CE1	2:D:258:LEU:HD11	2.38	0.58
2:B:81:PRO:HG2	2:B:176:VAL:HG22	1.86	0.58
2:B:172:GLY:O	2:B:173:LYS:HD2	2.02	0.58
1:A:875:HIS:O	1:A:879:LEU:HD21	2.04	0.58
2:B:178:ILE:HG12	2:B:259:MET:HB2	1.86	0.58
2:B:146:ARG:HB2	2:B:251:GLN:HG3	1.85	0.58
1:C:470:ILE:HG12	1:C:485:ILE:O	2.04	0.58
1:A:852:MET:O	1:A:856:LEU:HG	2.04	0.58
2:B:276:CYS:HB2	2:B:295:PHE:CD1	2.38	0.58
1:A:195:ASP:CB	1:A:253:TYR:HB2	2.31	0.58
1:A:266:LEU:O	1:A:270:LEU:HG	2.03	0.58
1:A:865:ILE:HD12	1:A:980:TRP:CE2	2.38	0.58
2:B:102:VAL:O	2:B:105:ILE:HG12	2.03	0.58
1:C:824:ILE:O	1:C:827:ARG:HG2	2.04	0.58
2:D:102:VAL:O	2:D:106:VAL:HG23	2.04	0.58
2:D:178:ILE:HG12	2:D:259:MET:HB2	1.86	0.58
2:D:246:TYR:HB2	2:D:251:GLN:CD	2.28	0.58
2:B:183:VAL:CG1	2:B:186:PHE:HB2	2.34	0.57
1:C:155:LYS:O	1:C:155:LYS:CG	2.51	0.57
1:C:649:ASN:HD22	1:C:650:PRO:HD2	1.69	0.57
1:A:370:LYS:HG3	1:A:608:MET:HE2	1.86	0.57
2:B:62:SER:OG	2:B:64:PHE:N	2.38	0.57
1:C:266:LEU:O	1:C:270:LEU:HG	2.04	0.57
1:C:688:PRO:HG3	1:C:713:ASN:HB2	1.85	0.57
2:D:146:ARG:HB2	2:D:251:GLN:HG3	1.85	0.57
1:A:507:ILE:HG23	1:A:549:CYS:SG	2.44	0.57
2:D:148:VAL:HG11	2:D:254:TYR:HA	1.87	0.57
2:D:178:ILE:HD11	2:D:211:VAL:HG11	1.86	0.57
2:D:183:VAL:CG1	2:D:186:PHE:HB2	2.34	0.57
1:A:802:CYS:HB3	1:A:916:PHE:CE2	2.40	0.57
1:A:807:THR:HB	1:A:954:GLU:CG	2.18	0.57
2:B:36:LEU:O	2:B:40:VAL:HG23	2.05	0.57
2:B:204:TYR:CA	2:B:206:PRO:HD2	2.35	0.57
2:D:156:LEU:HD22	2:D:260:ALA:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:PHE:CG	1:A:239:SER:N	2.72	0.57
2:D:62:SER:OG	2:D:64:PHE:N	2.34	0.57
1:C:370:LYS:HG3	1:C:608:MET:HE2	1.85	0.57
2:D:80:ILE:CD1	2:D:177:ILE:HG23	2.34	0.57
1:A:632:GLU:HB3	1:A:636:ASP:HB2	1.85	0.57
1:C:725:VAL:HG22	1:C:741:MET:HB2	1.87	0.57
1:A:547:GLY:HA2	1:A:581:LEU:HD23	1.87	0.57
2:B:156:LEU:HD22	2:B:260:ALA:H	1.69	0.57
2:B:210:PRO:HG2	2:B:279:TYR:HB2	1.86	0.57
1:C:611:GLY:HA2	1:C:686:THR:N	2.18	0.57
1:C:852:MET:O	1:C:856:LEU:HG	2.05	0.57
1:C:990:LEU:CD1	2:D:49:ILE:HD13	2.35	0.57
1:A:260:MET:CE	1:A:712:VAL:CG1	2.78	0.57
1:A:514:ILE:HD11	1:A:523:LEU:HG	1.87	0.57
1:A:611:GLY:C	1:A:685:ARG:HA	2.30	0.57
1:A:824:ILE:O	1:A:827:ARG:HG2	2.04	0.57
1:A:949:PHE:CE1	3:G:45:ILE:HD13	2.39	0.57
2:B:112:TYR:CE1	2:B:258:LEU:HD11	2.40	0.57
2:B:204:TYR:CE1	2:B:235:TYR:CE1	2.92	0.57
1:C:35:ASP:OD2	1:C:229:PRO:HB3	2.05	0.57
1:C:949:PHE:CZ	1:C:953:GLU:HG3	2.40	0.57
1:A:95:MET:HA	1:A:95:MET:CE	2.33	0.56
1:A:492:ALA:C	1:A:494:PRO:HD3	2.30	0.56
2:B:202:MET:HE3	2:B:203:LYS:H	1.70	0.56
1:A:868:GLU:HA	2:B:67:THR:CG2	2.35	0.56
1:A:949:PHE:CZ	1:A:953:GLU:HG3	2.40	0.56
1:C:229:PRO:O	1:C:237:PHE:CZ	2.58	0.56
1:C:495:ARG:CG	1:C:555:ASP:HB3	2.29	0.56
1:C:989:LEU:HD23	1:C:989:LEU:C	2.30	0.56
1:A:549:CYS:HB3	1:A:578:PHE:HA	1.87	0.56
1:A:611:GLY:HA2	1:A:686:THR:H	1.69	0.56
1:A:688:PRO:HG3	1:A:713:ASN:HB2	1.86	0.56
1:C:55:GLY:HA3	1:C:165:ILE:O	2.05	0.56
1:A:101:ALA:HA	1:A:104:CYS:SG	2.45	0.56
1:A:183:LEU:HD21	1:A:248:ARG:HH21	1.71	0.56
1:A:321:ILE:HD12	1:A:322:VAL:N	2.21	0.56
1:A:381:VAL:HG22	1:A:584:MET:HE2	1.87	0.56
1:A:649:ASN:HD22	1:A:650:PRO:HD2	1.70	0.56
1:A:165:ILE:HD13	1:A:170:LYS:HB3	1.87	0.56
1:A:374:LEU:O	1:A:592:VAL:HG21	2.05	0.56
1:A:821:GLU:CD	1:A:933:ARG:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:238:PHE:CG	1:C:239:SER:N	2.73	0.56
1:C:564:PHE:HD2	1:C:571:PHE:CD2	2.24	0.56
1:A:238:PHE:CE2	1:A:260:MET:CG	2.87	0.56
1:A:663:LEU:HD21	1:A:671:LEU:HD22	1.88	0.56
1:A:873:PRO:CD	2:B:58:LEU:HD21	2.36	0.56
1:A:917:VAL:HG12	1:A:918:THR:N	2.19	0.56
2:B:102:VAL:O	2:B:106:VAL:HG23	2.06	0.56
1:C:162:ALA:O	1:C:172:SER:HA	2.05	0.56
1:A:238:PHE:HE2	1:A:260:MET:HG2	1.68	0.56
2:B:102:VAL:HA	2:B:105:ILE:CD1	2.35	0.56
2:B:130:PRO:CD	2:B:204:TYR:OH	2.53	0.56
2:B:204:TYR:O	2:B:206:PRO:HD2	1.99	0.56
1:C:57:THR:HG22	1:C:59:ALA:H	1.70	0.56
1:C:312:GLU:CA	1:C:315:ILE:HG22	2.35	0.56
1:C:549:CYS:HB3	1:C:578:PHE:HA	1.88	0.56
1:C:725:VAL:HG22	1:C:741:MET:CB	2.35	0.56
1:C:898:GLN:NE2	2:D:182:ARG:N	2.50	0.56
1:A:35:ASP:HB2	1:A:229:PRO:HG3	1.87	0.56
1:A:41:LEU:H	1:A:41:LEU:HD12	1.71	0.56
1:A:688:PRO:HB2	1:A:689:GLN:OE1	2.06	0.56
2:B:175:CYS:HA	2:B:262:GLN:CB	2.35	0.56
1:C:56:LEU:HD12	1:C:56:LEU:H	1.70	0.56
1:C:381:VAL:HG22	1:C:584:MET:HE2	1.87	0.56
1:C:777:ILE:HD13	1:C:780:ILE:HD12	1.88	0.56
2:D:207:TYR:O	2:D:208:VAL:HG23	2.06	0.56
1:A:101:ALA:CB	1:A:129:LEU:HB2	2.32	0.56
2:B:80:ILE:HG22	2:B:108:PHE:CG	2.41	0.56
1:C:284:PHE:CD1	1:C:838:VAL:HG21	2.40	0.56
1:C:507:ILE:HG23	1:C:549:CYS:SG	2.46	0.56
2:D:157:GLY:O	2:D:159:CYS:N	2.39	0.56
2:D:173:LYS:CB	2:D:263:PHE:O	2.54	0.56
2:D:246:TYR:O	2:D:250:LEU:HB2	2.06	0.56
1:A:369:PHD:OD2	1:A:369:PHD:OP2	2.21	0.55
1:A:480:LYS:HG2	1:A:506:ARG:NH1	2.20	0.55
1:A:783:PHE:CE1	4:A:1:OBN:C16	2.84	0.55
2:B:148:VAL:HG11	2:B:254:TYR:HA	1.87	0.55
1:C:404:PHE:CD2	1:C:404:PHE:N	2.59	0.55
1:C:860:PHE:CD1	2:D:54:ILE:HD12	2.41	0.55
1:C:887:TRP:O	1:C:889:ASN:ND2	2.39	0.55
1:C:29:LYS:O	1:C:689:GLN:HG2	2.06	0.55
1:C:909:PHE:CE2	1:C:972:ARG:HD3	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:931:LYS:HG2	1:C:932:THR:HG23	1.87	0.55
1:A:54:ARG:HD3	1:A:168:GLY:HA3	1.89	0.55
2:B:202:MET:CG	2:B:203:LYS:H	2.20	0.55
1:C:797:THR:OG1	4:C:1:OBN:C15	2.54	0.55
1:C:802:CYS:HB3	1:C:916:PHE:CE2	2.42	0.55
2:B:265:ASN:C	2:B:266:LEU:HD23	2.30	0.55
1:A:312:GLU:CA	1:A:315:ILE:HG22	2.34	0.55
1:A:853:ILE:HD13	1:A:990:LEU:HD22	1.88	0.55
2:B:66:PRO:HG2	2:B:69:GLN:HG2	1.87	0.55
2:B:92:PRO:HD2	2:B:303:SER:CB	2.37	0.55
2:B:130:PRO:CB	2:B:204:TYR:CZ	2.89	0.55
1:C:71:ASN:ND2	1:C:255:GLY:H	2.04	0.55
1:C:911:CYS:C	1:C:914:PRO:HD2	2.32	0.55
2:D:193:ASN:HA	2:D:203:LYS:HZ3	1.70	0.55
1:A:795:LEU:HD13	1:A:915:PHE:CD2	2.42	0.55
1:A:880:ARG:NH2	4:A:1:OBN:H6'3	2.22	0.55
1:C:260:MET:CE	1:C:712:VAL:HG11	2.37	0.55
1:C:875:HIS:O	1:C:879:LEU:HD21	2.07	0.55
1:C:1011:GLU:HA	1:C:1015:TYR:HB2	1.89	0.55
2:D:102:VAL:HA	2:D:105:ILE:CD1	2.35	0.55
2:D:264:THR:CG2	2:D:265:ASN:N	2.69	0.55
1:A:57:THR:HG22	1:A:59:ALA:H	1.71	0.55
1:C:93:PHE:CG	1:C:330:LEU:HD21	2.41	0.55
1:C:165:ILE:HD13	1:C:170:LYS:HB3	1.89	0.55
1:C:585:ILE:O	1:C:587:PRO:CD	2.53	0.55
2:D:120:ASP:O	2:D:123:PHE:N	2.40	0.55
2:D:276:CYS:HB2	2:D:295:PHE:CD1	2.37	0.55
1:A:564:PHE:HD2	1:A:571:PHE:CD2	2.24	0.55
1:A:967:MET:CE	1:A:971:LEU:HD12	2.37	0.55
1:A:1011:GLU:HA	1:A:1015:TYR:HB2	1.88	0.55
1:C:492:ALA:C	1:C:494:PRO:HD3	2.31	0.55
1:C:663:LEU:HD21	1:C:671:LEU:HD22	1.88	0.55
1:C:868:GLU:HA	2:D:67:THR:CG2	2.37	0.55
2:D:80:ILE:HD11	2:D:177:ILE:H	1.72	0.55
1:A:162:ALA:O	1:A:172:SER:HA	2.07	0.55
2:B:80:ILE:CG1	2:B:177:ILE:HG12	2.24	0.55
1:C:48:TYR:OH	1:C:252:VAL:HG12	2.07	0.55
1:C:897:GLN:HE21	2:D:184:LEU:H	1.53	0.55
1:A:260:MET:CE	1:A:712:VAL:CG2	2.83	0.55
1:C:312:GLU:HA	1:C:315:ILE:CG2	2.37	0.55
1:C:374:LEU:O	1:C:592:VAL:HG21	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:795:LEU:HD13	1:C:915:PHE:CD2	2.42	0.55
1:A:527:LEU:C	1:A:529:ASP:H	2.14	0.54
1:A:796:GLY:CA	1:A:912:HIS:CE1	2.90	0.54
1:A:909:PHE:CE2	1:A:972:ARG:HD3	2.42	0.54
1:C:527:LEU:C	1:C:529:ASP:H	2.15	0.54
1:C:611:GLY:C	1:C:685:ARG:HA	2.31	0.54
2:D:66:PRO:HG2	2:D:69:GLN:HG2	1.89	0.54
1:A:284:PHE:CD1	1:A:838:VAL:HG21	2.41	0.54
1:A:361:GLY:HA2	1:A:755:VAL:HG23	1.88	0.54
1:A:850:ILE:HD12	1:A:991:ILE:HG23	1.88	0.54
2:B:80:ILE:HD11	2:B:177:ILE:H	1.72	0.54
2:B:173:LYS:HG2	2:B:264:THR:C	2.32	0.54
2:B:204:TYR:CE1	2:B:235:TYR:CZ	2.88	0.54
1:C:51:ASP:HB3	1:C:55:GLY:H	1.73	0.54
1:C:318:ILE:O	1:C:318:ILE:HG13	2.08	0.54
2:D:81:PRO:HG2	2:D:176:VAL:HG13	1.90	0.54
2:D:302:LYS:O	2:D:303:SER:HB2	2.06	0.54
2:B:246:TYR:O	2:B:250:LEU:HB2	2.07	0.54
2:B:302:LYS:O	2:B:303:SER:HB2	2.07	0.54
1:C:52:LEU:HG	1:C:199:ILE:CD1	2.31	0.54
1:C:802:CYS:HB3	1:C:916:PHE:HE2	1.72	0.54
2:D:37:LEU:HD23	2:D:37:LEU:O	2.07	0.54
2:B:90:PHE:CZ	2:B:174:PRO:CG	2.89	0.54
2:B:94:ASP:HB2	2:B:97:SER:CB	2.31	0.54
2:B:264:THR:CG2	2:B:265:ASN:N	2.70	0.54
1:C:166:ARG:O	1:C:167:ASN:HB2	2.07	0.54
1:C:803:ILE:HD13	1:C:807:THR:OG1	2.07	0.54
1:C:876:LEU:HD23	1:C:879:LEU:HD12	1.88	0.54
1:C:1000:LEU:C	1:C:1000:LEU:HD13	2.33	0.54
2:D:178:ILE:HD12	2:D:211:VAL:HG11	1.89	0.54
1:A:35:ASP:OD2	1:A:229:PRO:HB3	2.08	0.54
1:A:857:GLY:HA2	1:A:987:TYR:CD1	2.42	0.54
2:B:37:LEU:O	2:B:37:LEU:HD23	2.08	0.54
2:B:143:ARG:HB2	2:B:146:ARG:NH2	2.23	0.54
1:C:514:ILE:HD11	1:C:523:LEU:HG	1.89	0.54
1:C:551:LEU:HD23	1:C:552:PHE:N	2.23	0.54
1:C:1008:GLY:N	1:C:1012:LYS:HE2	2.22	0.54
2:D:92:PRO:HD2	2:D:303:SER:CB	2.36	0.54
1:A:616:THR:O	1:A:619:ALA:HB3	2.08	0.54
1:A:887:TRP:O	1:A:889:ASN:ND2	2.37	0.54
2:B:157:GLY:C	2:B:159:CYS:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:73:ALA:CB	2:D:74:PRO:HD3	2.30	0.54
1:A:29:LYS:O	1:A:689:GLN:HG2	2.08	0.54
1:A:413:ALA:O	1:A:417:ILE:HG13	2.08	0.54
1:A:775:SER:O	1:A:779:GLU:HG3	2.08	0.54
1:A:909:PHE:CZ	1:A:972:ARG:HD3	2.43	0.54
2:B:130:PRO:CG	2:B:204:TYR:CE2	2.90	0.54
1:C:611:GLY:HA2	1:C:686:THR:H	1.73	0.54
1:C:790:ASN:CB	1:C:878:GLY:HA2	2.38	0.54
1:C:967:MET:CE	1:C:971:LEU:HD12	2.38	0.54
1:A:312:GLU:HA	1:A:315:ILE:CG2	2.36	0.54
1:A:369:PHD:HB2	1:A:373:THR:OG1	2.07	0.54
1:A:797:THR:OG1	4:A:1:OBN:C15	2.55	0.54
2:B:80:ILE:CD1	2:B:177:ILE:HG23	2.38	0.54
1:C:947:LEU:HD23	1:C:947:LEU:C	2.33	0.54
1:A:56:LEU:HD12	1:A:56:LEU:H	1.72	0.54
1:A:78:THR:C	1:A:80:PRO:HD3	2.32	0.54
1:A:559:PRO:HD2	1:A:562:PHE:HD1	1.72	0.54
1:A:802:CYS:HB3	1:A:916:PHE:HE2	1.72	0.54
2:B:33:PHE:CE2	2:B:37:LEU:HD12	2.43	0.54
2:B:117:GLN:HB3	2:B:123:PHE:CE2	2.42	0.54
1:C:547:GLY:HA2	1:C:581:LEU:HD23	1.89	0.54
1:A:763:ASP:O	1:A:766:LYS:HB2	2.07	0.54
2:B:120:ASP:O	2:B:123:PHE:N	2.41	0.54
1:C:361:GLY:HA2	1:C:755:VAL:HG23	1.89	0.54
1:C:413:ALA:O	1:C:417:ILE:HG13	2.07	0.54
1:A:404:PHE:HD2	1:A:404:PHE:N	1.96	0.53
1:C:763:ASP:O	1:C:766:LYS:HB2	2.09	0.53
1:C:850:ILE:HD12	1:C:991:ILE:HG23	1.90	0.53
1:C:853:ILE:HD13	1:C:990:LEU:HD22	1.87	0.53
1:C:868:GLU:HA	2:D:67:THR:HG23	1.88	0.53
1:A:37:HIS:CD2	1:A:37:HIS:N	2.75	0.53
2:B:65:LYS:HE3	2:B:69:GLN:HE22	1.73	0.53
1:C:667:THR:HG22	1:C:670:GLN:NE2	2.21	0.53
1:A:790:ASN:CB	1:A:878:GLY:HA2	2.37	0.53
1:A:980:TRP:CE3	1:A:980:TRP:HA	2.44	0.53
1:C:331:ALA:O	1:C:335:VAL:HG23	2.07	0.53
1:C:783:PHE:CZ	4:C:1:OBN:H17	2.43	0.53
2:B:213:CYS:O	2:B:227:MET:SD	2.67	0.53
1:C:326:PRO:CB	1:C:329:LEU:HB2	2.39	0.53
1:A:192:ILE:HG22	1:A:194:ALA:O	2.08	0.53
1:A:420:LEU:CD1	1:A:463:MET:HB3	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:ILE:HD13	1:A:780:ILE:HD12	1.89	0.53
1:C:35:ASP:HB2	1:C:229:PRO:HG3	1.90	0.53
1:C:52:LEU:CG	1:C:199:ILE:HD12	2.32	0.53
1:C:54:ARG:HG3	1:C:54:ARG:NH1	2.08	0.53
1:C:688:PRO:HB2	1:C:689:GLN:OE1	2.09	0.53
1:C:853:ILE:HD13	1:C:990:LEU:HD21	1.91	0.53
1:A:725:VAL:HG22	1:A:741:MET:HB2	1.91	0.53
2:B:183:VAL:CB	2:B:186:PHE:HB2	2.38	0.53
1:C:197:ARG:HG2	1:C:235:ILE:CD1	2.38	0.53
1:C:321:ILE:CD1	1:C:322:VAL:HG23	2.39	0.53
1:C:980:TRP:HA	1:C:980:TRP:CE3	2.43	0.53
2:D:31:SER:HA	2:D:34:LYS:HG3	1.91	0.53
2:D:183:VAL:CB	2:D:186:PHE:HB2	2.37	0.53
1:A:667:THR:HG22	1:A:670:GLN:NE2	2.24	0.53
1:A:755:VAL:HG22	1:A:825:MET:HE1	1.90	0.53
1:A:968:GLY:HA2	1:A:973:MET:O	2.08	0.53
1:C:118:PRO:CG	4:C:1:OBN:C19	2.78	0.53
1:C:612:ASP:OD2	1:C:613:HIS:N	2.37	0.53
1:C:967:MET:HE1	1:C:971:LEU:HD12	1.91	0.53
1:A:52:LEU:HG	1:A:199:ILE:CD1	2.31	0.53
2:B:212:HIS:CD2	2:B:213:CYS:N	2.77	0.53
1:C:675:LEU:HD23	1:C:698:CYS:SG	2.49	0.53
1:C:909:PHE:CZ	1:C:972:ARG:HD3	2.43	0.53
1:A:467:TYR:CE1	1:A:489:PRO:HG3	2.44	0.53
1:A:911:CYS:C	1:A:914:PRO:HD2	2.33	0.53
1:A:952:PHE:HE2	3:G:40:VAL:HG11	1.74	0.53
1:C:29:LYS:HB2	1:C:266:LEU:HD13	1.91	0.53
1:C:309:THR:HG23	1:C:311:LEU:H	1.74	0.53
1:C:755:VAL:HG22	1:C:825:MET:HE1	1.90	0.53
1:C:968:GLY:HA2	1:C:973:MET:O	2.09	0.53
1:A:166:ARG:O	1:A:167:ASN:HB2	2.09	0.52
1:C:315:ILE:HD12	1:C:318:ILE:HG21	1.91	0.52
1:C:350:LEU:HG	1:C:351:VAL:N	2.24	0.52
2:D:117:GLN:HB3	2:D:123:PHE:CE2	2.44	0.52
1:A:52:LEU:CG	1:A:199:ILE:HD12	2.32	0.52
1:A:331:ALA:O	1:A:335:VAL:HG23	2.09	0.52
2:B:81:PRO:HG2	2:B:176:VAL:HG13	1.90	0.52
1:C:95:MET:HA	1:C:95:MET:CE	2.33	0.52
1:A:321:ILE:CD1	1:A:322:VAL:HG23	2.39	0.52
1:A:967:MET:HE1	1:A:971:LEU:HD12	1.91	0.52
2:B:173:LYS:CE	2:B:264:THR:O	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:173:LYS:O	2:B:262:GLN:HG3	2.08	0.52
1:C:35:ASP:OD2	1:C:229:PRO:CB	2.58	0.52
1:C:54:ARG:CD	1:C:168:GLY:CA	2.87	0.52
1:C:467:TYR:CE1	1:C:489:PRO:HG3	2.45	0.52
1:C:839:ASN:ND2	1:C:841:GLN:HB2	2.24	0.52
1:C:1009:TRP:CD2	1:C:1009:TRP:O	2.62	0.52
1:A:550:HIS:CD2	1:A:550:HIS:C	2.87	0.52
2:B:49:ILE:O	2:B:53:THR:HG23	2.10	0.52
1:A:612:ASP:CG	1:A:613:HIS:H	2.17	0.52
2:B:193:ASN:HA	2:B:203:LYS:NZ	2.25	0.52
1:C:288:ILE:HG22	1:C:289:THR:N	2.24	0.52
1:C:783:PHE:CE1	4:C:1:OBN:C16	2.92	0.52
1:C:818:GLU:OE1	1:C:931:LYS:HG3	2.10	0.52
4:C:1:OBN:O11	4:C:1:OBN:H1	2.09	0.52
2:D:132:GLU:HB3	2:D:207:TYR:CE1	2.44	0.52
2:D:265:ASN:C	2:D:266:LEU:HD23	2.31	0.52
1:A:288:ILE:HG22	1:A:289:THR:N	2.23	0.52
2:B:71:ARG:NH2	3:G:23:TYR:CZ	2.76	0.52
1:C:42:ASP:C	1:C:42:ASP:OD1	2.52	0.52
1:C:93:PHE:CD2	1:C:330:LEU:HD22	2.44	0.52
1:C:165:ILE:HB	1:C:183:LEU:HB3	1.92	0.52
1:C:821:GLU:OE1	1:C:933:ARG:N	2.42	0.52
2:D:204:TYR:CD2	2:D:208:VAL:HB	2.44	0.52
1:A:725:VAL:HG22	1:A:741:MET:CB	2.39	0.52
1:A:817:TYR:CD1	1:A:817:TYR:N	2.78	0.52
2:B:31:SER:HA	2:B:34:LYS:HG3	1.92	0.52
2:D:173:LYS:CG	2:D:263:PHE:O	2.57	0.52
2:D:202:MET:CG	2:D:203:LYS:H	2.12	0.52
1:A:238:PHE:CD1	1:A:239:SER:N	2.78	0.52
1:A:318:ILE:HG13	1:A:318:ILE:O	2.09	0.52
1:A:351:VAL:HG12	1:A:353:ASN:H	1.75	0.52
1:A:384:MET:HG2	1:A:582:ILE:CG2	2.36	0.52
1:A:783:PHE:HZ	4:A:1:OBN:H122	1.73	0.52
1:A:824:ILE:HG22	1:A:827:ARG:CZ	2.40	0.52
1:C:37:HIS:CD2	1:C:37:HIS:N	2.77	0.52
1:C:420:LEU:CD1	1:C:463:MET:HB3	2.39	0.52
1:C:824:ILE:HG22	1:C:827:ARG:CZ	2.39	0.52
2:D:159:CYS:CB	2:D:175:CYS:SG	2.97	0.52
2:D:226:THR:HG23	2:D:264:THR:H	1.75	0.52
1:A:838:VAL:O	1:A:838:VAL:HG12	2.09	0.52
2:D:90:PHE:CE1	2:D:301:VAL:HG12	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:143:ARG:HB2	2:D:146:ARG:NH2	2.25	0.52
1:C:965:PRO:HD3	3:E:31:LEU:HD11	1.92	0.52
2:D:183:VAL:HB	2:D:186:PHE:CB	2.38	0.52
1:A:913:THR:O	1:A:916:PHE:HB3	2.10	0.51
1:A:1008:GLY:N	1:A:1012:LYS:HE2	2.24	0.51
2:B:207:TYR:O	2:B:208:VAL:HG23	2.11	0.51
1:C:857:GLY:HA2	1:C:987:TYR:CD1	2.45	0.51
1:C:995:ASP:O	1:C:999:LYS:HG3	2.10	0.51
2:D:33:PHE:CE2	2:D:37:LEU:HD12	2.46	0.51
1:A:947:LEU:HD23	1:A:947:LEU:C	2.34	0.51
1:A:1009:TRP:CD2	1:A:1009:TRP:O	2.63	0.51
2:B:178:ILE:HD12	2:B:211:VAL:HG11	1.89	0.51
1:C:192:ILE:HG22	1:C:194:ALA:O	2.10	0.51
2:D:41:ILE:O	2:D:41:ILE:HG22	2.11	0.51
1:A:52:LEU:O	1:A:52:LEU:HD23	2.11	0.51
1:A:315:ILE:HD12	1:A:318:ILE:HG21	1.92	0.51
1:A:381:VAL:HB	1:A:452:CYS:SG	2.51	0.51
1:A:515:LEU:HB2	1:A:577:CYS:SG	2.50	0.51
1:C:52:LEU:O	1:C:52:LEU:HD23	2.10	0.51
1:C:71:ASN:HD22	1:C:255:GLY:H	1.59	0.51
1:C:980:TRP:HA	1:C:980:TRP:HE3	1.74	0.51
2:D:91:ARG:HA	2:D:302:LYS:O	2.11	0.51
2:D:146:ARG:HB2	2:D:251:GLN:CG	2.40	0.51
1:A:51:ASP:HB3	1:A:55:GLY:H	1.75	0.51
1:A:608:MET:HE3	1:A:626:ILE:HD12	1.92	0.51
2:B:173:LYS:HG2	2:B:264:THR:O	2.10	0.51
2:B:183:VAL:HB	2:B:186:PHE:CB	2.39	0.51
2:D:119:ASP:C	2:D:121:MET:N	2.67	0.51
2:D:213:CYS:O	2:D:227:MET:SD	2.68	0.51
2:B:130:PRO:CB	2:B:204:TYR:OH	2.58	0.51
1:C:612:ASP:CG	1:C:613:HIS:H	2.16	0.51
1:A:56:LEU:HD11	1:A:182:ASP:CB	2.39	0.51
1:A:93:PHE:CE1	1:A:284:PHE:HD2	2.29	0.51
1:A:151:MET:O	1:A:151:MET:HG2	2.11	0.51
1:A:689:GLN:O	1:A:692:LEU:HB3	2.10	0.51
1:A:821:GLU:OE1	1:A:933:ARG:N	2.44	0.51
2:D:170:LYS:HD3	2:D:173:LYS:H	1.76	0.51
2:D:204:TYR:CE1	2:D:235:TYR:CZ	2.95	0.51
1:A:45:HIS:HD2	1:A:50:THR:O	1.94	0.51
1:A:531:PHE:CD1	1:A:531:PHE:C	2.88	0.51
2:B:88:ILE:HB	2:B:299:ILE:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:321:ILE:HD12	1:C:322:VAL:HG23	1.92	0.51
1:C:468:THR:HG22	1:C:487:LYS:HB2	1.93	0.51
1:C:608:MET:HE3	1:C:626:ILE:HD12	1.93	0.51
1:A:54:ARG:CD	1:A:168:GLY:CA	2.89	0.51
1:A:76:PRO:O	1:A:78:THR:N	2.40	0.51
1:A:591:ALA:O	1:A:592:VAL:C	2.52	0.51
1:C:550:HIS:C	1:C:550:HIS:CD2	2.89	0.51
1:C:796:GLY:CA	1:C:912:HIS:CE1	2.93	0.51
1:A:215:SER:O	1:A:216:GLU:C	2.52	0.51
1:A:1011:GLU:O	1:A:1015:TYR:CB	2.59	0.51
2:B:130:PRO:HD2	2:B:204:TYR:OH	2.11	0.51
2:B:226:THR:HG23	2:B:264:THR:H	1.75	0.51
1:C:495:ARG:CD	1:C:553:LEU:O	2.59	0.51
1:C:873:PRO:O	1:C:876:LEU:HB2	2.11	0.51
2:B:90:PHE:CE1	2:B:174:PRO:HG2	2.45	0.51
1:C:531:PHE:CD1	1:C:531:PHE:C	2.89	0.51
2:D:274:ILE:HD12	2:D:299:ILE:HD11	1.93	0.51
1:A:321:ILE:HD12	1:A:322:VAL:HG23	1.92	0.50
2:B:90:PHE:CE1	2:B:301:VAL:HG12	2.45	0.50
2:B:207:TYR:CB	2:B:240:LEU:HB2	2.24	0.50
1:C:54:ARG:HD3	1:C:168:GLY:HA3	1.92	0.50
1:C:791:ILE:HG22	1:C:876:LEU:O	2.11	0.50
1:C:817:TYR:N	1:C:817:TYR:CD1	2.78	0.50
1:C:900:THR:HG23	1:C:903:GLN:OE1	2.11	0.50
1:A:281:ILE:CG2	1:A:282:GLU:N	2.75	0.50
1:A:868:GLU:HA	2:B:67:THR:HG23	1.93	0.50
2:B:41:ILE:HG22	2:B:41:ILE:O	2.11	0.50
2:B:184:LEU:HD21	2:B:247:GLY:CA	2.41	0.50
2:D:81:PRO:HG2	2:D:176:VAL:HG22	1.92	0.50
1:A:197:ARG:HG2	1:A:235:ILE:CD1	2.40	0.50
1:A:322:VAL:HB	4:A:1:OBN:O23	2.10	0.50
1:A:977:LYS:O	1:A:980:TRP:HB2	2.11	0.50
2:B:90:PHE:HB2	2:B:97:SER:O	2.12	0.50
1:C:1013:GLU:OE2	2:D:35:ILE:HD11	2.11	0.50
1:A:35:ASP:OD2	1:A:229:PRO:CB	2.58	0.50
1:A:141:TYR:C	1:A:141:TYR:CD2	2.89	0.50
1:A:839:ASN:ND2	1:A:841:GLN:HB2	2.27	0.50
1:A:980:TRP:HA	1:A:980:TRP:HE3	1.75	0.50
1:C:270:LEU:O	1:C:719:LYS:HE3	2.11	0.50
1:C:515:LEU:HB2	1:C:577:CYS:SG	2.51	0.50
1:C:962:SER:OG	1:C:975:PRO:HA	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1013:GLU:OE2	2:D:35:ILE:CD1	2.59	0.50
2:D:88:ILE:HB	2:D:299:ILE:HG22	1.93	0.50
2:D:207:TYR:CB	2:D:240:LEU:HB2	2.24	0.50
1:A:143:GLN:OE1	1:A:143:GLN:HA	2.12	0.50
1:A:571:PHE:HB2	1:A:572:PRO:CD	2.41	0.50
1:A:790:ASN:C	1:A:880:ARG:HG2	2.37	0.50
2:B:146:ARG:HB2	2:B:251:GLN:CG	2.41	0.50
2:B:226:THR:HG23	2:B:226:THR:O	2.12	0.50
1:C:56:LEU:HD11	1:C:182:ASP:CB	2.38	0.50
1:C:238:PHE:CD1	1:C:239:SER:N	2.79	0.50
1:C:616:THR:O	1:C:619:ALA:HB3	2.11	0.50
2:B:155:TRP:CD2	2:B:232:LEU:HD22	2.47	0.50
1:C:103:LEU:O	1:C:318:ILE:HD11	2.12	0.50
1:C:247:ALA:O	1:C:248:ARG:HG3	2.12	0.50
1:C:612:ASP:CG	1:C:613:HIS:N	2.70	0.50
1:C:807:THR:HB	1:C:954:GLU:CG	2.21	0.50
2:D:184:LEU:HD21	2:D:247:GLY:CA	2.41	0.50
1:A:165:ILE:HB	1:A:183:LEU:HB3	1.92	0.50
1:A:271:GLU:OE1	1:A:271:GLU:HA	2.12	0.50
1:C:80:PRO:O	1:C:81:GLU:HG2	2.12	0.50
1:A:447:SER:O	1:A:451:LYS:HG3	2.12	0.50
1:A:495:ARG:CD	1:A:553:LEU:O	2.60	0.50
1:A:910:THR:O	1:A:910:THR:CG2	2.59	0.50
1:C:326:PRO:HB3	1:C:329:LEU:HB2	1.92	0.50
1:C:591:ALA:O	1:C:592:VAL:C	2.54	0.50
2:D:226:THR:HG23	2:D:226:THR:O	2.12	0.50
1:A:326:PRO:CB	1:A:329:LEU:HB2	2.42	0.50
1:A:329:LEU:HD11	1:A:769:ILE:HD13	1.93	0.50
1:C:54:ARG:CD	1:C:168:GLY:HA3	2.42	0.50
1:C:141:TYR:C	1:C:141:TYR:CD2	2.90	0.50
2:D:65:LYS:HE3	2:D:69:GLN:HE22	1.76	0.50
2:D:129:VAL:CB	2:D:130:PRO:HD2	2.37	0.50
1:A:915:PHE:C	1:A:918:THR:HG22	2.37	0.49
2:B:101:TYR:O	2:B:105:ILE:HD13	2.11	0.49
1:C:228:ASN:C	1:C:230:LEU:N	2.70	0.49
1:C:351:VAL:HG12	1:C:353:ASN:H	1.76	0.49
1:C:671:LEU:O	1:C:675:LEU:HD13	2.12	0.49
1:C:889:ASN:CG	2:D:291:PHE:CD2	2.90	0.49
1:C:913:THR:O	1:C:916:PHE:HB3	2.12	0.49
2:D:157:GLY:C	2:D:159:CYS:H	2.19	0.49
1:A:748:PHE:O	1:A:751:ILE:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:817:TYR:N	1:A:817:TYR:HD1	2.10	0.49
1:A:871:PHE:HZ	1:A:899:TRP:CD1	2.30	0.49
1:A:900:THR:HG23	1:A:903:GLN:OE1	2.12	0.49
2:B:191:PRO:HD3	2:B:280:GLY:HA2	1.93	0.49
1:C:281:ILE:CG2	1:C:282:GLU:N	2.74	0.49
1:C:559:PRO:CD	1:C:562:PHE:HB2	2.41	0.49
1:C:712:VAL:C	1:C:714:ASP:H	2.20	0.49
1:C:1008:GLY:H	1:C:1012:LYS:HG3	1.77	0.49
1:C:1011:GLU:O	1:C:1015:TYR:CB	2.58	0.49
2:D:49:ILE:O	2:D:53:THR:HG23	2.12	0.49
2:D:213:CYS:O	2:D:227:MET:HE1	2.13	0.49
1:A:559:PRO:CD	1:A:562:PHE:HB2	2.42	0.49
2:B:157:GLY:C	2:B:159:CYS:N	2.70	0.49
1:C:370:LYS:HB2	1:C:610:THR:HB	1.93	0.49
1:C:460:VAL:HA	1:C:463:MET:HE3	1.94	0.49
1:C:471:VAL:HG21	1:C:564:PHE:HB2	1.94	0.49
1:C:708:THR:HA	1:C:725:VAL:O	2.12	0.49
1:C:775:SER:O	1:C:779:GLU:HG3	2.12	0.49
1:C:871:PHE:HZ	1:C:899:TRP:CD1	2.29	0.49
1:A:228:ASN:C	1:A:230:LEU:N	2.69	0.49
1:A:995:ASP:O	1:A:999:LYS:HG3	2.12	0.49
1:C:93:PHE:CE1	1:C:284:PHE:HD2	2.29	0.49
1:C:792:PRO:O	1:C:794:PRO:HD3	2.12	0.49
1:C:817:TYR:N	1:C:817:TYR:HD1	2.10	0.49
1:A:195:ASP:HB2	1:A:253:TYR:CB	2.35	0.49
1:A:270:LEU:O	1:A:719:LYS:HE3	2.13	0.49
1:A:743:LEU:HD11	1:A:751:ILE:HD11	1.94	0.49
2:B:73:ALA:CB	2:B:74:PRO:HD3	2.32	0.49
1:C:980:TRP:O	1:C:983:CYS:SG	2.68	0.49
1:A:659:HIS:CE1	1:A:685:ARG:HG2	2.48	0.49
1:A:1008:GLY:H	1:A:1012:LYS:HG3	1.77	0.49
1:C:360:LEU:HD13	1:C:723:ILE:CD1	2.42	0.49
1:C:797:THR:OG1	4:C:1:OBN:O14	2.28	0.49
1:C:850:ILE:HG21	1:C:926:ASP:OD1	2.12	0.49
2:D:83:SER:O	2:D:84:GLN:C	2.56	0.49
1:A:37:HIS:HB3	1:A:235:ILE:HD11	1.94	0.49
1:C:92:GLY:O	1:C:95:MET:HB2	2.13	0.49
1:C:659:HIS:CE1	1:C:685:ARG:HG2	2.47	0.49
1:C:818:GLU:CD	1:C:931:LYS:HG3	2.37	0.49
1:A:54:ARG:CD	1:A:168:GLY:HA3	2.43	0.49
1:A:612:ASP:CG	1:A:613:HIS:N	2.70	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:226:THR:HG21	2:B:264:THR:HG22	1.95	0.49
1:C:277:ILE:HG23	1:C:278:ALA:N	2.27	0.49
1:C:750:SER:O	1:C:754:GLY:N	2.45	0.49
2:D:90:PHE:HB2	2:D:97:SER:O	2.13	0.49
1:A:63:GLU:C	1:A:65:LEU:H	2.19	0.49
1:A:468:THR:HG22	1:A:487:LYS:HB2	1.93	0.49
1:A:799:THR:HG23	1:A:916:PHE:HB2	1.95	0.49
1:A:803:ILE:HD13	1:A:807:THR:OG1	2.12	0.49
2:B:119:ASP:C	2:B:121:MET:N	2.68	0.49
2:B:132:GLU:HB3	2:B:207:TYR:CE1	2.47	0.49
2:B:267:THR:HG23	2:B:269:ASP:H	1.76	0.49
1:C:127:VAL:O	1:C:130:SER:HB3	2.13	0.49
1:C:559:PRO:HD2	1:C:562:PHE:HD1	1.73	0.49
1:A:370:LYS:HB2	1:A:610:THR:HB	1.95	0.49
1:A:924:TRP:HA	1:A:951:LEU:HD21	1.95	0.49
1:C:381:VAL:HB	1:C:452:CYS:SG	2.53	0.49
1:C:799:THR:HG23	1:C:916:PHE:HB2	1.95	0.49
2:D:172:GLY:O	2:D:173:LYS:HD2	2.13	0.49
2:D:267:THR:HG23	2:D:269:ASP:H	1.77	0.49
1:A:42:ASP:C	1:A:42:ASP:OD1	2.56	0.48
1:A:299:PHE:CE2	1:A:784:LEU:HD22	2.48	0.48
1:A:309:THR:HG23	1:A:311:LEU:H	1.77	0.48
1:A:565:ASP:OD2	1:A:568:ASP:HB2	2.12	0.48
1:A:991:ILE:O	1:A:992:PHE:C	2.56	0.48
2:B:171:ASP:OD1	2:B:172:GLY:N	2.46	0.48
1:C:131:ALA:O	1:C:135:ILE:HG12	2.13	0.48
1:C:480:LYS:CB	1:C:506:ARG:NH1	2.76	0.48
1:A:92:GLY:O	1:A:95:MET:HB2	2.13	0.48
1:A:125:LEU:HD21	1:A:322:VAL:HG22	1.96	0.48
1:A:127:VAL:O	1:A:130:SER:HB3	2.13	0.48
1:A:350:LEU:HG	1:A:351:VAL:N	2.28	0.48
1:A:506:ARG:CG	1:A:506:ARG:NH1	2.72	0.48
1:A:548:PHE:CE1	1:A:582:ILE:HG12	2.49	0.48
1:A:712:VAL:C	1:A:714:ASP:H	2.21	0.48
1:A:733:ASP:O	1:A:736:LYS:HB2	2.13	0.48
1:A:850:ILE:HG21	1:A:926:ASP:OD1	2.13	0.48
1:C:82:TRP:C	1:C:84:LYS:N	2.69	0.48
1:C:93:PHE:CE1	1:C:284:PHE:CD2	3.01	0.48
1:C:805:LEU:HA	1:C:809:MET:HG2	1.95	0.48
2:D:184:LEU:CD2	2:D:247:GLY:H	2.25	0.48
1:A:93:PHE:CE1	1:A:284:PHE:CD2	3.00	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:LEU:CD1	2:B:180:LEU:HD12	2.43	0.48
2:B:229:TYR:CD1	2:B:261:VAL:HG22	2.48	0.48
1:C:37:HIS:HB3	1:C:235:ILE:HD11	1.95	0.48
1:C:781:THR:HA	1:C:784:LEU:HD12	1.95	0.48
1:C:797:THR:HG1	4:C:1:OBN:HOF	1.60	0.48
1:C:898:GLN:HE21	2:D:182:ARG:N	2.09	0.48
1:C:947:LEU:HD23	1:C:947:LEU:O	2.13	0.48
2:B:213:CYS:O	2:B:227:MET:HE1	2.13	0.48
1:C:63:GLU:C	1:C:65:LEU:H	2.20	0.48
1:C:548:PHE:CE1	1:C:582:ILE:HG12	2.48	0.48
1:C:879:LEU:O	1:C:880:ARG:C	2.56	0.48
1:A:852:MET:HE3	2:B:43:TYR:OH	2.13	0.48
1:A:860:PHE:CZ	2:B:57:MET:HG3	2.49	0.48
2:B:193:ASN:HA	2:B:203:LYS:HZ3	1.77	0.48
1:C:84:LYS:HA	1:C:84:LYS:HD2	1.48	0.48
1:C:508:LEU:HD11	1:C:528:LYS:HG3	1.95	0.48
1:C:915:PHE:C	1:C:918:THR:HG22	2.37	0.48
1:C:1000:LEU:HD23	1:C:1003:ARG:HH21	1.78	0.48
2:B:91:ARG:HA	2:B:302:LYS:O	2.12	0.48
2:D:101:TYR:O	2:D:105:ILE:HD13	2.13	0.48
1:A:691:LYS:CB	1:A:717:ALA:HB2	2.43	0.48
4:A:1:OBN:H1	4:A:1:OBN:O11	2.13	0.48
2:B:129:VAL:CB	2:B:130:PRO:HD2	2.43	0.48
1:C:238:PHE:CD2	1:C:260:MET:CB	2.91	0.48
1:C:260:MET:HE1	1:C:712:VAL:CB	2.42	0.48
1:C:506:ARG:NH1	1:C:506:ARG:HG3	2.25	0.48
1:C:691:LYS:CB	1:C:717:ALA:HB2	2.43	0.48
1:C:819:GLN:H	1:C:819:GLN:CD	2.21	0.48
1:C:963:TYR:O	3:E:31:LEU:HD21	2.14	0.48
2:D:204:TYR:O	2:D:206:PRO:CD	2.56	0.48
1:A:121:ASP:OD1	4:A:1:OBN:H72	2.14	0.48
1:A:471:VAL:HG21	1:A:564:PHE:HB2	1.95	0.48
1:A:585:ILE:O	1:A:587:PRO:CD	2.56	0.48
1:C:51:ASP:HB3	1:C:55:GLY:N	2.28	0.48
1:C:611:GLY:O	1:C:685:ARG:HD2	2.14	0.48
1:C:838:VAL:HG12	1:C:838:VAL:O	2.13	0.48
2:D:212:HIS:CD2	2:D:213:CYS:N	2.81	0.48
2:D:226:THR:HG21	2:D:264:THR:HG22	1.95	0.48
1:A:323:ALA:O	1:A:776:ASN:ND2	2.46	0.48
1:A:750:SER:O	1:A:754:GLY:N	2.47	0.48
1:A:873:PRO:O	1:A:876:LEU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:TRP:C	1:C:84:LYS:H	2.22	0.48
1:C:271:GLU:OE1	1:C:271:GLU:HA	2.14	0.48
1:C:508:LEU:O	1:C:508:LEU:HD13	2.14	0.48
1:C:565:ASP:OD2	1:C:568:ASP:HB2	2.13	0.48
1:C:990:LEU:HD11	2:D:49:ILE:HD13	1.95	0.48
2:D:155:TRP:CD2	2:D:232:LEU:HD22	2.48	0.48
1:A:142:TYR:O	1:A:146:LYS:HG2	2.14	0.48
1:A:853:ILE:HD13	1:A:990:LEU:HD21	1.92	0.48
1:C:195:ASP:CG	1:C:258:THR:HB	2.38	0.48
1:C:790:ASN:C	1:C:880:ARG:HG2	2.39	0.48
2:D:209:LEU:O	2:D:237:GLY:HA2	2.14	0.48
1:A:879:LEU:O	1:A:880:ARG:C	2.57	0.47
3:G:17:ASP:C	3:G:19:PHE:H	2.22	0.47
1:C:48:TYR:CE2	1:C:252:VAL:HG13	2.49	0.47
1:C:63:GLU:C	1:C:65:LEU:N	2.72	0.47
1:C:192:ILE:HG13	1:C:240:THR:OG1	2.14	0.47
1:C:281:ILE:HG23	1:C:282:GLU:N	2.29	0.47
1:C:480:LYS:HB3	1:C:506:ARG:HG3	1.96	0.47
1:C:924:TRP:HA	1:C:951:LEU:HD21	1.95	0.47
1:C:984:ALA:O	1:C:985:PHE:C	2.57	0.47
2:D:204:TYR:O	2:D:205:ASN:C	2.56	0.47
1:A:42:ASP:CG	1:A:43:GLU:N	2.71	0.47
1:A:118:PRO:CB	4:A:1:OBN:H192	2.42	0.47
1:A:316:PHE:O	1:A:319:GLY:N	2.47	0.47
1:A:624:VAL:CG2	1:A:626:ILE:HG13	2.44	0.47
1:A:687:SER:O	1:A:688:PRO:C	2.57	0.47
1:A:819:GLN:CD	1:A:819:GLN:H	2.22	0.47
1:C:98:TRP:CD1	1:C:133:VAL:HG21	2.48	0.47
1:C:329:LEU:HD11	1:C:769:ILE:HD13	1.96	0.47
1:C:447:SER:O	1:C:451:LYS:HG3	2.13	0.47
1:C:970:ALA:O	1:C:971:LEU:HD23	2.14	0.47
1:A:63:GLU:C	1:A:65:LEU:N	2.72	0.47
1:A:255:GLY:O	1:A:258:THR:HG23	2.13	0.47
1:A:805:LEU:HA	1:A:809:MET:HG2	1.97	0.47
1:C:253:TYR:HB3	1:C:258:THR:HA	1.96	0.47
1:C:323:ALA:O	1:C:776:ASN:ND2	2.46	0.47
1:A:228:ASN:O	1:A:230:LEU:N	2.47	0.47
1:A:488:ASN:OD1	1:A:489:PRO:HD2	2.14	0.47
1:A:691:LYS:HB3	1:A:717:ALA:HB2	1.97	0.47
1:A:1016:TYR:CD1	1:A:1016:TYR:N	2.76	0.47
1:C:741:MET:O	1:C:742:ILE:HD13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:865:ILE:CD1	1:C:980:TRP:CD2	2.97	0.47
1:C:949:PHE:CD1	3:E:45:ILE:HG23	2.50	0.47
1:C:977:LYS:O	1:C:980:TRP:HB2	2.14	0.47
2:D:275:GLU:HB2	2:D:296:ASP:OD1	2.14	0.47
1:A:52:LEU:HD23	1:A:52:LEU:C	2.40	0.47
1:A:460:VAL:HA	1:A:463:MET:HE3	1.95	0.47
2:D:157:GLY:C	2:D:159:CYS:N	2.72	0.47
1:A:232:THR:HG21	1:A:235:ILE:HG12	1.96	0.47
1:A:281:ILE:HG23	1:A:282:GLU:N	2.29	0.47
1:A:427:GLN:OE1	1:A:441:ALA:HB2	2.15	0.47
1:A:611:GLY:O	1:A:685:ARG:HD2	2.15	0.47
1:A:825:MET:HA	1:A:825:MET:CE	2.40	0.47
1:C:91:GLY:O	1:C:92:GLY:C	2.57	0.47
1:C:143:GLN:OE1	1:C:143:GLN:HA	2.14	0.47
1:C:380:THR:HB	1:C:587:PRO:HG3	1.97	0.47
1:C:397:GLU:O	1:C:436:LEU:HD12	2.14	0.47
1:C:743:LEU:HD11	1:C:751:ILE:HD11	1.95	0.47
1:A:42:ASP:O	1:A:45:HIS:N	2.40	0.47
1:A:508:LEU:HD11	1:A:528:LYS:HG3	1.96	0.47
1:A:1000:LEU:HD23	1:A:1003:ARG:HH21	1.78	0.47
2:B:184:LEU:CD2	2:B:247:GLY:H	2.28	0.47
2:B:204:TYR:CE1	2:B:235:TYR:CE2	3.03	0.47
2:B:250:LEU:HD23	2:B:250:LEU:HA	1.74	0.47
1:C:82:TRP:O	1:C:84:LYS:N	2.47	0.47
1:C:299:PHE:CE2	1:C:784:LEU:HD22	2.50	0.47
1:C:488:ASN:OD1	1:C:489:PRO:HD2	2.14	0.47
1:C:691:LYS:HB3	1:C:717:ALA:HB2	1.95	0.47
2:D:77:LEU:CD1	2:D:180:LEU:HD12	2.45	0.47
2:D:120:ASP:O	2:D:123:PHE:O	2.33	0.47
2:D:124:GLU:CG	2:D:147:LYS:HD2	2.44	0.47
2:D:191:PRO:HD3	2:D:280:GLY:HA2	1.96	0.47
1:A:977:LYS:HD3	2:B:68:TYR:CZ	2.49	0.47
2:B:156:LEU:HD22	2:B:260:ALA:HB2	1.97	0.47
2:B:205:ASN:O	2:B:206:PRO:O	2.33	0.47
2:B:229:TYR:HD1	2:B:261:VAL:HG22	1.80	0.47
1:C:76:PRO:O	1:C:78:THR:N	2.47	0.47
1:C:79:THR:N	1:C:80:PRO:HD3	2.30	0.47
1:C:868:GLU:O	2:D:67:THR:HG23	2.15	0.47
1:C:949:PHE:CD2	1:C:949:PHE:C	2.92	0.47
2:B:205:ASN:O	2:B:206:PRO:C	2.57	0.47
1:A:860:PHE:CE1	2:B:53:THR:HB	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:PHE:CD1	1:C:285:ILE:HD11	2.43	0.47
1:C:689:GLN:O	1:C:692:LEU:HB3	2.15	0.47
1:C:733:ASP:O	1:C:736:LYS:HB2	2.15	0.47
2:D:187:LYS:O	2:D:189:LYS:HG3	2.15	0.47
2:D:207:TYR:HA	2:D:240:LEU:HD22	1.96	0.47
2:D:229:TYR:CD1	2:D:261:VAL:HG22	2.50	0.47
3:E:17:ASP:C	3:E:19:PHE:H	2.23	0.47
1:A:380:THR:HB	1:A:587:PRO:HG3	1.96	0.46
1:A:708:THR:HA	1:A:725:VAL:O	2.14	0.46
1:A:792:PRO:O	1:A:794:PRO:HD3	2.15	0.46
1:A:980:TRP:O	1:A:983:CYS:SG	2.70	0.46
2:B:202:MET:CG	2:B:203:LYS:N	2.78	0.46
3:G:36:LEU:HD23	3:G:36:LEU:HA	1.76	0.46
1:C:54:ARG:CG	1:C:54:ARG:NH1	2.71	0.46
1:C:915:PHE:HA	1:C:918:THR:HG22	1.97	0.46
1:A:93:PHE:HD2	1:A:330:LEU:HD22	1.77	0.46
1:A:508:LEU:O	1:A:508:LEU:HD13	2.14	0.46
1:A:781:THR:HA	1:A:784:LEU:HD12	1.96	0.46
1:A:970:ALA:O	1:A:971:LEU:HD23	2.15	0.46
2:B:83:SER:O	2:B:84:GLN:C	2.58	0.46
2:B:90:PHE:CZ	2:B:174:PRO:HG3	2.50	0.46
2:B:120:ASP:O	2:B:123:PHE:O	2.33	0.46
2:B:124:GLU:CG	2:B:147:LYS:HD2	2.42	0.46
1:C:468:THR:CG2	1:C:487:LYS:HB2	2.46	0.46
1:C:624:VAL:CG2	1:C:626:ILE:HG13	2.45	0.46
1:C:687:SER:O	1:C:688:PRO:C	2.57	0.46
1:C:910:THR:O	1:C:910:THR:CG2	2.62	0.46
2:D:156:LEU:HD22	2:D:260:ALA:HB2	1.97	0.46
1:A:612:ASP:O	1:A:685:ARG:N	2.48	0.46
1:A:741:MET:O	1:A:742:ILE:HD13	2.16	0.46
2:B:214:THR:O	2:B:274:ILE:HA	2.16	0.46
1:C:48:TYR:O	1:C:49:GLY:C	2.58	0.46
1:C:384:MET:HG2	1:C:582:ILE:CG2	2.38	0.46
1:C:443:ASP:OD1	1:C:446:GLU:HB2	2.16	0.46
1:C:571:PHE:HB2	1:C:572:PRO:CD	2.43	0.46
2:D:78:THR:O	2:D:295:PHE:HE2	1.99	0.46
1:A:192:ILE:HG13	1:A:240:THR:OG1	2.15	0.46
1:A:443:ASP:OD1	1:A:446:GLU:HB2	2.15	0.46
1:A:785:ILE:CD1	1:A:859:PHE:CZ	2.93	0.46
1:A:934:ARG:HB2	1:A:1015:TYR:CE1	2.51	0.46
1:A:934:ARG:HB2	1:A:1015:TYR:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:PHE:CZ	2:B:174:PRO:HG2	2.49	0.46
2:B:202:MET:CE	2:B:203:LYS:H	2.28	0.46
1:C:232:THR:HG21	1:C:235:ILE:HG12	1.97	0.46
1:C:916:PHE:CD1	1:C:916:PHE:C	2.94	0.46
1:C:948:ILE:HG22	1:C:949:PHE:N	2.30	0.46
2:D:159:CYS:SG	2:D:260:ALA:HB1	2.55	0.46
1:A:668:SER:HB2	1:A:700:ARG:CZ	2.46	0.46
1:A:790:ASN:OD1	1:A:880:ARG:HD3	2.16	0.46
1:C:52:LEU:HD23	1:C:52:LEU:C	2.41	0.46
1:C:118:PRO:HG3	4:C:1:OBN:H192	1.91	0.46
1:C:751:ILE:HD13	1:C:751:ILE:N	2.31	0.46
1:C:899:TRP:CZ3	2:D:71:ARG:HB3	2.49	0.46
2:D:177:ILE:CD1	2:D:258:LEU:HD22	2.46	0.46
1:A:91:GLY:O	1:A:92:GLY:C	2.57	0.46
1:A:321:ILE:CG1	1:A:322:VAL:H	2.29	0.46
2:B:226:THR:HG21	2:B:264:THR:CG2	2.46	0.46
1:C:71:ASN:HD22	1:C:255:GLY:N	2.13	0.46
1:C:228:ASN:O	1:C:230:LEU:N	2.49	0.46
1:A:54:ARG:CG	1:A:54:ARG:NH1	2.71	0.46
1:A:326:PRO:HB3	1:A:329:LEU:HB2	1.98	0.46
1:A:554:PRO:O	1:A:558:PHE:HD1	1.98	0.46
1:A:690:GLN:O	1:A:691:LYS:C	2.58	0.46
1:A:899:TRP:CE3	2:B:72:VAL:HG13	2.51	0.46
1:A:984:ALA:O	1:A:985:PHE:C	2.59	0.46
4:A:1:OBN:H191	4:A:1:OBN:H8	1.64	0.46
2:B:103:VAL:HG11	2:B:107:ARG:NH2	2.31	0.46
2:B:275:GLU:HB2	2:B:296:ASP:OD1	2.16	0.46
1:C:40:SER:OG	1:C:43:GLU:HG3	2.16	0.46
1:C:119:GLN:O	1:C:119:GLN:HG2	2.16	0.46
1:A:612:ASP:OD2	1:A:613:HIS:N	2.37	0.46
1:A:818:GLU:OE1	1:A:931:LYS:HG3	2.16	0.46
2:B:179:LYS:HD3	2:B:256:GLN:OE1	2.14	0.46
1:C:135:ILE:O	1:C:138:CYS:N	2.48	0.46
1:C:721:ALA:O	1:C:722:ASP:C	2.59	0.46
1:C:825:MET:HA	1:C:825:MET:CE	2.40	0.46
1:C:981:TRP:N	1:C:981:TRP:CD1	2.83	0.46
1:A:135:ILE:O	1:A:138:CYS:N	2.48	0.46
1:A:323:ALA:HB1	1:A:780:ILE:HG12	1.98	0.46
1:A:468:THR:CG2	1:A:487:LYS:HB2	2.46	0.46
1:A:915:PHE:HA	1:A:918:THR:HG22	1.98	0.46
2:B:78:THR:O	2:B:295:PHE:HE2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:LEU:O	1:C:48:TYR:CD2	2.68	0.46
1:C:215:SER:O	1:C:216:GLU:C	2.56	0.46
2:D:103:VAL:HG12	2:D:107:ARG:CZ	2.46	0.46
2:D:119:ASP:O	2:D:121:MET:N	2.49	0.46
1:A:783:PHE:CZ	4:A:1:OBN:H17	2.51	0.46
1:A:886:ARG:CG	1:A:886:ARG:O	2.64	0.46
2:B:103:VAL:HG12	2:B:107:ARG:CZ	2.46	0.46
2:B:121:MET:HA	2:B:122:ILE:HA	1.44	0.46
2:B:129:VAL:CG2	2:B:130:PRO:HD3	2.31	0.46
1:C:554:PRO:O	1:C:558:PHE:HD1	1.98	0.46
1:C:934:ARG:HB2	1:C:1015:TYR:HE1	1.81	0.46
1:C:951:LEU:HD23	1:C:951:LEU:HA	1.81	0.46
2:D:272:ILE:HG12	2:D:299:ILE:O	2.16	0.46
2:B:173:LYS:CG	2:B:264:THR:O	2.64	0.45
2:B:204:TYR:O	2:B:205:ASN:C	2.59	0.45
2:B:272:ILE:HG12	2:B:299:ILE:O	2.16	0.45
1:C:612:ASP:O	1:C:685:ARG:N	2.48	0.45
2:D:226:THR:HG21	2:D:264:THR:CG2	2.46	0.45
1:A:207:ASP:OD2	1:A:209:SER:HB3	2.16	0.45
1:A:260:MET:HE3	1:A:712:VAL:HG21	1.97	0.45
2:B:187:LYS:O	2:B:189:LYS:HG3	2.16	0.45
1:C:934:ARG:HB2	1:C:1015:TYR:CE1	2.51	0.45
1:A:37:HIS:H	1:A:37:HIS:HD2	1.62	0.45
1:A:385:TRP:HB3	1:A:581:LEU:HB2	1.98	0.45
1:A:654:LYS:HA	1:A:654:LYS:CE	2.45	0.45
2:B:130:PRO:HB2	2:B:204:TYR:CZ	2.51	0.45
2:B:155:TRP:CE2	2:B:232:LEU:HD22	2.51	0.45
2:B:207:TYR:HA	2:B:240:LEU:HD22	1.97	0.45
2:B:210:PRO:C	2:B:211:VAL:HG23	2.41	0.45
1:C:48:TYR:OH	1:C:252:VAL:CG1	2.64	0.45
1:C:480:LYS:CD	1:C:506:ARG:HH12	2.29	0.45
2:D:90:PHE:HD2	2:D:98:TYR:CD1	2.35	0.45
2:D:229:TYR:HD1	2:D:261:VAL:HG22	1.80	0.45
1:A:284:PHE:HD1	1:A:838:VAL:HG21	1.80	0.45
1:C:991:ILE:O	1:C:992:PHE:C	2.58	0.45
2:D:77:LEU:HD12	2:D:179:LYS:O	2.17	0.45
1:A:48:TYR:HE2	1:A:252:VAL:HG13	1.76	0.45
1:A:103:LEU:O	1:A:318:ILE:HD11	2.16	0.45
1:A:195:ASP:OD2	1:A:259:VAL:N	2.37	0.45
1:A:287:ILE:HD13	1:A:287:ILE:HA	1.87	0.45
1:A:596:VAL:HG13	1:A:606:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:964:CYS:HB3	1:A:967:MET:HG2	1.99	0.45
2:B:117:GLN:HE22	2:B:150:ARG:CB	2.29	0.45
1:C:125:LEU:HD21	1:C:322:VAL:HG22	1.98	0.45
1:C:135:ILE:HG12	1:C:135:ILE:H	1.36	0.45
1:C:1001:ILE:CG2	1:C:1010:VAL:HG11	2.45	0.45
2:D:243:TYR:HB3	2:D:244:PRO:HA	1.98	0.45
1:A:93:PHE:HB3	1:A:330:LEU:CD2	2.47	0.45
1:A:780:ILE:C	1:A:782:PRO:HD2	2.42	0.45
1:A:949:PHE:CD2	1:A:949:PHE:C	2.95	0.45
2:B:192:LYS:C	2:B:194:GLU:H	2.25	0.45
1:C:330:LEU:HD23	1:C:330:LEU:N	2.32	0.45
1:C:852:MET:HG2	2:D:43:TYR:HE2	1.79	0.45
2:D:117:GLN:HE22	2:D:150:ARG:CB	2.30	0.45
2:D:130:PRO:CB	2:D:204:TYR:HE2	2.20	0.45
2:D:210:PRO:C	2:D:211:VAL:HG23	2.41	0.45
1:C:690:GLN:O	1:C:691:LYS:C	2.59	0.45
2:B:130:PRO:HB2	2:B:204:TYR:OH	2.17	0.45
1:C:301:ILE:HG13	1:C:302:LEU:N	2.31	0.45
1:C:321:ILE:CG1	1:C:322:VAL:H	2.30	0.45
1:C:852:MET:HE3	2:D:43:TYR:OH	2.17	0.45
2:D:39:TYR:O	2:D:40:VAL:C	2.60	0.45
2:D:171:ASP:CG	2:D:172:GLY:N	2.75	0.45
1:A:51:ASP:HB3	1:A:55:GLY:N	2.31	0.45
1:A:98:TRP:CD1	1:A:133:VAL:HG21	2.52	0.45
1:A:135:ILE:O	1:A:136:THR:C	2.57	0.45
1:A:831:ASN:HD22	1:A:831:ASN:C	2.25	0.45
2:B:130:PRO:HG2	2:B:204:TYR:CE2	2.38	0.45
1:C:157:MET:HB2	1:C:158:VAL:H	1.64	0.45
1:C:197:ARG:HG2	1:C:235:ILE:HD11	1.99	0.45
4:C:1:OBN:H21	4:C:1:OBN:H9	1.84	0.45
1:A:277:ILE:HG23	1:A:278:ALA:N	2.32	0.45
1:A:910:THR:O	1:A:910:THR:HG23	2.17	0.45
2:B:272:ILE:HG12	2:B:272:ILE:H	1.63	0.45
1:C:123:LEU:C	1:C:123:LEU:HD13	2.42	0.45
1:C:886:ARG:CG	1:C:886:ARG:O	2.64	0.45
1:C:238:PHE:CE2	1:C:239:SER:HB3	2.52	0.44
1:C:385:TRP:HB3	1:C:581:LEU:HB2	1.99	0.44
2:D:103:VAL:HG11	2:D:107:ARG:NH2	2.31	0.44
1:A:320:ILE:HG22	1:A:324:ASN:ND2	2.32	0.44
1:A:893:ASP:OD2	1:A:896:GLY:N	2.50	0.44
1:A:948:ILE:HG22	1:A:949:PHE:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:PHE:HD2	2:B:98:TYR:CD1	2.35	0.44
2:B:274:ILE:HD12	2:B:299:ILE:HD11	1.98	0.44
1:C:462:GLU:O	1:C:466:ARG:HG3	2.17	0.44
2:D:192:LYS:C	2:D:194:GLU:H	2.25	0.44
1:A:332:THR:O	1:A:333:VAL:C	2.60	0.44
1:A:571:PHE:CD2	1:A:571:PHE:N	2.86	0.44
1:A:721:ALA:O	1:A:722:ASP:C	2.59	0.44
1:A:916:PHE:CD1	1:A:916:PHE:C	2.96	0.44
1:A:985:PHE:HB2	1:A:986:PRO:HD3	1.99	0.44
2:B:90:PHE:CD2	2:B:98:TYR:HB3	2.53	0.44
2:B:202:MET:HE3	2:B:203:LYS:N	2.32	0.44
1:C:110:ILE:HD13	1:C:110:ILE:HA	1.81	0.44
1:C:670:GLN:O	1:C:674:ILE:HG13	2.17	0.44
1:C:952:PHE:HE2	3:E:40:VAL:HG11	1.82	0.44
1:C:977:LYS:HD3	2:D:68:TYR:CZ	2.52	0.44
2:D:90:PHE:CD2	2:D:98:TYR:HB3	2.52	0.44
1:A:42:ASP:O	1:A:43:GLU:C	2.60	0.44
1:A:670:GLN:O	1:A:674:ILE:HG13	2.17	0.44
1:A:770:ALA:O	1:A:771:TYR:C	2.60	0.44
2:B:133:LEU:CD2	2:B:243:TYR:HB2	2.47	0.44
2:B:171:ASP:O	2:B:172:GLY:C	2.61	0.44
1:C:207:ASP:OD2	1:C:209:SER:HB3	2.18	0.44
1:C:587:PRO:HA	1:C:588:PRO:HD3	1.88	0.44
1:C:596:VAL:HG13	1:C:606:VAL:HG21	2.00	0.44
1:A:225:THR:HG22	1:A:232:THR:CA	2.36	0.44
1:A:301:ILE:HG13	1:A:302:LEU:N	2.33	0.44
1:A:321:ILE:HG13	1:A:322:VAL:H	1.83	0.44
1:A:611:GLY:O	1:A:685:ARG:HA	2.18	0.44
1:A:818:GLU:CD	1:A:931:LYS:HG3	2.42	0.44
1:C:404:PHE:HD2	1:C:404:PHE:N	1.97	0.44
1:A:150:ILE:O	1:A:150:ILE:CG2	2.65	0.44
1:A:234:ASN:OD1	1:A:235:ILE:HG12	2.18	0.44
1:C:214:GLU:HG2	1:C:612:ASP:OD2	2.17	0.44
1:C:332:THR:O	1:C:333:VAL:C	2.60	0.44
1:C:893:ASP:OD2	1:C:896:GLY:N	2.51	0.44
1:A:93:PHE:CD1	1:A:285:ILE:HD11	2.45	0.44
1:A:790:ASN:HB3	1:A:880:ARG:HG2	1.99	0.44
1:A:861:THR:O	1:A:865:ILE:HG12	2.18	0.44
1:C:323:ALA:HB1	1:C:780:ILE:HG12	1.98	0.44
2:D:80:ILE:HG21	2:D:177:ILE:CD1	2.46	0.44
2:D:127:GLY:C	2:D:129:VAL:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:152:ARG:C	2:D:154:GLU:N	2.75	0.44
2:D:179:LYS:HD3	2:D:256:GLN:OE1	2.16	0.44
1:A:275:THR:HB	1:A:276:PRO:CD	2.43	0.44
1:A:506:ARG:HH11	1:A:506:ARG:HG2	1.79	0.44
2:B:152:ARG:C	2:B:154:GLU:N	2.75	0.44
1:C:142:TYR:O	1:C:146:LYS:HG2	2.17	0.44
1:C:761:ILE:O	1:C:761:ILE:HG12	2.18	0.44
2:D:226:THR:CG2	2:D:264:THR:HG22	2.48	0.44
1:A:54:ARG:HG3	1:A:54:ARG:NH1	2.09	0.44
1:A:238:PHE:CE2	1:A:239:SER:HB3	2.52	0.44
2:B:89:SER:HA	2:B:300:GLU:O	2.18	0.44
2:B:208:VAL:HG13	2:B:237:GLY:HA3	1.99	0.44
2:B:209:LEU:O	2:B:237:GLY:HA2	2.18	0.44
1:C:316:PHE:O	1:C:319:GLY:N	2.50	0.44
2:D:71:ARG:HD3	2:D:71:ARG:HA	1.81	0.44
2:D:124:GLU:CD	2:D:147:LYS:HD2	2.42	0.44
2:D:155:TRP:CE2	2:D:232:LEU:HD22	2.52	0.44
2:D:196:LEU:N	2:D:196:LEU:HD23	2.33	0.44
2:D:239:PRO:C	2:D:241:GLN:H	2.26	0.44
2:B:197:GLU:O	2:B:200:PRO:CD	2.60	0.43
2:B:226:THR:CG2	2:B:264:THR:HG22	2.48	0.43
1:C:277:ILE:CG2	1:C:355:GLU:HB3	2.48	0.43
1:C:317:LEU:HD23	1:C:317:LEU:C	2.43	0.43
1:C:565:ASP:O	1:C:568:ASP:O	2.36	0.43
1:C:765:LEU:O	1:C:769:ILE:HG12	2.18	0.43
1:C:996:GLU:OE1	1:C:996:GLU:HA	2.18	0.43
1:A:318:ILE:O	1:A:321:ILE:HG12	2.19	0.43
1:A:541:LEU:O	1:A:543:GLU:HG3	2.18	0.43
1:A:565:ASP:O	1:A:568:ASP:O	2.36	0.43
2:B:81:PRO:CG	2:B:176:VAL:HG13	2.48	0.43
1:C:214:GLU:HG2	1:C:612:ASP:CG	2.43	0.43
1:C:320:ILE:HG22	1:C:324:ASN:ND2	2.34	0.43
1:C:551:LEU:HD12	1:C:576:LEU:HD23	2.00	0.43
1:C:759:ARG:HH11	1:C:825:MET:HE2	1.82	0.43
1:C:957:LEU:HD23	1:C:957:LEU:C	2.43	0.43
4:C:1:OBN:H191	4:C:1:OBN:H8	1.53	0.43
2:D:88:ILE:HG23	2:D:101:TYR:CD2	2.53	0.43
1:C:96:LEU:O	1:C:99:ILE:HG22	2.17	0.43
1:C:103:LEU:HD23	1:C:103:LEU:C	2.42	0.43
1:C:508:LEU:HD22	1:C:508:LEU:HA	1.86	0.43
1:C:571:PHE:CD2	1:C:571:PHE:N	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:963:TYR:O	3:E:31:LEU:CG	2.66	0.43
1:C:985:PHE:HB2	1:C:986:PRO:HD3	2.00	0.43
2:D:90:PHE:CD2	2:D:98:TYR:CD1	3.06	0.43
2:D:130:PRO:CB	2:D:204:TYR:CZ	3.01	0.43
1:A:214:GLU:HG2	1:A:612:ASP:OD2	2.18	0.43
1:A:383:HIS:HB2	1:A:583:SER:OG	2.19	0.43
1:A:397:GLU:O	1:A:436:LEU:HD12	2.17	0.43
2:B:267:THR:HG23	2:B:268:MET:N	2.32	0.43
1:C:87:ARG:HD2	1:C:87:ARG:HA	1.81	0.43
1:C:321:ILE:HG13	1:C:322:VAL:H	1.84	0.43
1:C:427:GLN:OE1	1:C:441:ALA:HB2	2.19	0.43
1:C:688:PRO:HG3	1:C:713:ASN:CB	2.48	0.43
1:C:790:ASN:OD1	1:C:880:ARG:HD3	2.19	0.43
1:A:93:PHE:CZ	1:A:284:PHE:CE2	3.07	0.43
1:A:96:LEU:CA	1:A:99:ILE:HG22	2.45	0.43
1:A:204:CYS:O	1:A:220:ARG:N	2.50	0.43
1:A:369:PHD:OD2	1:A:371:THR:O	2.37	0.43
1:A:947:LEU:HD23	1:A:947:LEU:O	2.18	0.43
1:A:1000:LEU:HD13	1:A:1000:LEU:O	2.18	0.43
1:C:496:HIS:CE1	1:C:559:PRO:O	2.71	0.43
2:D:56:VAL:O	2:D:59:LEU:HB3	2.19	0.43
2:D:94:ASP:O	2:D:98:TYR:CE1	2.72	0.43
2:D:178:ILE:CG1	2:D:259:MET:HB2	2.48	0.43
1:A:87:ARG:HA	1:A:87:ARG:HD2	1.88	0.43
1:A:123:LEU:C	1:A:123:LEU:HD13	2.42	0.43
1:A:592:VAL:HG12	1:A:593:PRO:N	2.34	0.43
1:A:759:ARG:HH11	1:A:825:MET:HE2	1.84	0.43
1:A:764:ASN:ND2	1:A:818:GLU:HB2	2.34	0.43
1:A:765:LEU:O	1:A:769:ILE:HG12	2.18	0.43
1:A:831:ASN:C	1:A:831:ASN:ND2	2.77	0.43
2:B:196:LEU:N	2:B:196:LEU:HD23	2.34	0.43
1:C:284:PHE:HD1	1:C:838:VAL:HG21	1.80	0.43
1:C:790:ASN:HB3	1:C:880:ARG:HG2	2.01	0.43
1:A:35:ASP:HB2	1:A:229:PRO:CG	2.47	0.43
1:A:727:MET:HE3	1:A:746:ASP:CG	2.43	0.43
1:A:810:VAL:HG11	1:A:950:GLY:HA2	2.01	0.43
2:B:58:LEU:HD23	2:B:58:LEU:HA	1.86	0.43
1:C:37:HIS:H	1:C:37:HIS:HD2	1.63	0.43
1:C:88:GLN:OE1	1:C:140:SER:HB3	2.17	0.43
1:C:135:ILE:O	1:C:136:THR:C	2.60	0.43
1:C:831:ASN:C	1:C:831:ASN:HD22	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:889:ASN:O	1:C:900:THR:HA	2.19	0.43
1:C:964:CYS:HB3	1:C:967:MET:HG2	1.99	0.43
2:D:121:MET:HA	2:D:122:ILE:HA	1.42	0.43
1:A:462:GLU:O	1:A:466:ARG:HG3	2.18	0.43
1:A:802:CYS:O	1:A:916:PHE:HE2	2.02	0.43
1:A:960:PHE:C	1:A:962:SER:H	2.25	0.43
2:B:239:PRO:C	2:B:241:GLN:H	2.27	0.43
2:B:262:GLN:HE21	2:B:262:GLN:HB3	1.72	0.43
2:B:282:ASN:O	2:B:283:ILE:HD12	2.18	0.43
1:C:150:ILE:HD13	1:C:150:ILE:HA	1.78	0.43
1:C:298:SER:O	1:C:301:ILE:HG12	2.19	0.43
1:C:563:GLN:O	1:C:570:ASN:ND2	2.52	0.43
1:A:48:TYR:CE2	1:A:252:VAL:CG1	2.93	0.43
1:A:337:LEU:HD12	1:A:761:ILE:HD11	2.00	0.43
1:A:356:ALA:O	1:A:357:VAL:C	2.62	0.43
1:A:815:LEU:HD12	1:A:815:LEU:HA	1.76	0.43
1:A:981:TRP:N	1:A:981:TRP:CD1	2.84	0.43
2:B:39:TYR:O	2:B:40:VAL:C	2.60	0.43
2:B:119:ASP:O	2:B:121:MET:N	2.52	0.43
1:C:43:GLU:O	1:C:47:LYS:N	2.50	0.43
1:C:93:PHE:CB	1:C:330:LEU:HD11	2.37	0.43
1:C:144:GLU:CG	1:C:144:GLU:O	2.66	0.43
1:C:770:ALA:O	1:C:771:TYR:C	2.60	0.43
2:D:77:LEU:HD13	2:D:180:LEU:HD12	2.01	0.43
1:A:96:LEU:O	1:A:99:ILE:HG22	2.19	0.43
1:A:214:GLU:HG2	1:A:612:ASP:CG	2.43	0.43
1:A:298:SER:O	1:A:301:ILE:HG12	2.19	0.43
1:A:303:SER:O	1:A:308:TYR:HB2	2.19	0.43
1:A:305:ILE:O	1:A:305:ILE:HG22	2.17	0.43
1:A:385:TRP:CZ3	1:A:531:PHE:HB2	2.53	0.43
1:A:563:GLN:O	1:A:570:ASN:ND2	2.52	0.43
1:A:913:THR:HG22	1:A:976:LEU:HD11	2.01	0.43
2:B:243:TYR:HB3	2:B:244:PRO:HA	2.00	0.43
1:C:270:LEU:C	1:C:719:LYS:HE3	2.44	0.43
1:C:871:PHE:CZ	1:C:899:TRP:CD1	3.07	0.43
1:A:267:ALA:HB1	1:A:715:SER:HB2	2.01	0.42
1:A:865:ILE:CD1	1:A:980:TRP:CD2	3.01	0.42
2:B:241:GLN:HG3	2:B:242:TYR:CE1	2.54	0.42
1:C:35:ASP:HB2	1:C:229:PRO:CG	2.48	0.42
1:C:96:LEU:CA	1:C:99:ILE:HG22	2.46	0.42
1:C:385:TRP:CZ3	1:C:531:PHE:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:ILE:HD13	1:A:288:ILE:HA	1.93	0.42
1:A:312:GLU:C	1:A:315:ILE:HG22	2.44	0.42
1:A:360:LEU:HD13	1:A:723:ILE:CD1	2.44	0.42
1:A:761:ILE:O	1:A:761:ILE:HG12	2.19	0.42
2:B:77:LEU:HD12	2:B:179:LYS:O	2.19	0.42
2:B:173:LYS:HD2	2:B:173:LYS:N	2.30	0.42
2:B:212:HIS:CG	2:B:213:CYS:N	2.86	0.42
1:C:54:ARG:CD	1:C:168:GLY:N	2.81	0.42
1:C:234:ASN:OD1	1:C:235:ILE:HG12	2.19	0.42
2:D:78:THR:C	2:D:295:PHE:CE2	2.86	0.42
2:D:204:TYR:O	2:D:206:PRO:N	2.52	0.42
2:D:205:ASN:O	2:D:206:PRO:O	2.36	0.42
1:A:144:GLU:O	1:A:144:GLU:CG	2.67	0.42
1:A:170:LYS:C	1:A:171:MET:HG2	2.43	0.42
1:A:270:LEU:HA	1:A:270:LEU:HD23	1.82	0.42
1:A:794:PRO:O	1:A:912:HIS:HD2	2.02	0.42
1:A:889:ASN:O	1:A:900:THR:HA	2.18	0.42
1:A:902:GLU:O	1:A:906:ILE:HG12	2.18	0.42
2:B:77:LEU:HD13	2:B:180:LEU:HD12	2.02	0.42
2:B:204:TYR:HE1	2:B:235:TYR:CE2	2.34	0.42
1:C:305:ILE:HG22	1:C:305:ILE:O	2.18	0.42
1:C:771:TYR:OH	1:C:923:GLN:HB3	2.20	0.42
2:D:89:SER:HA	2:D:300:GLU:O	2.19	0.42
1:A:627:ILE:HA	1:A:680:GLU:OE1	2.19	0.42
1:A:887:TRP:O	1:A:888:ILE:C	2.63	0.42
2:B:127:GLY:C	2:B:129:VAL:N	2.78	0.42
2:B:130:PRO:HB3	2:B:204:TYR:CE2	2.51	0.42
2:B:173:LYS:CD	2:B:264:THR:O	2.67	0.42
1:C:149:LYS:HD2	1:C:149:LYS:HA	1.68	0.42
1:C:887:TRP:O	1:C:888:ILE:C	2.63	0.42
2:D:282:ASN:O	2:D:283:ILE:HD12	2.18	0.42
1:A:99:ILE:O	1:A:102:ILE:HG22	2.20	0.42
1:A:797:THR:HG1	4:A:1:OBN:HOF	1.61	0.42
2:B:127:GLY:C	2:B:129:VAL:H	2.26	0.42
2:B:131:SER:OG	2:B:241:GLN:CB	2.64	0.42
1:C:853:ILE:HG12	2:D:46:LEU:HD11	2.01	0.42
2:D:208:VAL:HG13	2:D:237:GLY:HA3	2.00	0.42
1:A:267:ALA:CB	1:A:715:SER:HB2	2.50	0.42
1:A:794:PRO:HA	1:A:862:TYR:CE1	2.55	0.42
1:C:303:SER:O	1:C:308:TYR:HB2	2.19	0.42
1:C:854:GLN:HE21	1:C:922:VAL:HB	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:957:LEU:HD23	1:C:957:LEU:O	2.19	0.42
2:D:80:ILE:HD12	2:D:105:ILE:CG2	2.39	0.42
1:A:36:ASP:HB2	1:A:39:LEU:CD1	2.50	0.42
1:A:211:LEU:HD21	1:A:237:PHE:CB	2.50	0.42
1:A:513:SER:C	1:A:514:ILE:HG13	2.43	0.42
1:A:824:ILE:C	1:A:826:LYS:N	2.77	0.42
2:B:72:VAL:O	2:B:73:ALA:C	2.63	0.42
2:B:94:ASP:O	2:B:98:TYR:CE1	2.72	0.42
1:C:238:PHE:CE2	1:C:260:MET:HB3	2.55	0.42
1:C:287:ILE:HD13	1:C:287:ILE:HA	1.88	0.42
1:C:503:ALA:HA	1:C:504:PRO:HD3	1.84	0.42
1:C:910:THR:O	1:C:910:THR:HG23	2.19	0.42
1:C:914:PRO:O	1:C:918:THR:N	2.37	0.42
1:A:84:LYS:HD2	1:A:84:LYS:HA	1.48	0.42
1:A:102:ILE:HG23	1:A:103:LEU:N	2.34	0.42
1:A:369:PHD:OP2	1:A:370:LYS:N	2.49	0.42
1:A:1015:TYR:O	1:A:1016:TYR:C	2.62	0.42
1:C:211:LEU:N	1:C:211:LEU:CD1	2.82	0.42
1:C:277:ILE:CG2	1:C:278:ALA:N	2.83	0.42
1:C:337:LEU:HD12	1:C:761:ILE:HD11	2.01	0.42
1:C:513:SER:C	1:C:514:ILE:HG13	2.45	0.42
1:C:536:LEU:HD23	1:C:536:LEU:HA	1.89	0.42
1:C:727:MET:HE3	1:C:746:ASP:CG	2.43	0.42
1:C:861:THR:O	1:C:865:ILE:HG12	2.20	0.42
2:D:204:TYR:CE1	2:D:235:TYR:CE1	3.07	0.42
1:A:93:PHE:CB	1:A:330:LEU:HD11	2.36	0.42
1:A:99:ILE:C	1:A:102:ILE:HG22	2.45	0.42
1:A:372:GLY:HA3	1:A:710:ASP:OD1	2.19	0.42
1:A:472:GLU:HG3	1:A:474:PRO:HD3	2.02	0.42
1:A:651:ARG:HA	1:A:651:ARG:HE	1.85	0.42
1:A:666:MET:HB3	1:A:671:LEU:HD21	2.02	0.42
2:B:122:ILE:O	2:B:122:ILE:HG13	2.20	0.42
1:C:216:GLU:HA	1:C:217:PRO:HD2	1.79	0.42
1:C:831:ASN:ND2	1:C:833:LYS:H	2.18	0.42
2:D:127:GLY:C	2:D:129:VAL:N	2.77	0.42
2:D:267:THR:HG23	2:D:268:MET:N	2.35	0.42
1:A:309:THR:HG22	1:A:312:GLU:CD	2.44	0.42
1:A:860:PHE:HD1	2:B:54:ILE:HD12	1.85	0.42
1:A:886:ARG:HE	1:A:886:ARG:HB2	1.54	0.42
2:B:56:VAL:O	2:B:59:LEU:HB3	2.20	0.42
2:B:90:PHE:CD2	2:B:98:TYR:CD1	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:SER:O	1:C:41:LEU:C	2.61	0.42
1:C:383:HIS:HB2	1:C:583:SER:OG	2.19	0.42
1:C:960:PHE:C	1:C:962:SER:H	2.28	0.42
1:A:320:ILE:HG22	1:A:324:ASN:HD22	1.85	0.41
1:A:480:LYS:CG	1:A:506:ARG:NH1	2.83	0.41
1:A:511:CYS:SG	1:A:578:PHE:HB2	2.60	0.41
1:A:618:LYS:NZ	1:A:636:ASP:OD1	2.53	0.41
1:A:781:THR:OG1	1:A:782:PRO:HD3	2.20	0.41
1:A:876:LEU:C	1:A:879:LEU:HG	2.44	0.41
1:A:951:LEU:HD23	1:A:951:LEU:HA	1.80	0.41
1:A:967:MET:C	1:A:969:VAL:N	2.77	0.41
2:B:28:THR:O	2:B:32:TRP:NE1	2.53	0.41
1:C:356:ALA:O	1:C:357:VAL:C	2.63	0.41
1:C:372:GLY:HA3	1:C:710:ASP:OD1	2.20	0.41
1:C:794:PRO:O	1:C:912:HIS:HD2	2.03	0.41
1:C:816:ALA:HB3	1:C:817:TYR:CD1	2.55	0.41
1:C:963:TYR:O	3:E:31:LEU:HG	2.20	0.41
2:D:72:VAL:O	2:D:73:ALA:C	2.63	0.41
1:A:351:VAL:HG12	1:A:352:LYS:N	2.35	0.41
1:A:820:ALA:C	1:A:822:SER:H	2.28	0.41
1:A:871:PHE:CZ	1:A:899:TRP:CD1	3.08	0.41
1:C:43:GLU:C	1:C:45:HIS:N	2.64	0.41
1:C:51:ASP:OD2	1:C:54:ARG:HB2	2.21	0.41
1:C:351:VAL:HG12	1:C:352:LYS:N	2.35	0.41
1:C:369:PHD:O	1:C:373:THR:HB	2.19	0.41
1:C:511:CYS:SG	1:C:578:PHE:HB2	2.60	0.41
1:C:831:ASN:C	1:C:831:ASN:ND2	2.78	0.41
1:C:886:ARG:HE	1:C:886:ARG:HB2	1.54	0.41
1:A:211:LEU:N	1:A:211:LEU:CD1	2.82	0.41
1:A:317:LEU:C	1:A:317:LEU:HD23	2.45	0.41
1:A:370:LYS:HG3	1:A:608:MET:CE	2.50	0.41
1:A:831:ASN:ND2	1:A:833:LYS:H	2.19	0.41
1:A:868:GLU:CA	2:B:67:THR:HG23	2.50	0.41
2:B:90:PHE:HZ	2:B:174:PRO:CG	2.30	0.41
1:C:354:LEU:HD12	1:C:354:LEU:HA	1.75	0.41
1:C:643:ILE:HG13	1:C:644:PRO:O	2.19	0.41
1:C:654:LYS:HA	1:C:654:LYS:CE	2.46	0.41
1:C:899:TRP:HH2	2:D:71:ARG:HB2	1.86	0.41
1:C:967:MET:C	1:C:969:VAL:N	2.78	0.41
1:A:102:ILE:CG2	1:A:103:LEU:N	2.83	0.41
1:A:216:GLU:HA	1:A:217:PRO:HD2	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:THR:HG23	1:A:255:GLY:N	2.33	0.41
1:A:254:THR:HG22	1:A:257:ARG:HH21	1.86	0.41
1:A:309:THR:HG22	1:A:312:GLU:OE1	2.21	0.41
1:A:341:ALA:HB2	1:A:357:VAL:CG2	2.39	0.41
1:A:369:PHD:O	1:A:373:THR:HB	2.20	0.41
1:A:1001:ILE:CG2	1:A:1010:VAL:HG11	2.45	0.41
1:C:88:GLN:CD	1:C:140:SER:HB3	2.46	0.41
1:C:234:ASN:O	1:C:235:ILE:HD13	2.21	0.41
1:C:592:VAL:HG12	1:C:593:PRO:N	2.34	0.41
1:C:764:ASN:ND2	1:C:818:GLU:HB2	2.35	0.41
1:C:798:VAL:HG13	1:C:971:LEU:HD22	2.03	0.41
1:C:882:ASN:O	1:C:885:ASP:HB3	2.21	0.41
2:D:117:GLN:NE2	2:D:150:ARG:HG2	2.35	0.41
2:D:184:LEU:HD22	2:D:184:LEU:HA	1.90	0.41
2:D:226:THR:CG2	2:D:265:ASN:H	2.32	0.41
2:D:239:PRO:HG2	2:D:242:TYR:HD1	1.81	0.41
1:A:60:ARG:O	1:A:64:ILE:HG13	2.20	0.41
1:A:321:ILE:O	1:A:325:VAL:N	2.53	0.41
1:A:675:LEU:HD22	1:A:698:CYS:SG	2.60	0.41
1:A:907:VAL:O	1:A:911:CYS:N	2.54	0.41
1:A:957:LEU:HD23	1:A:957:LEU:C	2.46	0.41
2:B:81:PRO:CD	2:B:176:VAL:HG13	2.50	0.41
2:B:241:GLN:HG3	2:B:242:TYR:CD1	2.55	0.41
1:C:93:PHE:CZ	1:C:284:PHE:CE2	3.08	0.41
1:C:132:VAL:O	1:C:133:VAL:C	2.62	0.41
1:C:276:PRO:HG2	1:C:277:ILE:H	1.85	0.41
1:C:370:LYS:HE3	1:C:370:LYS:HB3	1.86	0.41
1:C:472:GLU:HG3	1:C:474:PRO:HD3	2.02	0.41
1:C:495:ARG:HD2	1:C:553:LEU:O	2.21	0.41
1:C:762:PHE:O	1:C:765:LEU:HB2	2.20	0.41
1:C:847:TYR:O	1:C:852:MET:HE2	2.21	0.41
1:C:1000:LEU:HD13	1:C:1000:LEU:O	2.21	0.41
1:C:1000:LEU:HA	1:C:1003:ARG:CZ	2.50	0.41
1:A:54:ARG:CD	1:A:168:GLY:N	2.82	0.41
1:A:270:LEU:C	1:A:719:LYS:HE3	2.45	0.41
1:A:480:LYS:HB3	1:A:506:ARG:HG3	2.01	0.41
1:A:962:SER:OG	1:A:975:PRO:HA	2.20	0.41
1:A:967:MET:C	1:A:969:VAL:H	2.28	0.41
4:A:1:OBN:H71	4:A:1:OBN:H151	1.72	0.41
2:B:65:LYS:HE3	2:B:69:GLN:NE2	2.34	0.41
2:B:117:GLN:HE22	2:B:150:ARG:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:206:PRO:HB2	2:B:207:TYR:H	1.61	0.41
2:B:227:MET:HG2	2:B:263:PHE:CZ	2.55	0.41
1:C:370:LYS:HG3	1:C:608:MET:CE	2.49	0.41
1:C:541:LEU:O	1:C:543:GLU:HG3	2.21	0.41
1:C:651:ARG:HA	1:C:651:ARG:HE	1.85	0.41
1:C:810:VAL:HG11	1:C:950:GLY:HA2	2.02	0.41
1:C:915:PHE:CA	1:C:918:THR:HG22	2.51	0.41
1:C:1015:TYR:O	1:C:1016:TYR:C	2.62	0.41
1:A:118:PRO:CG	4:A:1:OBN:C19	2.77	0.41
1:A:232:THR:HG21	1:A:235:ILE:CG1	2.51	0.41
1:A:360:LEU:HA	1:A:360:LEU:HD12	1.81	0.41
1:A:996:GLU:OE1	1:A:996:GLU:HA	2.20	0.41
2:B:178:ILE:CG1	2:B:259:MET:HB2	2.48	0.41
2:B:205:ASN:HD22	2:B:205:ASN:HA	1.66	0.41
1:C:611:GLY:O	1:C:685:ARG:HA	2.20	0.41
1:C:615:ILE:HD13	1:C:615:ILE:N	2.34	0.41
1:C:618:LYS:NZ	1:C:636:ASP:OD1	2.53	0.41
1:C:820:ALA:C	1:C:822:SER:H	2.29	0.41
1:C:901:TYR:HA	1:C:904:ARG:NH1	2.35	0.41
2:D:109:LEU:HD12	2:D:169:TYR:OH	2.20	0.41
2:D:122:ILE:O	2:D:122:ILE:HG13	2.19	0.41
1:A:110:ILE:HD13	1:A:110:ILE:HA	1.84	0.41
1:A:206:VAL:HA	1:A:243:VAL:H	1.86	0.41
2:B:209:LEU:HD12	2:B:209:LEU:HA	1.85	0.41
2:B:239:PRO:HG2	2:B:242:TYR:HD1	1.81	0.41
1:C:225:THR:HG22	1:C:232:THR:CA	2.31	0.41
1:C:675:LEU:N	1:C:675:LEU:CD1	2.84	0.41
1:C:824:ILE:C	1:C:826:LYS:N	2.77	0.41
2:D:56:VAL:CG2	2:D:57:MET:N	2.84	0.41
2:D:241:GLN:HG3	2:D:242:TYR:CE1	2.56	0.41
1:A:144:GLU:O	1:A:144:GLU:HG3	2.20	0.41
1:A:205:LYS:HE2	1:A:219:THR:OG1	2.20	0.41
1:A:234:ASN:O	1:A:235:ILE:HD13	2.21	0.41
1:A:901:TYR:HA	1:A:904:ARG:NH1	2.36	0.41
2:B:88:ILE:HG23	2:B:101:TYR:CD2	2.55	0.41
2:B:117:GLN:NE2	2:B:150:ARG:HG2	2.36	0.41
2:B:159:CYS:SG	2:B:260:ALA:HB1	2.61	0.41
2:B:207:TYR:CD2	2:B:207:TYR:N	2.89	0.41
1:C:36:ASP:C	1:C:38:LYS:N	2.78	0.41
1:C:144:GLU:O	1:C:144:GLU:HG3	2.20	0.41
1:C:266:LEU:O	1:C:266:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:319:GLY:O	1:C:321:ILE:N	2.48	0.41
1:C:794:PRO:HA	1:C:862:TYR:CE1	2.56	0.41
1:C:815:LEU:HA	1:C:815:LEU:HD12	1.75	0.41
2:D:117:GLN:HE22	2:D:150:ARG:HB3	1.86	0.41
2:D:204:TYR:HE1	2:D:235:TYR:CE1	2.38	0.41
1:A:354:LEU:HD12	1:A:354:LEU:HA	1.74	0.41
1:A:615:ILE:N	1:A:615:ILE:HD13	2.36	0.41
1:A:762:PHE:O	1:A:765:LEU:HB2	2.21	0.41
1:A:771:TYR:OH	1:A:923:GLN:HB3	2.21	0.41
1:C:60:ARG:O	1:C:64:ILE:HG13	2.21	0.41
1:C:201:ALA:HB3	1:C:222:PRO:HD3	2.04	0.41
1:C:318:ILE:O	1:C:321:ILE:HG12	2.21	0.41
1:C:482:GLN:O	1:C:500:MET:HA	2.21	0.41
1:C:668:SER:HB2	1:C:700:ARG:CZ	2.50	0.41
1:C:1009:TRP:O	1:C:1013:GLU:HB2	2.21	0.41
1:A:323:ALA:N	4:A:1:OBN:O23	2.54	0.40
1:A:383:HIS:C	1:A:384:MET:HG3	2.46	0.40
1:A:506:ARG:HG3	1:A:506:ARG:NH1	2.33	0.40
1:A:860:PHE:O	1:A:864:VAL:HG23	2.20	0.40
1:A:924:TRP:CD1	1:A:951:LEU:HD22	2.57	0.40
1:C:93:PHE:HD2	1:C:330:LEU:HD22	1.86	0.40
1:C:195:ASP:OD2	1:C:259:VAL:N	2.50	0.40
1:C:255:GLY:C	1:C:257:ARG:H	2.29	0.40
1:C:751:ILE:O	1:C:755:VAL:HG12	2.21	0.40
1:C:850:ILE:HD13	1:C:850:ILE:HA	1.82	0.40
2:D:119:ASP:C	2:D:121:MET:H	2.29	0.40
2:D:227:MET:HG2	2:D:263:PHE:CZ	2.55	0.40
2:D:250:LEU:HD23	2:D:250:LEU:HA	1.75	0.40
2:D:293:GLY:O	2:D:294:ARG:HB3	2.21	0.40
1:A:751:ILE:O	1:A:755:VAL:HG12	2.20	0.40
2:B:46:LEU:HA	2:B:46:LEU:HD23	1.73	0.40
2:B:52:GLY:O	2:B:56:VAL:HG13	2.20	0.40
1:C:683:PHE:HB3	1:C:686:THR:HG21	2.03	0.40
1:C:795:LEU:HD11	1:C:799:THR:HG21	2.03	0.40
4:C:1:OBN:H151	4:C:1:OBN:H71	1.71	0.40
2:D:133:LEU:CD2	2:D:243:TYR:HB2	2.50	0.40
1:A:30:LYS:C	1:A:31:GLU:HG3	2.46	0.40
1:A:103:LEU:HD23	1:A:103:LEU:C	2.46	0.40
1:A:165:ILE:CD1	1:A:170:LYS:HB3	2.51	0.40
2:B:27:ARG:HA	2:B:27:ARG:HD2	1.72	0.40
1:C:43:GLU:O	1:C:45:HIS:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:PHE:HD1	1:C:285:ILE:CD1	2.29	0.40
1:C:102:ILE:HG23	1:C:103:LEU:N	2.36	0.40
1:C:183:LEU:HD21	1:C:248:ARG:HH21	1.86	0.40
1:C:312:GLU:C	1:C:315:ILE:HG22	2.46	0.40
1:C:777:ILE:HD13	1:C:777:ILE:HA	1.72	0.40
1:C:853:ILE:HG12	2:D:46:LEU:CD1	2.51	0.40
1:A:112:ALA:C	1:A:114:THR:N	2.78	0.40
2:B:78:THR:C	2:B:295:PHE:CE2	2.85	0.40
1:C:165:ILE:CG1	1:C:183:LEU:HD23	2.45	0.40
1:C:292:ALA:HA	1:C:324:ASN:ND2	2.36	0.40
1:C:384:MET:HE3	1:C:384:MET:HB2	1.91	0.40
1:C:392:GLU:O	1:C:392:GLU:HG3	2.21	0.40
1:C:921:VAL:O	1:C:921:VAL:HG12	2.21	0.40
1:C:924:TRP:CD1	1:C:951:LEU:HD22	2.57	0.40
2:D:65:LYS:HE3	2:D:69:GLN:NE2	2.36	0.40
2:D:130:PRO:HB2	2:D:204:TYR:CZ	2.54	0.40
2:D:272:ILE:HG12	2:D:272:ILE:H	1.64	0.40
1:A:132:VAL:O	1:A:133:VAL:C	2.64	0.40
1:A:197:ARG:HG2	1:A:235:ILE:HD11	2.02	0.40
1:A:496:HIS:CE1	1:A:559:PRO:O	2.74	0.40
1:A:688:PRO:HG3	1:A:713:ASN:CB	2.50	0.40
1:A:831:ASN:HA	1:A:832:PRO:HD2	1.93	0.40
1:A:917:VAL:O	1:A:918:THR:C	2.65	0.40
4:A:1:OBN:H21	4:A:1:OBN:H9	1.99	0.40
2:B:151:PHE:HE1	2:B:232:LEU:HD23	1.84	0.40
2:B:177:ILE:CD1	2:B:258:LEU:HD22	2.51	0.40
2:B:226:THR:CG2	2:B:265:ASN:H	2.31	0.40
1:C:326:PRO:HB2	1:C:329:LEU:HB2	2.03	0.40
2:D:94:ASP:HA	2:D:95:PRO:HD3	1.98	0.40
2:D:181:ASN:O	2:D:183:VAL:HG23	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ARG:NH2	2:D:132:GLU:O[4_545]	2.05	0.15

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	989/992 (100%)	807 (82%)	171 (17%)	11 (1%)	11	45
1	C	989/992 (100%)	809 (82%)	168 (17%)	12 (1%)	10	42
2	B	258/277 (93%)	197 (76%)	56 (22%)	5 (2%)	6	32
2	D	258/277 (93%)	195 (76%)	56 (22%)	7 (3%)	4	25
3	E	29/31 (94%)	25 (86%)	4 (14%)	0	100	100
3	G	29/31 (94%)	25 (86%)	4 (14%)	0	100	100
All	All	2552/2600 (98%)	2058 (81%)	459 (18%)	35 (1%)	9	39

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	158	ASN
2	B	206	PRO
2	D	158	ASN
2	D	206	PRO
2	B	120	ASP
2	D	120	ASP
1	A	444	ALA
1	C	444	ALA
1	C	881	VAL
1	A	117	GLU
1	A	586	ASP
1	A	881	VAL
1	A	888	ILE
2	B	223	LYS
1	C	117	GLU
2	D	125	ASP
2	D	129	VAL
2	D	223	LYS
1	A	229	PRO
1	A	965	PRO

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Mol	Chain	Res	Type
2	B	211	VAL
1	C	229	PRO
1	C	586	ASP
1	C	888	ILE
1	C	965	PRO
1	C	83	VAL
2	D	211	VAL
1	A	320	ILE
1	C	320	ILE
1	C	874	ILE
1	C	873	PRO
1	A	615	ILE
1	A	873	PRO
1	A	874	ILE
1	C	615	ILE

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	842/842 (100%)	730 (87%)	112 (13%)	4	16
1	C	842/842 (100%)	736 (87%)	106 (13%)	4	17
2	B	236/248 (95%)	201 (85%)	35 (15%)	3	14
2	D	236/248 (95%)	200 (85%)	36 (15%)	3	13
3	E	25/25 (100%)	24 (96%)	1 (4%)	28	49
3	G	25/25 (100%)	24 (96%)	1 (4%)	28	49
All	All	2206/2230 (99%)	1915 (87%)	291 (13%)	4	16

All (291) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	32	VAL
1	A	34	MET

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Mol	Chain	Res	Type
1	A	42	ASP
1	A	44	LEU
1	A	45	HIS
1	A	54	ARG
1	A	56	LEU
1	A	60	ARG
1	A	74	THR
1	A	82	TRP
1	A	84	LYS
1	A	86	CYS
1	A	90	PHE
1	A	95	MET
1	A	96	LEU
1	A	97	LEU
1	A	110	ILE
1	A	115	GLU
1	A	116	GLU
1	A	119	GLN
1	A	120	ASN
1	A	135	ILE
1	A	140	SER
1	A	142	TYR
1	A	143	GLN
1	A	149	LYS
1	A	150	ILE
1	A	153	SER
1	A	154	PHE
1	A	157	MET
1	A	161	GLN
1	A	171	MET
1	A	179	VAL
1	A	186	VAL
1	A	205	LYS
1	A	214	GLU
1	A	224	PHE
1	A	238	PHE
1	A	250	ILE
1	A	252	VAL
1	A	254	THR
1	A	257	ARG
1	A	260	MET
1	A	263	ILE

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Mol	Chain	Res	Type
1	A	266	LEU
1	A	268	SER
1	A	271	GLU
1	A	277	ILE
1	A	298	SER
1	A	302	LEU
1	A	304	LEU
1	A	310	TRP
1	A	318	ILE
1	A	320	ILE
1	A	321	ILE
1	A	330	LEU
1	A	334	THR
1	A	336	CYS
1	A	352	LYS
1	A	363	THR
1	A	404	PHE
1	A	420	LEU
1	A	450	LEU
1	A	464	ARG
1	A	478	THR
1	A	495	ARG
1	A	506	ARG
1	A	508	LEU
1	A	516	ILE
1	A	523	LEU
1	A	531	PHE
1	A	550	HIS
1	A	551	LEU
1	A	552	PHE
1	A	571	PHE
1	A	585	ILE
1	A	592	VAL
1	A	645	VAL
1	A	663	LEU
1	A	671	LEU
1	A	712	VAL
1	A	715	SER
1	A	719	LYS
1	A	723	ILE
1	A	735	SER
1	A	741	MET

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Mol	Chain	Res	Type
1	A	751	ILE
1	A	755	VAL
1	A	761	ILE
1	A	777	ILE
1	A	814	SER
1	A	815	LEU
1	A	817	TYR
1	A	819	GLN
1	A	826	LYS
1	A	831	ASN
1	A	881	VAL
1	A	910	THR
1	A	917	VAL
1	A	931	LYS
1	A	933	ARG
1	A	936	SER
1	A	948	ILE
1	A	949	PHE
1	A	961	LEU
1	A	980	TRP
1	A	982	PHE
1	A	1000	LEU
1	A	1009	TRP
1	A	1014	THR
1	A	1016	TYR
2	B	54	ILE
2	B	56	VAL
2	B	67	THR
2	B	72	VAL
2	B	79	GLN
2	B	80	ILE
2	B	83	SER
2	B	84	GLN
2	B	88	ILE
2	B	117	GLN
2	B	118	LYS
2	B	129	VAL
2	B	132	GLU
2	B	133	LEU
2	B	175	CYS
2	B	177	ILE
2	B	184	LEU

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Mol	Chain	Res	Type
2	B	192	LYS
2	B	196	LEU
2	B	199	TYR
2	B	201	VAL
2	B	203	LYS
2	B	205	ASN
2	B	207	TYR
2	B	208	VAL
2	B	262	GLN
2	B	266	LEU
2	B	267	THR
2	B	268	MET
2	B	272	ILE
2	B	274	ILE
2	B	285	TYR
2	B	295	PHE
2	B	299	ILE
2	B	301	VAL
3	G	32	ILE
1	C	27	GLU
1	C	32	VAL
1	C	34	MET
1	C	37	HIS
1	C	42	ASP
1	C	44	LEU
1	C	54	ARG
1	C	56	LEU
1	C	60	ARG
1	C	74	THR
1	C	82	TRP
1	C	84	LYS
1	C	86	CYS
1	C	90	PHE
1	C	96	LEU
1	C	97	LEU
1	C	103	LEU
1	C	110	ILE
1	C	115	GLU
1	C	116	GLU
1	C	120	ASN
1	C	135	ILE
1	C	140	SER

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Mol	Chain	Res	Type
1	C	142	TYR
1	C	150	ILE
1	C	157	MET
1	C	158	VAL
1	C	161	GLN
1	C	171	MET
1	C	179	VAL
1	C	186	VAL
1	C	187	LYS
1	C	205	LYS
1	C	214	GLU
1	C	221	SER
1	C	224	PHE
1	C	238	PHE
1	C	250	ILE
1	C	252	VAL
1	C	254	THR
1	C	263	ILE
1	C	268	SER
1	C	277	ILE
1	C	298	SER
1	C	302	LEU
1	C	304	LEU
1	C	310	TRP
1	C	318	ILE
1	C	320	ILE
1	C	321	ILE
1	C	330	LEU
1	C	334	THR
1	C	336	CYS
1	C	352	LYS
1	C	363	THR
1	C	404	PHE
1	C	420	LEU
1	C	450	LEU
1	C	464	ARG
1	C	495	ARG
1	C	506	ARG
1	C	508	LEU
1	C	516	ILE
1	C	523	LEU
1	C	531	PHE

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Mol	Chain	Res	Type
1	C	550	HIS
1	C	551	LEU
1	C	552	PHE
1	C	571	PHE
1	C	585	ILE
1	C	592	VAL
1	C	645	VAL
1	C	663	LEU
1	C	671	LEU
1	C	712	VAL
1	C	715	SER
1	C	719	LYS
1	C	723	ILE
1	C	735	SER
1	C	741	MET
1	C	751	ILE
1	C	755	VAL
1	C	761	ILE
1	C	777	ILE
1	C	814	SER
1	C	815	LEU
1	C	817	TYR
1	C	819	GLN
1	C	826	LYS
1	C	831	ASN
1	C	881	VAL
1	C	910	THR
1	C	913	THR
1	C	917	VAL
1	C	931	LYS
1	C	933	ARG
1	C	936	SER
1	C	948	ILE
1	C	949	PHE
1	C	961	LEU
1	C	980	TRP
1	C	982	PHE
1	C	1000	LEU
1	C	1009	TRP
1	C	1014	THR
1	C	1016	TYR
2	D	54	ILE

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Mol	Chain	Res	Type
2	D	56	VAL
2	D	67	THR
2	D	72	VAL
2	D	79	GLN
2	D	80	ILE
2	D	83	SER
2	D	84	GLN
2	D	88	ILE
2	D	117	GLN
2	D	118	LYS
2	D	129	VAL
2	D	132	GLU
2	D	133	LEU
2	D	173	LYS
2	D	175	CYS
2	D	177	ILE
2	D	184	LEU
2	D	192	LYS
2	D	196	LEU
2	D	199	TYR
2	D	201	VAL
2	D	203	LYS
2	D	205	ASN
2	D	207	TYR
2	D	208	VAL
2	D	262	GLN
2	D	266	LEU
2	D	267	THR
2	D	268	MET
2	D	272	ILE
2	D	274	ILE
2	D	285	TYR
2	D	295	PHE
2	D	299	ILE
2	D	301	VAL
3	E	32	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	71	ASN

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Mol	Chain	Res	Type
1	A	122	ASN
1	A	161	GLN
1	A	324	ASN
1	A	383	HIS
1	A	391	HIS
1	A	427	GLN
1	A	496	HIS
1	A	550	HIS
1	A	570	ASN
1	A	649	ASN
1	A	690	GLN
1	A	747	ASN
1	A	764	ASN
1	A	831	ASN
1	A	854	GLN
1	A	897	GLN
2	B	69	GLN
2	B	117	GLN
2	B	158	ASN
2	B	262	GLN
1	C	37	HIS
1	C	71	ASN
1	C	161	GLN
1	C	324	ASN
1	C	383	HIS
1	C	391	HIS
1	C	427	GLN
1	C	550	HIS
1	C	570	ASN
1	C	649	ASN
1	C	690	GLN
1	C	747	ASN
1	C	764	ASN
1	C	831	ASN
1	C	854	GLN
1	C	897	GLN
1	C	898	GLN
2	D	69	GLN
2	D	117	GLN
2	D	158	ASN
2	D	262	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	$\# Z > 2$
1	PHD	C	369	5,1	9,11,12	2.22	2 (22%)	9,15,17	1.97	3 (33%)
1	PHD	A	369	5,1	9,11,12	2.21	2 (22%)	9,15,17	2.09	3 (33%)

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
1	PHD	C	369	5,1	-	0/8/11/13	-
1	PHD	A	369	5,1	-	2/8/11/13	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	369	PHD	OD2-CG	5.28	1.38	1.22
1	A	369	PHD	OD2-CG	5.20	1.38	1.22
1	A	369	PHD	P-OD1	-2.30	1.55	1.59
1	C	369	PHD	P-OD1	-2.21	1.55	1.59

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	369	PHD	OD2-CG-CB	-4.41	114.40	124.65
1	A	369	PHD	OD2-CG-CB	-4.01	115.34	124.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	PHD	CA-CB-CG	3.96	121.28	112.78
1	C	369	PHD	CA-CB-CG	3.11	119.44	112.78
1	A	369	PHD	OP2-P-OD1	2.05	111.28	105.32
1	C	369	PHD	OP2-P-OD1	2.02	111.20	105.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	369	PHD	CG-OD1-P-OP1
1	A	369	PHD	CA-CB-CG-OD1

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	369	PHD	5	0
1	A	369	PHD	7	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OBN	A	1	-	44,46,46	0.80	1 (2%)	69,76,76	2.01	13 (18%)
4	OBN	C	1	-	44,46,46	0.88	1 (2%)	69,76,76	2.18	18 (26%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OBN	A	1	-	-	4/11/116/116	0/6/6/6
4	OBN	C	1	-	-	4/11/116/116	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1	OBN	O21-C23	3.84	1.45	1.36
4	A	1	OBN	O21-C23	3.49	1.44	1.36

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	OBN	C15-C14-C13	8.01	109.34	103.37
4	A	1	OBN	C15-C14-C13	7.52	108.98	103.37
4	C	1	OBN	C16-C17-C13	6.20	111.63	105.01
4	A	1	OBN	C16-C17-C13	5.41	110.79	105.01
4	A	1	OBN	C16-C17-C20	-5.07	104.18	113.62
4	C	1	OBN	C15-C14-C8	-5.04	108.96	116.07
4	A	1	OBN	C15-C14-C8	-4.85	109.23	116.07
4	C	1	OBN	C18-C13-C12	-4.43	104.96	111.08
4	C	1	OBN	C16-C17-C20	-4.10	105.99	113.62
4	A	1	OBN	C18-C13-C12	-4.07	105.45	111.08
4	A	1	OBN	C13-C14-C8	3.95	118.64	113.84
4	C	1	OBN	C12-C13-C14	3.74	116.27	109.03
4	C	1	OBN	C12-C11-C9	-3.73	107.44	112.66
4	C	1	OBN	C17-C20-C22	-3.66	119.19	128.83
4	A	1	OBN	C17-C20-C22	-3.48	119.66	128.83
4	A	1	OBN	C12-C11-C9	-3.46	107.82	112.66
4	C	1	OBN	C13-C14-C8	3.40	117.97	113.84
4	C	1	OBN	C21-C20-C22	3.06	115.04	108.48
4	A	1	OBN	C12-C13-C14	3.04	114.91	109.03
4	C	1	OBN	O23-C23-C22	-3.03	124.85	130.80
4	A	1	OBN	C21-C20-C22	2.87	114.63	108.48
4	A	1	OBN	O23-C23-C22	-2.70	125.50	130.80
4	C	1	OBN	C1'-O3-C3	2.66	120.11	114.84
4	C	1	OBN	O21-C23-O23	2.48	125.73	120.50
4	C	1	OBN	C7-C6-C5	-2.48	109.80	112.72
4	C	1	OBN	O21-C21-C20	-2.42	100.47	104.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1	OBN	C20-C22-C23	-2.39	104.26	108.89
4	C	1	OBN	C20-C22-C23	-2.34	104.34	108.89
4	C	1	OBN	O3-C1'-C2'	-2.32	102.38	108.09
4	C	1	OBN	O11-C11-C9	2.18	116.25	111.29
4	A	1	OBN	C7-C6-C5	-2.08	110.27	112.72

There are no chirality outliers.

All (8) torsion outliers are listed below:

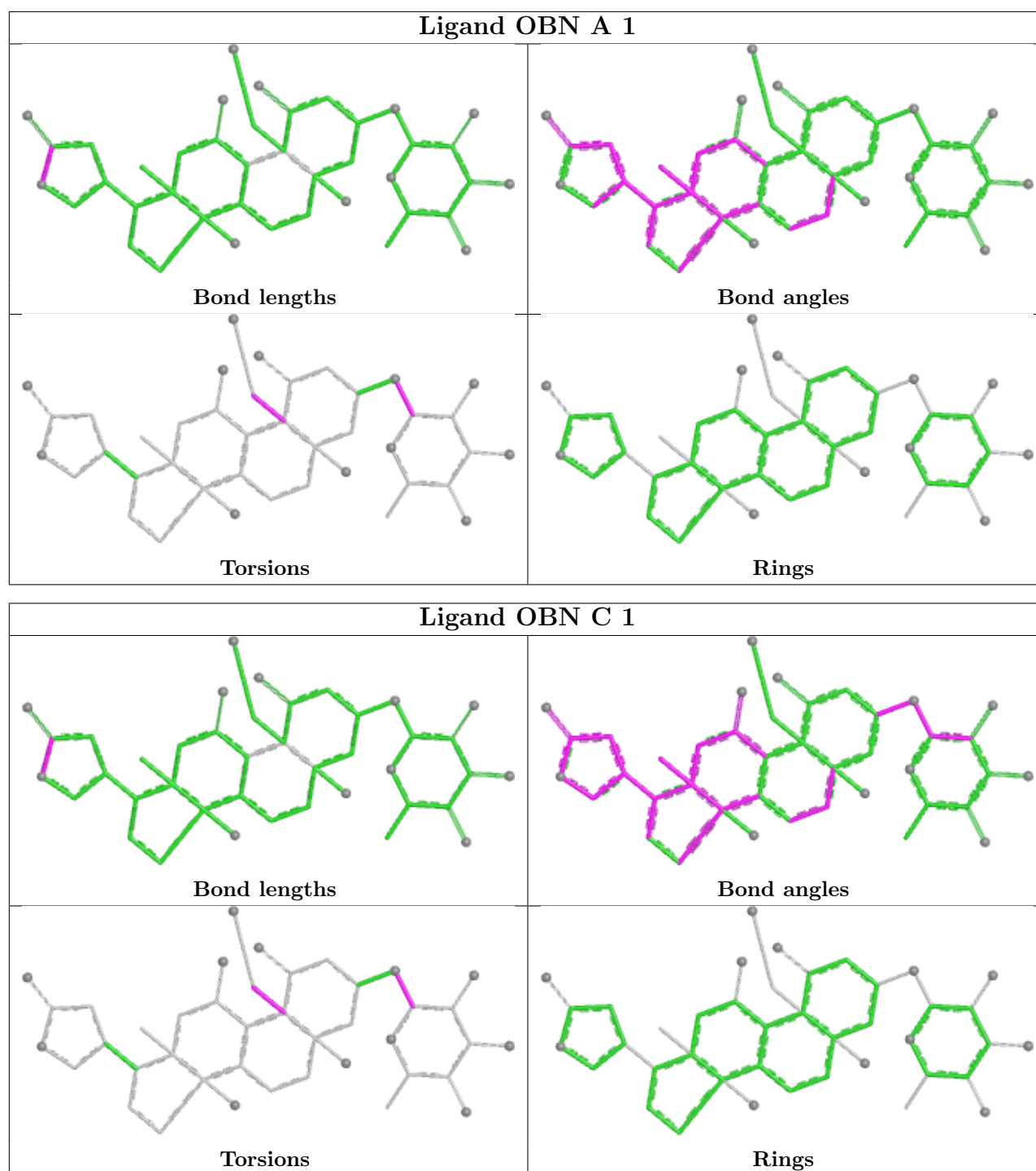
Mol	Chain	Res	Type	Atoms
4	A	1	OBN	C1-C10-C19-O19
4	C	1	OBN	C1-C10-C19-O19
4	A	1	OBN	C9-C10-C19-O19
4	C	1	OBN	C9-C10-C19-O19
4	A	1	OBN	O5'-C1'-O3-C3
4	C	1	OBN	O5'-C1'-O3-C3
4	C	1	OBN	C2'-C1'-O3-C3
4	A	1	OBN	C2'-C1'-O3-C3

There are no ring outliers.

2 monomers are involved in 49 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	OBN	25	0
4	C	1	OBN	24	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	991/992 (99%)	0.49	67 (6%)	23 25	158, 252, 353, 457	0
1	C	991/992 (99%)	0.42	62 (6%)	26 27	175, 274, 412, 550	0
2	B	264/277 (95%)	0.60	31 (11%)	9 14	207, 280, 383, 469	0
2	D	264/277 (95%)	0.58	19 (7%)	21 24	207, 280, 383, 469	0
3	E	31/31 (100%)	-0.05	2 (6%)	25 26	177, 249, 313, 421	0
3	G	31/31 (100%)	0.46	1 (3%)	50 41	158, 247, 330, 396	0
All	All	2572/2600 (98%)	0.48	182 (7%)	22 24	158, 266, 391, 550	0

All (182) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	168	GLY	6.3
2	B	158	ASN	5.9
1	A	223	ASP	5.7
1	C	573	LEU	5.3
2	D	168	GLY	4.8
1	A	501	LYS	4.8
1	A	869	ASN	4.7
1	C	971	LEU	4.6
2	B	276	CYS	4.2
2	B	258	LEU	4.2
1	A	837	LEU	4.1
1	C	488	ASN	4.1
2	B	79	GLN	4.0
1	C	840	GLU	3.9
1	A	48	TYR	3.9
1	C	978	PRO	3.9
2	D	126	CYS	3.9
1	A	934	ARG	3.9
2	B	215	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	938	PHE	3.7
1	C	366	ILE	3.7
1	C	177	GLU	3.7
1	A	259	VAL	3.6
1	C	64	ILE	3.6
1	C	748	PHE	3.5
1	C	466	ARG	3.5
1	C	498	LEU	3.4
1	A	978	PRO	3.4
1	A	355	GLU	3.3
2	B	184	LEU	3.3
1	C	752	VAL	3.3
2	B	260	ALA	3.3
1	A	961	LEU	3.3
1	C	397	GLU	3.2
1	A	268	SER	3.2
1	A	509	ASP	3.2
1	C	942	MET	3.2
2	B	278	ALA	3.1
2	D	73	ALA	3.1
2	B	159	CYS	3.1
1	A	992	PHE	3.1
1	C	268	SER	3.1
2	D	57	MET	3.1
1	C	456	CYS	3.0
2	D	276	CYS	3.0
1	A	1011	GLU	3.0
2	D	125	ASP	2.9
1	A	187	LYS	2.9
1	C	938	PHE	2.9
1	A	971	LEU	2.9
1	C	367	CYS	2.9
2	B	175	CYS	2.9
2	D	258	LEU	2.9
1	C	687	SER	2.9
3	G	47	SER	2.8
2	B	211	VAL	2.8
3	E	47	SER	2.8
1	A	277	ILE	2.8
1	A	92	GLY	2.8
2	D	79	GLN	2.8
1	A	44	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
2	D	222	GLU	2.7
1	C	241	ASN	2.7
1	C	708	THR	2.7
2	B	299	ILE	2.7
2	B	86	THR	2.7
1	A	838	VAL	2.7
1	A	763	ASP	2.7
1	C	418	ALA	2.7
2	D	64	PHE	2.7
1	C	703	ALA	2.6
2	B	83	SER	2.6
2	D	41	ILE	2.6
1	A	907	VAL	2.6
1	C	178	VAL	2.6
1	C	606	VAL	2.6
1	A	748	PHE	2.6
1	A	538	LEU	2.6
1	A	868	GLU	2.6
2	B	111	LYS	2.6
2	B	71	ARG	2.6
2	D	255	LEU	2.6
1	A	354	LEU	2.6
2	B	61	ILE	2.5
2	B	213	CYS	2.5
1	A	30	LYS	2.5
1	A	581	LEU	2.5
2	B	57	MET	2.5
2	B	174	PRO	2.5
1	A	210	SER	2.5
2	B	243	TYR	2.5
1	C	289	THR	2.5
1	C	210	SER	2.5
1	C	874	ILE	2.5
1	C	550	HIS	2.5
1	C	659	HIS	2.5
1	A	720	LYS	2.5
1	A	545	VAL	2.5
1	C	403	SER	2.5
1	C	237	PHE	2.4
1	C	1016	TYR	2.4
2	D	169	TYR	2.4
1	A	592	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	384	MET	2.4
2	B	113	LYS	2.4
1	C	485	ILE	2.4
2	B	112	TYR	2.4
1	C	188	GLY	2.4
1	C	107	ALA	2.4
2	D	45	CYS	2.4
1	A	239	SER	2.4
1	A	600	ARG	2.4
1	A	41	LEU	2.4
2	D	193	ASN	2.4
1	A	982	PHE	2.3
1	C	259	VAL	2.3
2	B	209	LEU	2.3
1	A	776	ASN	2.3
1	C	589	ARG	2.3
1	A	337	LEU	2.3
3	E	17	ASP	2.3
1	C	599	CYS	2.3
1	C	49	GLY	2.3
1	C	144	GLU	2.3
1	C	32	VAL	2.3
1	A	98	TRP	2.3
2	B	188	PRO	2.3
1	C	409	ALA	2.3
2	B	186	PHE	2.3
1	A	634	VAL	2.3
1	A	884	ASP	2.3
2	B	180	LEU	2.3
1	C	756	GLU	2.3
1	A	421	CYS	2.3
1	A	870	GLY	2.3
1	A	209	SER	2.2
1	A	306	LEU	2.2
1	A	895	TYR	2.2
1	A	491	THR	2.2
2	B	277	LYS	2.2
1	A	224	PHE	2.2
1	C	299	PHE	2.2
1	C	355	GLU	2.2
1	A	941	GLY	2.2
2	D	215	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	260	MET	2.2
1	A	599	CYS	2.2
1	C	892	GLU	2.2
1	C	487	LYS	2.2
1	C	211	LEU	2.2
1	C	489	PRO	2.2
1	A	366	ILE	2.2
1	A	687	SER	2.2
1	A	305	ILE	2.2
1	A	683	PHE	2.2
2	D	211	VAL	2.1
1	C	630	GLY	2.1
2	D	127	GLY	2.1
1	C	572	PRO	2.1
1	C	541	LEU	2.1
1	C	836	LYS	2.1
2	B	178	ILE	2.1
1	C	979	THR	2.1
1	A	540	GLY	2.1
1	C	875	HIS	2.1
2	B	279	TYR	2.1
1	A	717	ALA	2.1
1	A	979	THR	2.1
1	C	819	GLN	2.1
1	A	191	ARG	2.1
1	C	173	ILE	2.1
1	A	863	PHE	2.0
1	C	478	THR	2.0
1	A	32	VAL	2.0
1	A	601	SER	2.0
1	C	515	LEU	2.0
1	C	59	ALA	2.0
1	A	227	GLU	2.0
1	A	505	GLU	2.0
2	D	234	GLY	2.0
1	C	491	THR	2.0
1	A	985	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	PHD	A	369	12/13	0.96	0.17	249,249,377,377	0
1	PHD	C	369	12/13	0.96	0.14	288,288,461,461	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

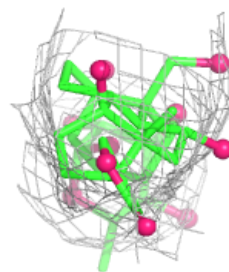
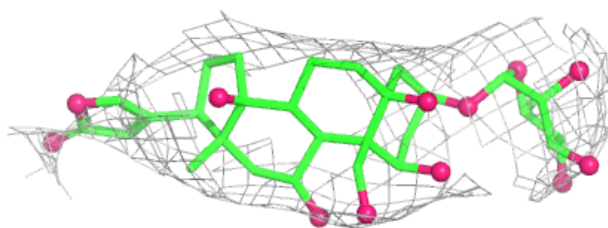
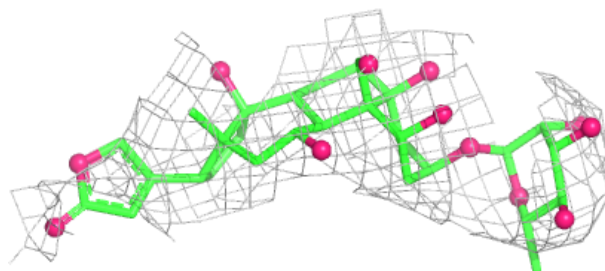
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	C	1017	1/1	0.78	0.25	274,274,274,274	0
5	MG	A	1017	1/1	0.87	0.23	274,274,274,274	0
4	OBN	A	1	41/41	0.95	0.13	274,274,274,274	0
4	OBN	C	1	41/41	0.95	0.12	274,274,274,274	0

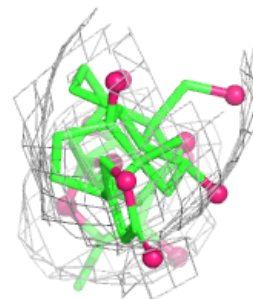
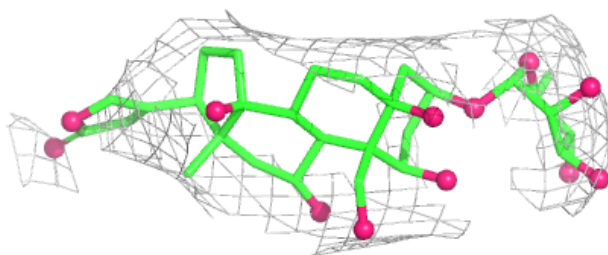
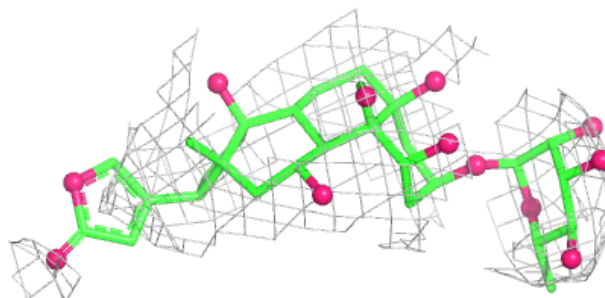
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around OBN A 1:

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

**Electron density around OBN C 1:**

$2mF_o-DF_c$ (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.