



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:08 am GMT

PDB ID : 1N8P
Title : Crystal Structure of cystathionine gamma-lyase from yeast
Authors : Messerschmidt, A.; Worbs, M.; Steegborn, C.; Wahl, M.C.; Huber, R.; Clausen, T.
Deposited on : 2002-11-21
Resolution : 2.60 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

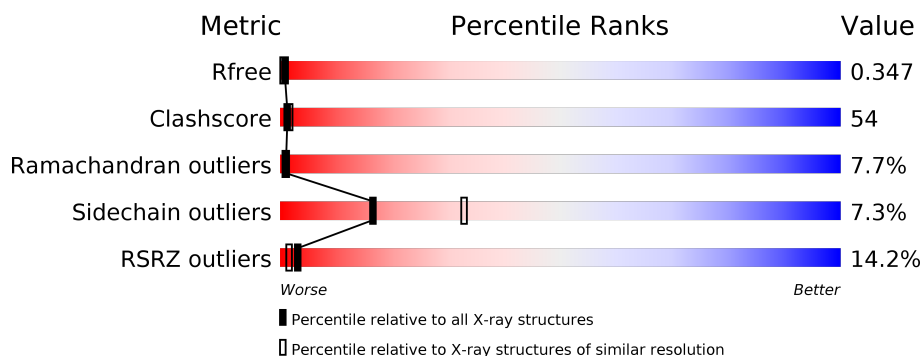
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	393	<div> <div>12%</div> <div>35%</div> <div>55%</div> <div>8%</div> </div>
1	B	393	<div> <div>15%</div> <div>35%</div> <div>53%</div> <div>11%</div> </div>
1	C	393	<div> <div>17%</div> <div>30%</div> <div>61%</div> <div>9%</div> </div>
1	D	393	<div> <div>13%</div> <div>40%</div> <div>50%</div> <div>10%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PLP	D	400	-	-	-	X

2 Entry composition [i](#)

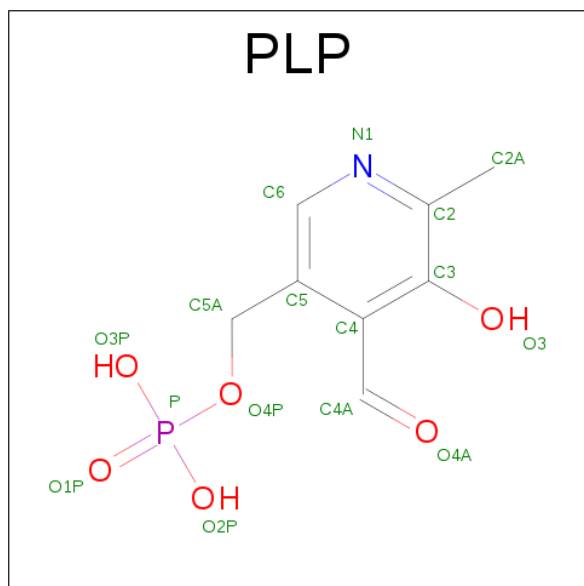
There are 3 unique types of molecules in this entry. The entry contains 12287 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cystathionine gamma-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			2969	1871	518	578	2			
1	B	393	Total	C	N	O	S	0	0	0
			2969	1871	518	578	2			
1	C	393	Total	C	N	O	S	0	0	0
			2969	1871	518	578	2			
1	D	393	Total	C	N	O	S	0	0	0
			2969	1871	518	578	2			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

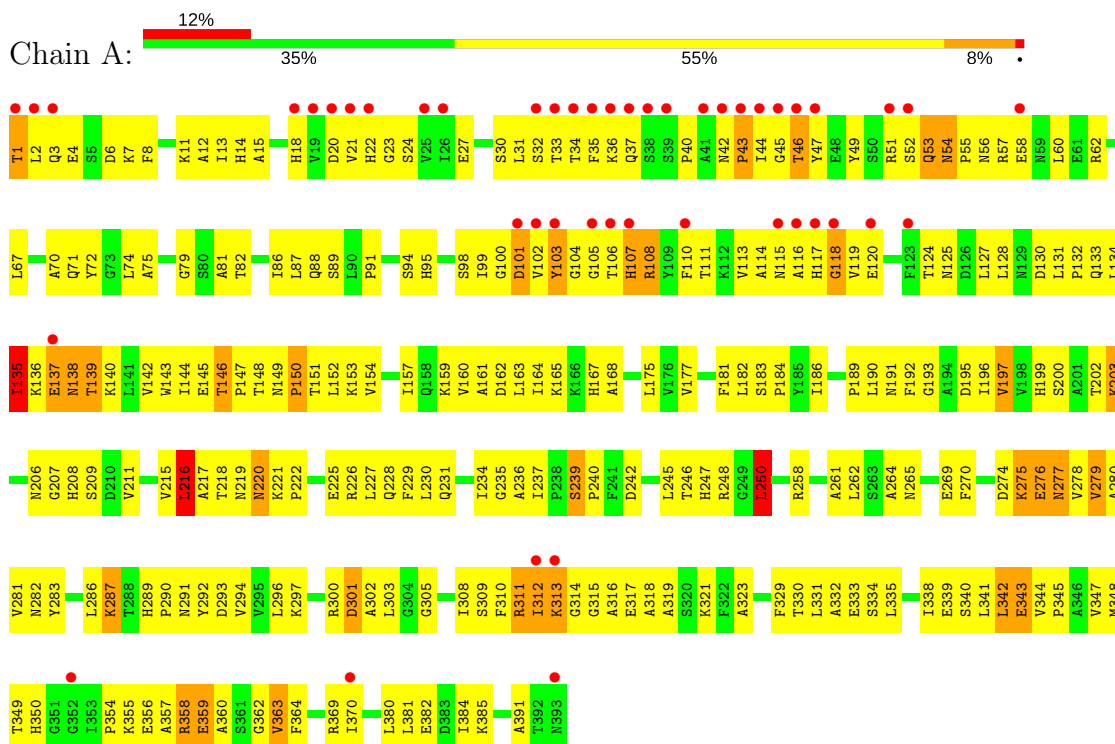
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	74	Total	O	0	0
			74	74		
3	B	94	Total	O	0	0
			94	94		
3	C	95	Total	O	0	0
			95	95		
3	D	88	Total	O	0	0
			88	88		

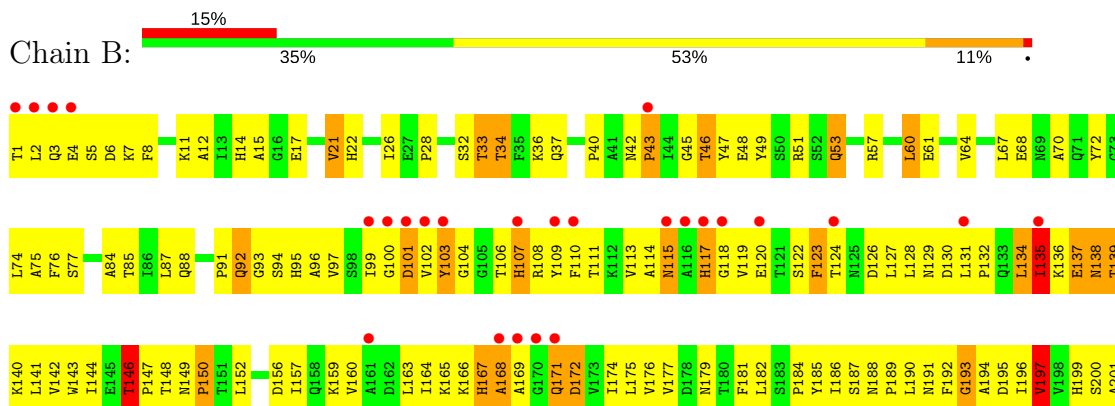
3 Residue-property plots [i](#)

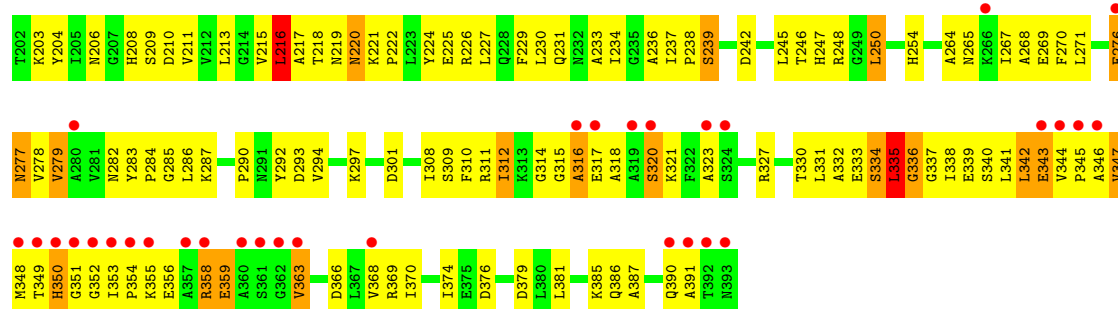
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

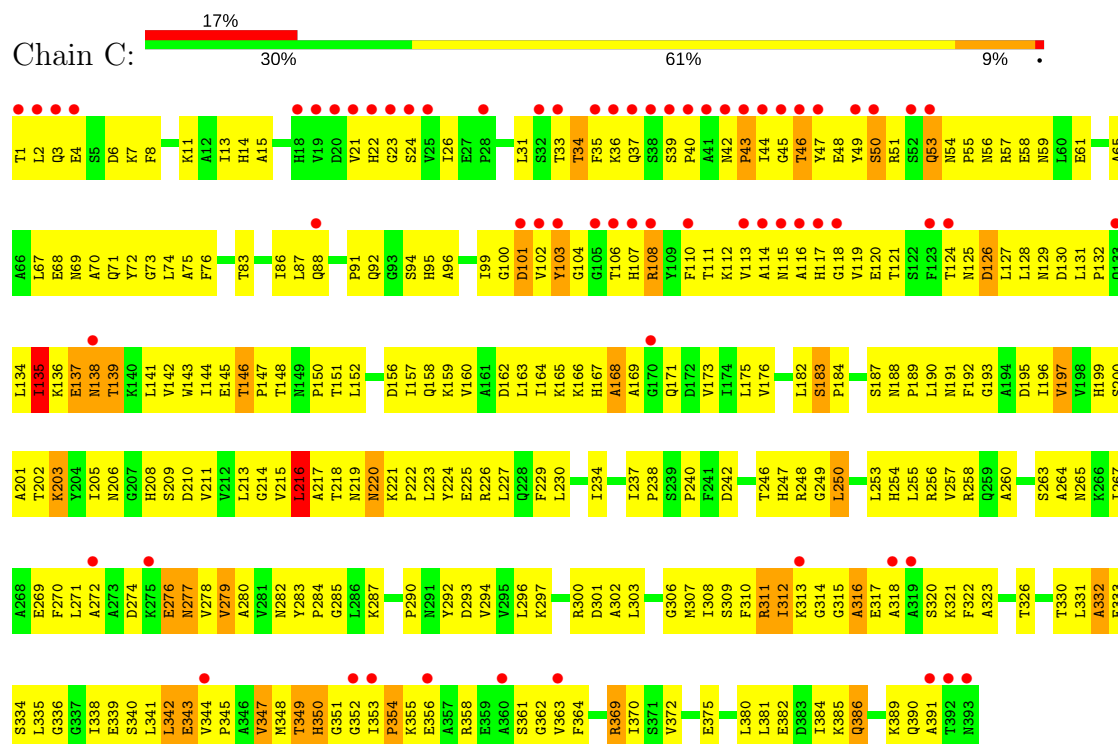


• Molecule 1: Cystathionine gamma-lyase

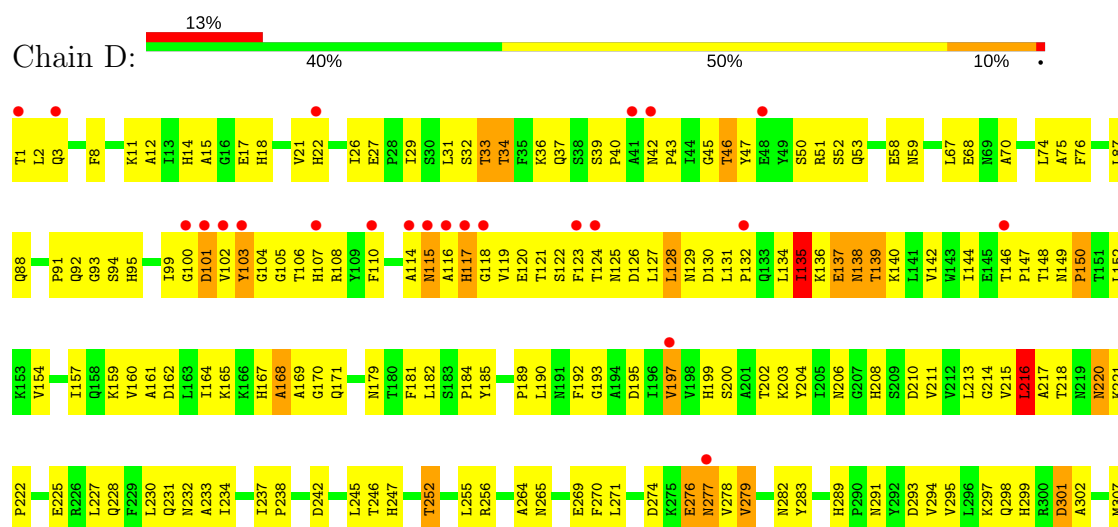


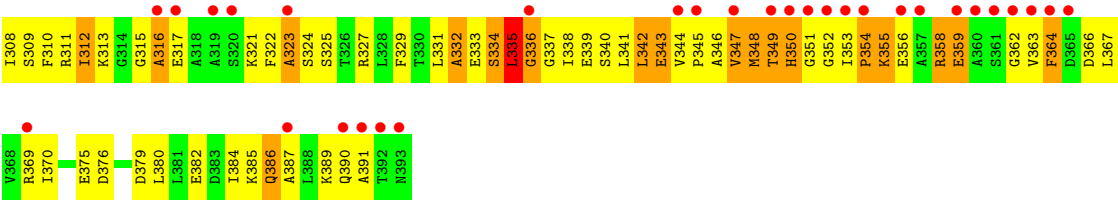


- Molecule 1: Cystathionine gamma-lyase



- Molecule 1: Cystathionine gamma-lyase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.82Å 62.16Å 160.84Å 90.00° 105.42° 90.00°	Depositor
Resolution (Å)	6.00 – 2.60 19.90 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.1 (6.00-2.60) 98.9 (19.90-2.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.59Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.253 , 0.346 0.257 , 0.347	Depositor DCC
R_{free} test set	2075 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.556	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 72.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12287	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.54	0/3026	0.80	3/4121 (0.1%)
1	B	0.52	0/3026	0.80	5/4121 (0.1%)
1	C	0.50	0/3026	0.78	2/4121 (0.0%)
1	D	0.56	0/3026	0.79	2/4121 (0.0%)
All	All	0.53	0/12104	0.79	12/16484 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	216	LEU	CA-CB-CG	8.30	134.38	115.30
1	A	216	LEU	CA-CB-CG	6.59	130.45	115.30
1	B	200	SER	N-CA-C	-6.49	93.47	111.00
1	D	216	LEU	CA-CB-CG	6.44	130.11	115.30
1	D	200	SER	N-CA-C	-6.33	93.89	111.00
1	C	216	LEU	CA-CB-CG	6.20	129.57	115.30
1	A	250	LEU	CA-CB-CG	6.11	129.35	115.30
1	B	250	LEU	CA-CB-CG	5.93	128.93	115.30
1	A	200	SER	N-CA-C	-5.80	95.33	111.00
1	B	194	ALA	N-CA-C	-5.43	96.33	111.00
1	B	197	VAL	CB-CA-C	-5.30	101.33	111.40
1	C	200	SER	N-CA-C	-5.08	97.28	111.00

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	2969	0	2939	345	0
1	B	2969	0	2939	323	0
1	C	2969	0	2939	373	0
1	D	2969	0	2939	333	0
2	A	15	0	6	0	0
2	B	15	0	6	1	0
2	C	15	0	6	0	0
2	D	15	0	6	0	0
3	A	74	0	0	3	0
3	B	94	0	0	20	0
3	C	95	0	0	17	0
3	D	88	0	0	18	0
All	All	12287	0	11780	1281	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 54.

All (1281) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:LYS:HG2	1:B:391:ALA:HA	1.21	1.20
1:C:321:LYS:HG2	1:C:391:ALA:HA	1.28	1.16
1:A:36:LYS:H	1:C:23:GLY:HA3	1.17	1.09
1:D:321:LYS:HG2	1:D:391:ALA:HA	1.35	1.08
1:C:95:HIS:ND1	1:C:139:THR:HG22	1.69	1.08
1:A:95:HIS:ND1	1:A:139:THR:HG22	1.68	1.08
1:D:220:ASN:ND2	1:D:222:PRO:HD2	1.70	1.06
1:D:279:VAL:HB	1:D:311:ARG:HG3	1.36	1.06
1:D:95:HIS:ND1	1:D:139:THR:HG22	1.69	1.06
1:A:348:MET:HG2	1:B:40:PRO:O	1.55	1.05
1:C:37:GLN:HE21	1:C:43:PRO:HG3	1.13	1.05
1:B:347:VAL:HG23	1:B:348:MET:H	1.23	1.03
1:A:321:LYS:HG2	1:A:391:ALA:HA	1.42	1.01
1:C:115:ASN:O	1:D:92:GLN:HB2	1.59	1.01
1:B:95:HIS:ND1	1:B:139:THR:HG22	1.76	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:VAL:HB	1:B:311:ARG:HG3	1.42	1.00
1:A:220:ASN:ND2	1:A:222:PRO:HD2	1.77	0.98
1:A:3:GLN:HE22	1:A:15:ALA:HB2	1.28	0.98
1:A:37:GLN:HE21	1:A:43:PRO:HG3	1.25	0.98
1:B:323:ALA:HB1	1:B:331:LEU:HD13	1.46	0.97
1:A:136:LYS:HG3	1:A:137:GLU:H	1.27	0.96
1:A:206:ASN:HB2	1:A:246:THR:HG23	1.47	0.96
1:D:75:ALA:HA	1:D:215:VAL:HG12	1.46	0.95
1:B:342:LEU:HB2	1:B:370:ILE:HG22	1.45	0.95
1:B:195:ASP:O	1:B:218:THR:HG22	1.64	0.95
1:C:323:ALA:HB1	1:C:331:LEU:HD13	1.48	0.94
1:D:347:VAL:HG23	1:D:348:MET:H	1.33	0.94
1:C:279:VAL:HB	1:C:311:ARG:HG3	1.48	0.94
1:D:136:LYS:HG3	1:D:137:GLU:H	1.33	0.94
1:A:347:VAL:HG23	1:A:348:MET:H	1.35	0.92
1:C:347:VAL:HG23	1:C:348:MET:H	1.32	0.92
1:A:36:LYS:H	1:C:23:GLY:CA	1.82	0.92
1:B:335:LEU:O	1:B:337:GLY:N	2.04	0.91
1:A:323:ALA:HB1	1:A:331:LEU:HD13	1.54	0.89
1:A:23:GLY:HA3	1:C:36:LYS:H	1.34	0.89
1:A:279:VAL:HB	1:A:311:ARG:HG3	1.54	0.89
1:C:68:GLU:OE1	1:C:184:PRO:HG3	1.72	0.89
1:D:317:GLU:HB3	3:D:448:HOH:O	1.70	0.89
1:B:342:LEU:O	1:B:342:LEU:HD23	1.73	0.89
1:A:342:LEU:HB2	1:A:370:ILE:HG22	1.52	0.89
1:C:87:LEU:HD13	1:C:110:PHE:HA	1.55	0.88
1:A:23:GLY:CA	1:C:36:LYS:H	1.88	0.87
1:C:265:ASN:O	1:C:269:GLU:HG3	1.75	0.86
1:C:137:GLU:O	1:C:138:ASN:HB2	1.76	0.86
1:C:340:SER:O	1:C:341:LEU:HD23	1.75	0.86
1:C:144:ILE:HD11	1:C:160:VAL:HG11	1.58	0.86
1:A:36:LYS:N	1:C:23:GLY:HA3	1.90	0.86
1:B:99:ILE:O	1:B:102:VAL:HG23	1.76	0.85
1:C:37:GLN:NE2	1:C:43:PRO:HG3	1.91	0.85
1:A:71:GLN:H	1:A:219:ASN:ND2	1.75	0.84
1:B:277:ASN:HD22	1:B:277:ASN:N	1.76	0.84
1:A:340:SER:O	1:A:341:LEU:HD23	1.77	0.84
1:A:1:THR:HG21	1:A:14:HIS:CG	2.12	0.84
1:B:149:ASN:HB2	1:B:181:PHE:HE2	1.42	0.84
1:C:344:VAL:H	1:C:348:MET:CE	1.90	0.83
1:A:35:PHE:HB3	1:C:22:HIS:O	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:ASN:HD22	1:C:246:THR:HA	1.42	0.83
1:C:277:ASN:HD22	1:C:277:ASN:N	1.77	0.83
1:B:346:ALA:HB3	3:B:492:HOH:O	1.79	0.82
1:B:220:ASN:ND2	1:B:222:PRO:HD2	1.95	0.82
1:A:338:ILE:HG22	3:A:416:HOH:O	1.79	0.82
1:D:349:THR:HG22	1:D:350:HIS:N	1.93	0.82
1:B:95:HIS:HD2	1:B:120:GLU:HB3	1.45	0.81
1:A:118:GLY:HA3	3:B:424:HOH:O	1.79	0.81
1:A:136:LYS:O	1:A:137:GLU:HB3	1.77	0.81
1:C:220:ASN:ND2	1:C:222:PRO:HD2	1.96	0.81
1:C:1:THR:HG21	1:C:14:HIS:CG	2.16	0.81
1:C:342:LEU:HD23	1:C:342:LEU:O	1.82	0.80
1:C:3:GLN:HE21	1:C:11:LYS:HG2	1.45	0.80
1:D:344:VAL:H	1:D:348:MET:HE3	1.45	0.80
1:A:95:HIS:HB3	1:A:138:ASN:C	2.02	0.80
1:D:51:ARG:HG3	1:D:237:ILE:HD13	1.63	0.79
1:D:75:ALA:CA	1:D:215:VAL:HG12	2.11	0.79
1:B:150:PRO:O	1:B:152:LEU:HG	1.82	0.78
1:A:23:GLY:HA3	1:C:36:LYS:N	1.97	0.78
1:A:343:GLU:HA	1:A:348:MET:HE1	1.65	0.78
1:C:206:ASN:HB2	1:C:246:THR:HG23	1.66	0.78
1:D:146:THR:OG1	1:D:147:PRO:HD3	1.84	0.78
1:B:70:ALA:HB2	1:B:190:LEU:HD12	1.65	0.78
1:D:344:VAL:H	1:D:348:MET:CE	1.96	0.78
1:B:135:ILE:HG21	1:B:167:HIS:O	1.84	0.78
1:B:114:ALA:CB	1:B:119:VAL:H	1.97	0.78
1:B:379:ASP:OD1	1:C:7:LYS:HG2	1.83	0.78
1:A:242:ASP:OD1	1:B:239:SER:HB2	1.82	0.78
1:B:149:ASN:HB2	1:B:181:PHE:CE2	2.19	0.78
1:C:95:HIS:O	1:C:139:THR:HA	1.84	0.77
1:A:3:GLN:HE21	1:A:11:LYS:HG2	1.48	0.77
1:A:382:GLU:HG3	3:A:420:HOH:O	1.83	0.77
1:B:95:HIS:HB3	1:B:139:THR:N	1.99	0.77
1:C:95:HIS:HB3	1:C:139:THR:N	2.00	0.77
1:D:114:ALA:HA	1:D:119:VAL:H	1.49	0.77
1:A:136:LYS:HA	1:A:139:THR:HG23	1.65	0.77
1:A:95:HIS:HB3	1:A:139:THR:N	1.99	0.77
1:A:23:GLY:C	1:C:36:LYS:H	1.87	0.77
1:D:3:GLN:HE21	1:D:11:LYS:HG2	1.50	0.77
1:A:137:GLU:O	1:A:138:ASN:HB2	1.83	0.77
1:D:335:LEU:O	1:D:337:GLY:N	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LYS:O	1:B:169:ALA:HB2	1.85	0.76
1:C:293:ASP:O	1:C:297:LYS:HG2	1.84	0.76
1:D:220:ASN:HD22	1:D:220:ASN:C	1.88	0.76
1:C:146:THR:OG1	1:C:147:PRO:HD3	1.85	0.76
1:B:143:TRP:CZ3	1:B:176:VAL:HG11	2.21	0.75
1:D:342:LEU:HD23	1:D:342:LEU:O	1.87	0.75
1:D:95:HIS:HB3	1:D:138:ASN:C	2.06	0.75
1:A:87:LEU:HD13	1:A:110:PHE:HA	1.67	0.75
1:C:220:ASN:C	1:C:220:ASN:HD22	1.89	0.75
1:D:136:LYS:CG	1:D:137:GLU:H	1.98	0.75
1:A:142:VAL:HG21	1:A:164:ILE:HD11	1.69	0.75
1:B:157:ILE:HG22	1:B:192:PHE:O	1.87	0.75
1:B:70:ALA:HA	1:B:219:ASN:HD21	1.50	0.75
1:B:95:HIS:HB3	1:B:138:ASN:C	2.07	0.74
1:D:323:ALA:HA	1:D:342:LEU:HD11	1.67	0.74
1:C:142:VAL:HG21	1:C:164:ILE:HD11	1.69	0.74
1:A:22:HIS:O	1:C:35:PHE:HB3	1.87	0.74
1:B:344:VAL:HG21	3:B:443:HOH:O	1.86	0.74
1:D:195:ASP:O	1:D:218:THR:HG22	1.87	0.74
1:A:135:ILE:HD12	1:A:167:HIS:HB2	1.69	0.74
1:A:206:ASN:HD22	1:A:246:THR:HA	1.51	0.74
1:A:220:ASN:HD22	1:A:222:PRO:HD2	1.52	0.74
1:C:3:GLN:HE22	1:C:15:ALA:HB2	1.52	0.74
1:D:68:GLU:HG3	3:D:439:HOH:O	1.86	0.74
1:A:75:ALA:HA	1:A:215:VAL:HG12	1.69	0.74
1:B:74:LEU:HB2	1:B:216:LEU:HD22	1.70	0.74
1:C:114:ALA:CB	1:C:119:VAL:H	2.01	0.74
1:D:136:LYS:O	1:D:137:GLU:HB3	1.85	0.74
1:D:114:ALA:CB	1:D:119:VAL:H	1.99	0.73
3:C:458:HOH:O	1:D:33:THR:HG21	1.88	0.73
1:C:150:PRO:HG3	1:C:345:PRO:HG3	1.70	0.73
1:C:150:PRO:O	1:C:152:LEU:HG	1.88	0.73
1:C:282:ASN:HB2	1:C:309:SER:HB3	1.70	0.73
1:C:116:ALA:HB3	1:D:92:GLN:CB	2.18	0.73
1:A:99:ILE:O	1:A:102:VAL:HG23	1.88	0.73
1:D:347:VAL:HA	3:D:438:HOH:O	1.86	0.73
1:A:71:GLN:H	1:A:219:ASN:HD22	1.35	0.73
1:D:230:LEU:O	1:D:234:ILE:HG12	1.89	0.73
1:A:277:ASN:HD22	1:A:277:ASN:N	1.87	0.72
1:D:3:GLN:HE22	1:D:15:ALA:HB2	1.54	0.72
1:D:88:GLN:OE1	1:D:234:ILE:HD13	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:220:ASN:HD21	1:D:222:PRO:HD2	1.53	0.72
1:D:349:THR:HG22	1:D:350:HIS:H	1.55	0.72
1:D:106:THR:HG22	1:D:110:PHE:CE1	2.24	0.72
1:D:342:LEU:HB2	1:D:370:ILE:HG22	1.71	0.72
1:B:26:ILE:HB	1:D:32:SER:HB3	1.71	0.72
1:D:95:HIS:NE2	1:D:122:SER:OG	2.22	0.72
1:C:31:LEU:HD23	1:C:240:PRO:HB2	1.72	0.72
1:D:220:ASN:HD22	1:D:222:PRO:HD2	1.50	0.72
1:C:87:LEU:HD11	1:C:110:PHE:CD1	2.25	0.72
1:B:321:LYS:HG2	1:B:391:ALA:CA	2.11	0.71
1:D:149:ASN:HB2	1:D:181:PHE:HE2	1.55	0.71
1:A:162:ASP:HA	1:A:165:LYS:NZ	2.05	0.71
1:D:317:GLU:HB2	3:D:442:HOH:O	1.91	0.71
1:A:347:VAL:HG23	1:A:348:MET:N	2.04	0.71
1:B:136:LYS:HA	1:B:139:THR:HG23	1.71	0.71
1:C:102:VAL:HG12	1:C:103:TYR:O	1.91	0.71
1:D:277:ASN:N	1:D:277:ASN:HD22	1.89	0.71
1:C:348:MET:HE2	1:D:40:PRO:HB3	1.72	0.71
1:B:293:ASP:O	1:B:297:LYS:HG2	1.90	0.71
1:C:95:HIS:HB3	1:C:138:ASN:C	2.11	0.71
1:A:220:ASN:HD21	1:A:222:PRO:HD2	1.55	0.71
1:A:258:ARG:NH1	1:A:303:LEU:HD11	2.06	0.70
1:D:3:GLN:NE2	1:D:11:LYS:HG2	2.05	0.70
1:B:100:GLY:O	1:B:102:VAL:N	2.24	0.70
1:C:75:ALA:HA	1:C:215:VAL:HG12	1.74	0.70
1:C:342:LEU:HB2	1:C:370:ILE:HG22	1.72	0.70
1:B:344:VAL:H	1:B:348:MET:CE	2.05	0.70
1:A:146:THR:OG1	1:A:147:PRO:HD3	1.92	0.70
1:A:150:PRO:HB3	1:A:369:ARG:HD2	1.72	0.70
1:D:315:GLY:O	1:D:317:GLU:N	2.25	0.70
1:D:362:GLY:O	1:D:364:PHE:N	2.24	0.70
1:C:254:HIS:CE1	1:C:255:LEU:HG	2.26	0.70
1:C:349:THR:HG22	1:C:350:HIS:N	2.07	0.70
1:D:106:THR:HA	1:D:110:PHE:CD1	2.27	0.70
1:A:37:GLN:NE2	1:A:43:PRO:HG3	2.03	0.70
1:A:95:HIS:O	1:A:139:THR:HA	1.92	0.70
1:B:127:LEU:HD23	1:B:160:VAL:HG21	1.74	0.70
1:B:220:ASN:HD22	1:B:220:ASN:C	1.94	0.70
1:B:390:GLN:HA	3:B:465:HOH:O	1.91	0.70
1:B:45:GLY:O	1:B:47:TYR:N	2.24	0.70
1:D:53:GLN:NE2	1:D:58:GLU:HB2	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:THR:OG1	1:B:147:PRO:HD3	1.91	0.69
1:B:152:LEU:HD12	1:B:282:ASN:O	1.92	0.69
1:C:277:ASN:H	1:C:277:ASN:HD22	1.38	0.69
1:B:128:LEU:HD22	3:B:413:HOH:O	1.91	0.69
1:B:206:ASN:HB2	1:B:246:THR:HG23	1.74	0.69
1:C:196:ILE:HG12	1:C:218:THR:HG21	1.74	0.69
1:D:279:VAL:CB	1:D:311:ARG:HG3	2.20	0.69
1:D:102:VAL:HG12	1:D:103:TYR:O	1.92	0.69
1:D:206:ASN:HB2	1:D:246:THR:HG23	1.73	0.69
1:D:1:THR:HG21	1:D:14:HIS:CB	2.23	0.69
1:C:116:ALA:HB3	1:D:92:GLN:HB2	1.75	0.69
1:D:99:ILE:O	1:D:102:VAL:HG23	1.93	0.69
1:B:347:VAL:HG23	1:B:348:MET:N	2.05	0.69
1:D:45:GLY:O	1:D:47:TYR:N	2.25	0.69
1:B:182:LEU:HD22	1:B:186:ILE:HG21	1.74	0.68
1:D:1:THR:HG21	1:D:14:HIS:CG	2.28	0.68
1:C:137:GLU:O	1:C:138:ASN:CB	2.41	0.68
1:B:184:PRO:HD3	1:B:199:HIS:CE1	2.28	0.68
1:D:220:ASN:ND2	1:D:222:PRO:CD	2.54	0.68
1:D:87:LEU:HD13	1:D:110:PHE:HA	1.74	0.68
1:B:131:LEU:N	1:B:132:PRO:HD2	2.07	0.68
1:B:315:GLY:O	1:B:317:GLU:N	2.27	0.68
1:C:165:LYS:O	1:C:169:ALA:HB2	1.93	0.68
1:A:33:THR:HG22	1:A:34:THR:HG23	1.76	0.68
1:A:102:VAL:HG12	1:A:103:TYR:N	2.09	0.68
1:B:3:GLN:HE22	1:B:15:ALA:HB2	1.58	0.68
1:C:106:THR:O	1:C:110:PHE:HB2	1.93	0.68
1:D:208:HIS:CE1	1:D:338:ILE:HD12	2.28	0.68
1:B:323:ALA:HA	1:B:342:LEU:HD11	1.75	0.68
1:A:137:GLU:O	1:A:138:ASN:CB	2.42	0.67
1:A:208:HIS:CE1	1:A:338:ILE:HD12	2.28	0.67
1:C:136:LYS:HA	1:C:139:THR:HG23	1.76	0.67
1:C:344:VAL:H	1:C:348:MET:HE3	1.57	0.67
1:D:126:ASP:OD2	1:D:129:ASN:HB2	1.93	0.67
1:A:95:HIS:ND1	1:A:139:THR:CG2	2.55	0.67
1:C:115:ASN:HD22	1:C:115:ASN:H	1.41	0.67
1:C:310:PHE:HE1	1:C:312:ILE:HG23	1.59	0.67
1:C:53:GLN:CD	1:C:58:GLU:HB2	2.14	0.67
1:D:114:ALA:CA	1:D:119:VAL:H	2.07	0.67
1:D:340:SER:O	1:D:341:LEU:HD23	1.93	0.67
1:A:91:PRO:HG2	1:A:94:SER:OG	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:270:PHE:CZ	1:C:385:LYS:HG2	2.29	0.67
1:D:70:ALA:HB2	1:D:190:LEU:HD12	1.75	0.67
1:A:3:GLN:NE2	1:A:11:LYS:HG2	2.09	0.67
1:A:128:LEU:HD13	1:A:159:LYS:HD3	1.76	0.67
1:B:343:GLU:OE1	1:B:369:ARG:HD3	1.95	0.67
1:D:136:LYS:O	1:D:137:GLU:CB	2.42	0.67
1:A:344:VAL:H	1:A:348:MET:CE	2.07	0.67
1:C:3:GLN:NE2	1:C:11:LYS:HG2	2.09	0.67
1:D:347:VAL:HG23	1:D:348:MET:N	2.09	0.67
1:B:106:THR:HG22	1:B:110:PHE:CE1	2.30	0.67
1:B:114:ALA:HB2	1:B:119:VAL:HB	1.77	0.67
1:B:379:ASP:OD2	1:C:6:ASP:HB3	1.95	0.67
1:D:147:PRO:HG2	1:D:182:LEU:HG	1.76	0.67
1:C:37:GLN:HG2	1:C:43:PRO:HA	1.77	0.66
1:A:248:ARG:NE	1:D:210:ASP:OD1	2.25	0.66
1:B:142:VAL:HG21	1:B:164:ILE:HD11	1.78	0.66
1:C:53:GLN:OE1	1:C:58:GLU:HB2	1.95	0.66
1:A:310:PHE:HE1	1:A:312:ILE:HG23	1.58	0.66
1:A:315:GLY:O	1:A:317:GLU:N	2.28	0.66
1:C:87:LEU:CD1	1:C:110:PHE:HA	2.25	0.66
1:C:369:ARG:HH11	1:C:369:ARG:HG2	1.58	0.66
1:C:331:LEU:HD21	1:D:40:PRO:N	2.10	0.66
1:D:3:GLN:HE21	1:D:11:LYS:HA	1.60	0.66
1:C:344:VAL:H	1:C:348:MET:HE1	1.61	0.66
1:C:53:GLN:HA	1:C:57:ARG:NH2	2.11	0.66
1:B:282:ASN:HB2	1:B:309:SER:HB3	1.78	0.65
1:C:375:GLU:N	1:C:375:GLU:OE2	2.26	0.65
1:C:258:ARG:HH11	1:C:303:LEU:HD11	1.60	0.65
1:D:204:TYR:CE2	1:D:336:GLY:HA2	2.31	0.65
1:A:106:THR:HA	1:A:110:PHE:CD1	2.32	0.65
1:A:134:LEU:O	1:A:136:LYS:N	2.30	0.65
1:D:137:GLU:O	1:D:138:ASN:CB	2.44	0.65
1:B:147:PRO:HG2	1:B:182:LEU:HG	1.79	0.65
1:C:106:THR:HA	1:C:110:PHE:CD1	2.32	0.65
1:A:35:PHE:HA	1:C:23:GLY:C	2.17	0.65
1:C:131:LEU:N	1:C:132:PRO:HD2	2.12	0.65
1:A:6:ASP:HB3	1:D:379:ASP:OD2	1.97	0.65
1:A:95:HIS:HB2	1:A:138:ASN:HB3	1.79	0.65
1:C:143:TRP:CZ3	1:C:176:VAL:HG11	2.31	0.65
1:C:355:LYS:HB2	1:C:358:ARG:NH2	2.11	0.65
1:B:26:ILE:HB	1:D:32:SER:CB	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:LYS:CA	1:A:139:THR:HG23	2.27	0.64
1:A:37:GLN:HA	1:A:43:PRO:HA	1.77	0.64
1:D:197:VAL:O	1:D:216:LEU:HA	1.97	0.64
1:B:210:ASP:OD1	1:C:248:ARG:NE	2.19	0.64
1:D:265:ASN:O	1:D:269:GLU:HG3	1.97	0.64
1:A:196:ILE:HG23	1:A:218:THR:CG2	2.28	0.64
1:A:23:GLY:O	1:C:36:LYS:N	2.30	0.64
1:C:351:GLY:O	1:C:353:ILE:N	2.29	0.64
1:C:100:GLY:O	1:C:102:VAL:N	2.31	0.64
1:C:88:GLN:OE1	1:C:234:ILE:HD13	1.97	0.64
1:A:23:GLY:O	1:C:36:LYS:HG3	1.98	0.64
1:B:21:VAL:HG23	1:D:21:VAL:HG21	1.80	0.64
1:D:271:LEU:O	1:D:278:VAL:HG11	1.97	0.64
1:A:3:GLN:NE2	1:A:15:ALA:HB2	2.08	0.64
1:B:333:GLU:OE1	1:B:343:GLU:HG3	1.97	0.64
1:B:358:ARG:HH11	1:B:358:ARG:HB3	1.62	0.64
1:D:331:LEU:HA	1:D:342:LEU:HD23	1.79	0.64
1:A:144:ILE:HD11	1:A:160:VAL:HG11	1.79	0.64
1:D:350:HIS:HA	3:D:421:HOH:O	1.96	0.63
1:A:196:ILE:HA	1:A:218:THR:HG22	1.80	0.63
1:C:95:HIS:HD2	1:C:120:GLU:HB3	1.61	0.63
1:C:71:GLN:H	1:C:219:ASN:ND2	1.97	0.63
1:D:181:PHE:CD1	1:D:335:LEU:HD11	2.32	0.63
1:A:332:ALA:HA	1:B:37:GLN:HG3	1.80	0.63
1:C:318:ALA:O	1:C:321:LYS:HB3	1.97	0.63
1:D:310:PHE:HE1	1:D:312:ILE:HG23	1.64	0.63
1:A:146:THR:CB	1:A:147:PRO:HD3	2.29	0.63
1:B:146:THR:CB	1:B:147:PRO:HD3	2.29	0.63
1:C:101:ASP:CB	1:C:148:THR:HB	2.28	0.63
1:A:270:PHE:CZ	1:A:385:LYS:HG2	2.34	0.63
1:D:1:THR:CG2	1:D:2:LEU:N	2.62	0.63
1:B:1:THR:HG21	1:B:14:HIS:CG	2.33	0.63
1:A:31:LEU:HD22	3:B:441:HOH:O	1.98	0.62
1:A:349:THR:HG22	1:A:350:HIS:N	2.14	0.62
1:D:27:GLU:OE1	1:D:59:ASN:ND2	2.28	0.62
1:C:333:GLU:O	1:D:34:THR:HG21	1.99	0.62
1:A:136:LYS:O	1:A:137:GLU:CB	2.45	0.62
1:B:135:ILE:HD12	1:B:167:HIS:HB2	1.80	0.62
1:D:131:LEU:N	1:D:132:PRO:HD2	2.14	0.62
1:B:265:ASN:O	1:B:269:GLU:HG3	1.98	0.62
1:D:211:VAL:HG23	1:D:245:LEU:HD23	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:PHE:CA	1:B:238:PRO:HD3	2.29	0.62
1:C:315:GLY:O	1:C:317:GLU:N	2.32	0.62
1:C:91:PRO:HG2	1:C:94:SER:OG	1.99	0.62
1:D:87:LEU:CD1	1:D:110:PHE:HA	2.28	0.62
1:A:274:ASP:OD1	1:A:274:ASP:O	2.17	0.62
1:A:46:THR:O	1:A:46:THR:HG22	1.99	0.62
1:B:99:ILE:O	1:B:102:VAL:CG2	2.46	0.62
1:A:53:GLN:NE2	1:A:58:GLU:HB2	2.15	0.62
1:C:221:LYS:HG2	1:C:225:GLU:OE2	1.98	0.62
1:D:3:GLN:NE2	1:D:11:LYS:HA	2.14	0.62
1:A:136:LYS:HG3	1:A:137:GLU:N	2.09	0.62
1:B:70:ALA:HB2	1:B:190:LEU:CD1	2.29	0.62
1:D:171:GLN:HB3	3:D:457:HOH:O	2.00	0.62
1:D:75:ALA:HA	1:D:215:VAL:CG1	2.26	0.62
1:A:157:ILE:HG22	1:A:192:PHE:O	1.99	0.62
1:B:264:ALA:O	1:B:308:ILE:HD11	2.00	0.62
1:D:137:GLU:O	1:D:138:ASN:HB2	1.97	0.62
1:D:149:ASN:HB2	1:D:181:PHE:CE2	2.35	0.62
1:A:51:ARG:HG3	1:A:237:ILE:HD13	1.81	0.62
1:C:369:ARG:NH1	1:C:369:ARG:HG2	2.15	0.62
1:C:104:GLY:O	1:C:107:HIS:HB3	1.99	0.61
1:D:114:ALA:CB	1:D:119:VAL:N	2.63	0.61
1:A:381:LEU:HG	1:A:385:LYS:HE3	1.81	0.61
1:A:124:THR:HG22	1:A:125:ASN:O	2.00	0.61
1:B:168:ALA:O	1:B:171:GLN:HG3	2.00	0.61
1:B:277:ASN:N	1:B:277:ASN:ND2	2.48	0.61
1:B:208:HIS:CE1	1:B:338:ILE:HD12	2.35	0.61
1:C:292:TYR:CE2	1:C:296:LEU:HD21	2.35	0.61
1:C:74:LEU:HB2	1:C:216:LEU:HD22	1.82	0.61
1:D:135:ILE:HG23	1:D:135:ILE:O	1.98	0.61
1:C:331:LEU:HA	1:C:342:LEU:HD23	1.82	0.61
1:C:347:VAL:HG23	1:C:348:MET:N	2.11	0.61
1:A:282:ASN:HB2	1:A:309:SER:HB3	1.82	0.61
1:B:128:LEU:HD13	1:B:159:LYS:HD3	1.83	0.61
1:B:163:LEU:O	1:B:166:LYS:HB3	2.00	0.61
1:B:95:HIS:HA	1:B:120:GLU:HB2	1.82	0.61
1:D:221:LYS:HG2	1:D:225:GLU:OE2	2.00	0.61
1:D:95:HIS:HA	1:D:120:GLU:HB2	1.83	0.61
1:C:114:ALA:HA	1:C:119:VAL:H	1.65	0.61
1:D:349:THR:CG2	1:D:350:HIS:N	2.64	0.61
1:A:131:LEU:N	1:A:132:PRO:HD2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:SER:HA	1:C:34:THR:O	2.01	0.61
1:A:184:PRO:HD3	1:A:199:HIS:CE1	2.36	0.61
1:D:322:PHE:O	1:D:324:SER:N	2.34	0.61
1:A:310:PHE:CE1	1:A:312:ILE:HG23	2.36	0.61
1:C:210:ASP:HA	1:D:31:LEU:O	2.01	0.61
1:D:321:LYS:CG	1:D:391:ALA:HA	2.21	0.61
1:A:124:THR:HG21	1:A:130:ASP:HB2	1.83	0.60
1:A:131:LEU:HG	1:A:135:ILE:HG13	1.83	0.60
1:B:72:TYR:O	1:B:217:ALA:HA	2.01	0.60
1:C:136:LYS:HG3	1:C:137:GLU:H	1.67	0.60
1:C:101:ASP:HB2	1:C:148:THR:HB	1.82	0.60
1:D:343:GLU:OE2	1:D:345:PRO:HA	2.00	0.60
1:C:37:GLN:CB	1:C:43:PRO:HA	2.30	0.60
1:B:60:LEU:HD12	1:B:64:VAL:HG23	1.82	0.60
1:C:196:ILE:HG12	1:C:218:THR:CG2	2.31	0.60
1:A:358:ARG:HB3	1:A:358:ARG:HH11	1.65	0.60
1:B:104:GLY:O	1:B:107:HIS:HB3	2.02	0.60
1:C:330:THR:HG21	1:D:36:LYS:HG2	1.84	0.60
1:A:102:VAL:HG12	1:A:103:TYR:O	2.02	0.60
1:A:258:ARG:HH11	1:A:303:LEU:HD11	1.67	0.60
1:D:135:ILE:HG21	1:D:168:ALA:HB2	1.83	0.60
1:D:211:VAL:CG2	1:D:245:LEU:HD23	2.32	0.60
1:A:103:TYR:C	1:A:105:GLY:H	2.04	0.60
1:A:110:PHE:O	1:A:114:ALA:HB2	2.02	0.60
1:A:45:GLY:O	1:A:47:TYR:N	2.35	0.60
1:C:349:THR:O	1:C:351:GLY:N	2.34	0.60
1:D:128:LEU:HD21	1:D:159:LYS:HB3	1.84	0.60
1:D:136:LYS:HA	1:D:139:THR:HG23	1.82	0.60
1:A:220:ASN:C	1:A:220:ASN:HD22	2.05	0.60
1:A:344:VAL:H	1:A:348:MET:HE3	1.66	0.60
1:C:264:ALA:O	1:C:308:ILE:HD11	2.02	0.60
1:C:386:GLN:HG2	3:C:413:HOH:O	2.02	0.60
1:D:165:LYS:O	1:D:169:ALA:HB2	2.01	0.60
1:D:277:ASN:O	1:D:313:LYS:N	2.35	0.60
1:C:134:LEU:O	1:C:136:LYS:N	2.35	0.60
1:B:354:PRO:C	1:B:356:GLU:H	2.04	0.59
1:B:150:PRO:HB3	1:B:369:ARG:HD2	1.83	0.59
1:C:277:ASN:ND2	1:C:277:ASN:N	2.50	0.59
1:A:53:GLN:CD	1:A:58:GLU:HB2	2.22	0.59
1:A:74:LEU:HB2	1:A:216:LEU:HD22	1.82	0.59
1:C:116:ALA:HB3	1:D:92:GLN:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:PRO:CB	1:C:167:HIS:CD2	2.85	0.59
1:D:135:ILE:CG2	1:D:168:ALA:HB2	2.32	0.59
1:A:265:ASN:O	1:A:269:GLU:HG3	2.01	0.59
1:B:156:ASP:HB3	1:B:159:LYS:HB2	1.84	0.59
1:B:3:GLN:HE22	1:B:15:ALA:CB	2.16	0.59
1:A:12:ALA:HA	1:A:67:LEU:HD21	1.85	0.59
1:A:36:LYS:H	1:C:23:GLY:C	2.06	0.59
1:D:170:GLY:N	3:D:465:HOH:O	2.34	0.59
1:A:242:ASP:O	1:A:246:THR:OG1	2.16	0.59
1:A:230:LEU:O	1:A:234:ILE:HG12	2.01	0.59
1:D:102:VAL:HG12	1:D:103:TYR:N	2.17	0.59
1:D:335:LEU:C	1:D:337:GLY:H	2.05	0.59
1:A:209:SER:O	1:B:33:THR:N	2.35	0.59
1:C:2:LEU:HD23	1:C:2:LEU:O	2.01	0.59
1:D:270:PHE:CZ	1:D:385:LYS:HG2	2.37	0.59
1:B:76:PHE:C	1:B:238:PRO:HD3	2.23	0.59
1:C:258:ARG:NH1	1:C:303:LEU:HD11	2.17	0.59
1:C:53:GLN:HE22	1:C:58:GLU:HG3	1.68	0.59
1:D:339:GLU:HG2	1:D:341:LEU:HD21	1.85	0.59
1:B:114:ALA:HA	1:B:119:VAL:H	1.66	0.59
1:B:128:LEU:HB3	3:B:413:HOH:O	2.01	0.59
1:B:134:LEU:O	1:B:136:LYS:N	2.36	0.59
1:A:190:LEU:C	1:A:192:PHE:H	2.06	0.58
1:B:137:GLU:O	1:B:138:ASN:CB	2.50	0.58
1:B:95:HIS:CD2	1:B:120:GLU:HB3	2.33	0.58
1:D:204:TYR:CZ	1:D:336:GLY:HA2	2.38	0.58
1:A:70:ALA:HA	1:A:219:ASN:HD21	1.67	0.58
1:C:144:ILE:CD1	1:C:175:LEU:HD11	2.34	0.58
1:A:264:ALA:O	1:A:308:ILE:HD11	2.02	0.58
1:A:131:LEU:O	1:A:135:ILE:HG13	2.03	0.58
1:A:142:VAL:HG21	1:A:164:ILE:CD1	2.33	0.58
1:B:114:ALA:HB1	1:B:119:VAL:H	1.68	0.58
1:D:1:THR:HG21	1:D:14:HIS:HB3	1.84	0.58
1:B:354:PRO:C	1:B:356:GLU:N	2.56	0.58
1:A:203:LYS:O	1:A:207:GLY:HA2	2.03	0.58
1:A:87:LEU:HD11	1:A:110:PHE:CD1	2.39	0.58
1:D:136:LYS:CG	1:D:137:GLU:N	2.67	0.58
1:D:46:THR:O	1:D:46:THR:CG2	2.51	0.58
1:A:135:ILE:O	1:A:139:THR:CG2	2.51	0.58
1:A:135:ILE:CD1	1:A:167:HIS:HB2	2.34	0.58
1:A:22:HIS:H	1:A:22:HIS:HD1	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:HIS:HD2	1:A:120:GLU:HB3	1.68	0.58
1:B:338:ILE:HG12	1:B:374:ILE:HD11	1.85	0.58
1:C:135:ILE:HD12	1:C:167:HIS:HB2	1.86	0.58
1:C:146:THR:CB	1:C:147:PRO:HD3	2.34	0.58
1:C:187:SER:C	1:C:188:ASN:HD22	2.07	0.58
1:C:45:GLY:O	1:C:47:TYR:N	2.37	0.58
1:C:135:ILE:CG2	1:C:168:ALA:HB2	2.34	0.57
1:A:35:PHE:HA	1:C:23:GLY:O	2.04	0.57
1:D:135:ILE:HG21	1:D:167:HIS:O	2.03	0.57
1:D:385:LYS:C	1:D:387:ALA:H	2.07	0.57
1:B:68:GLU:OE1	1:B:184:PRO:HG3	2.03	0.57
1:C:102:VAL:N	3:C:435:HOH:O	2.30	0.57
1:D:150:PRO:HG3	1:D:345:PRO:HG3	1.86	0.57
1:B:51:ARG:HG3	1:B:237:ILE:HD13	1.86	0.57
1:C:37:GLN:HE21	1:C:43:PRO:CG	2.03	0.57
1:B:87:LEU:HD13	1:B:110:PHE:HA	1.86	0.57
1:C:96:ALA:CB	1:C:141:LEU:HB3	2.35	0.57
1:A:150:PRO:CB	1:A:369:ARG:HD2	2.33	0.57
1:B:206:ASN:HD22	1:B:246:THR:HA	1.69	0.57
1:D:157:ILE:HD12	1:D:298:GLN:OE1	2.04	0.57
1:A:127:LEU:HD23	1:A:160:VAL:HG21	1.86	0.57
1:B:343:GLU:HG2	1:B:344:VAL:N	2.19	0.57
1:C:37:GLN:CG	1:C:43:PRO:HA	2.34	0.57
1:D:150:PRO:HB3	1:D:369:ARG:HD2	1.87	0.57
1:A:190:LEU:HD21	1:A:197:VAL:HG22	1.85	0.57
1:B:114:ALA:CA	1:B:119:VAL:H	2.17	0.57
1:A:362:GLY:O	1:A:364:PHE:N	2.37	0.57
1:B:221:LYS:HG2	1:B:225:GLU:OE2	2.03	0.57
1:D:317:GLU:O	1:D:321:LYS:N	2.37	0.57
1:A:102:VAL:HG11	1:A:106:THR:HG23	1.86	0.57
1:B:221:LYS:HB3	1:B:222:PRO:HD3	1.87	0.57
1:B:234:ILE:HG13	1:B:236:ALA:H	1.68	0.57
1:B:369:ARG:HH11	1:B:369:ARG:HG2	1.70	0.57
1:D:333:GLU:OE1	1:D:343:GLU:HG3	2.04	0.57
1:A:358:ARG:CB	1:A:358:ARG:HH11	2.18	0.57
1:B:3:GLN:HE22	1:B:15:ALA:CA	2.17	0.57
1:C:108:ARG:CZ	1:D:233:ALA:HA	2.34	0.57
1:D:335:LEU:C	1:D:337:GLY:N	2.56	0.57
1:C:95:HIS:HB2	1:C:138:ASN:HB3	1.87	0.56
1:D:136:LYS:NZ	1:D:138:ASN:HA	2.20	0.56
1:C:132:PRO:HB3	1:C:167:HIS:CD2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:203:LYS:HD2	1:C:203:LYS:N	2.19	0.56
1:C:280:ALA:HB3	1:C:311:ARG:HD3	1.86	0.56
1:B:128:LEU:CD1	1:B:159:LYS:HD3	2.35	0.56
1:C:280:ALA:H	1:C:311:ARG:HG3	1.71	0.56
1:D:152:LEU:HD12	1:D:282:ASN:O	2.05	0.56
1:A:114:ALA:HA	1:A:119:VAL:H	1.69	0.56
1:A:248:ARG:HG2	1:A:248:ARG:HH11	1.70	0.56
1:C:294:VAL:O	1:C:297:LYS:HG3	2.04	0.56
1:C:70:ALA:HB2	1:C:190:LEU:HD12	1.88	0.56
1:C:13:ILE:O	1:C:13:ILE:CG2	2.54	0.56
1:D:276:GLU:HA	3:D:461:HOH:O	2.04	0.56
1:B:61:GLU:OE2	1:B:74:LEU:HA	2.05	0.56
1:D:192:PHE:HE2	3:D:480:HOH:O	1.87	0.56
1:B:75:ALA:HA	1:B:215:VAL:HG12	1.87	0.56
1:C:196:ILE:HA	1:C:218:THR:HG22	1.88	0.56
1:C:354:PRO:C	1:C:356:GLU:N	2.56	0.56
1:B:187:SER:O	1:B:188:ASN:ND2	2.35	0.56
1:B:179:ASN:ND2	1:B:199:HIS:CE1	2.73	0.56
1:C:131:LEU:HG	1:C:135:ILE:HG13	1.87	0.56
1:C:201:ALA:HB3	1:C:213:LEU:O	2.05	0.56
1:D:102:VAL:HG11	1:D:106:THR:HG23	1.87	0.56
1:D:277:ASN:N	1:D:277:ASN:ND2	2.54	0.56
1:D:95:HIS:HD2	1:D:120:GLU:HB3	1.71	0.56
1:C:116:ALA:HB2	1:D:92:GLN:H	1.71	0.56
1:B:101:ASP:HA	3:B:491:HOH:O	2.05	0.56
1:B:102:VAL:HG11	1:B:106:THR:CG2	2.36	0.56
1:B:150:PRO:HG3	1:B:345:PRO:HG3	1.88	0.56
1:A:343:GLU:HG2	1:A:344:VAL:N	2.21	0.55
1:A:358:ARG:NH1	1:A:358:ARG:HB2	2.21	0.55
1:B:187:SER:C	1:B:188:ASN:HD22	2.09	0.55
1:B:312:ILE:HD12	1:B:318:ALA:HB1	1.87	0.55
1:B:343:GLU:OE1	1:B:345:PRO:HD3	2.06	0.55
1:C:128:LEU:HD13	1:C:159:LYS:HD3	1.88	0.55
1:D:95:HIS:CE1	1:D:139:THR:HG22	2.37	0.55
1:A:1:THR:HG21	1:A:14:HIS:CB	2.35	0.55
1:B:102:VAL:HG12	1:B:103:TYR:O	2.07	0.55
1:C:102:VAL:HG12	1:C:103:TYR:N	2.21	0.55
1:B:32:SER:CB	1:D:26:ILE:HB	2.36	0.55
1:A:102:VAL:CG1	1:A:103:TYR:N	2.69	0.55
1:A:358:ARG:CB	1:A:358:ARG:NH1	2.69	0.55
1:B:191:ASN:HA	3:B:461:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:TYR:CE1	1:B:336:GLY:HA3	2.42	0.55
1:A:333:GLU:O	1:B:34:THR:HG21	2.05	0.55
1:D:277:ASN:H	1:D:277:ASN:HD22	1.55	0.55
1:A:153:LYS:NZ	1:A:153:LYS:HB2	2.21	0.55
1:A:71:GLN:N	1:A:219:ASN:ND2	2.52	0.55
1:B:196:ILE:HG12	1:B:218:THR:CG2	2.37	0.55
1:B:358:ARG:NH1	1:B:358:ARG:CB	2.70	0.55
1:C:69:ASN:ND2	1:C:191:ASN:OD1	2.38	0.55
1:D:279:VAL:HG23	1:D:312:ILE:O	2.07	0.55
1:D:316:ALA:HA	3:D:488:HOH:O	2.05	0.55
1:A:106:THR:HG22	1:A:110:PHE:CE1	2.41	0.55
1:C:343:GLU:HA	1:C:348:MET:HE1	1.88	0.55
1:C:67:LEU:HD12	1:C:250:LEU:HD11	1.88	0.55
1:D:127:LEU:HD23	1:D:160:VAL:HG21	1.88	0.55
1:D:134:LEU:O	1:D:136:LYS:N	2.40	0.55
1:A:363:VAL:O	1:A:363:VAL:HG12	2.06	0.55
1:B:106:THR:O	1:B:110:PHE:HB2	2.06	0.55
1:A:3:GLN:HE21	1:A:11:LYS:CG	2.19	0.55
1:B:3:GLN:HE21	1:B:11:LYS:HA	1.72	0.55
1:B:123:PHE:H	1:B:123:PHE:HD1	1.55	0.55
1:B:192:PHE:HD2	3:B:484:HOH:O	1.90	0.55
1:B:196:ILE:HG23	1:B:218:THR:HG23	1.89	0.55
1:B:213:LEU:HD23	1:B:213:LEU:C	2.27	0.55
1:C:331:LEU:HD11	1:C:348:MET:HE2	1.89	0.55
1:B:346:ALA:CB	3:B:492:HOH:O	2.46	0.55
1:B:95:HIS:O	1:B:139:THR:HA	2.07	0.54
1:C:187:SER:O	1:C:188:ASN:ND2	2.38	0.54
1:C:311:ARG:HH11	1:C:311:ARG:HB3	1.72	0.54
1:B:327:ARG:NH2	1:C:6:ASP:OD1	2.27	0.54
1:A:323:ALA:HB1	1:A:331:LEU:CD1	2.32	0.54
1:A:348:MET:CE	1:B:40:PRO:HB3	2.38	0.54
1:A:7:LYS:HG3	1:D:376:ASP:OD2	2.06	0.54
1:A:95:HIS:HA	1:A:120:GLU:HB2	1.89	0.54
1:B:340:SER:O	1:B:341:LEU:HD23	2.07	0.54
1:C:249:GLY:HA2	3:C:417:HOH:O	2.08	0.54
1:C:294:VAL:HA	1:C:297:LYS:CG	2.38	0.54
1:D:68:GLU:HG2	1:D:197:VAL:HG21	1.89	0.54
1:A:103:TYR:C	1:A:105:GLY:N	2.60	0.54
1:B:76:PHE:CE2	1:B:231:GLN:HG3	2.42	0.54
1:B:363:VAL:HG12	1:B:363:VAL:O	2.08	0.54
1:C:111:THR:O	1:C:114:ALA:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:VAL:HG23	1:C:312:ILE:C	2.27	0.54
1:C:280:ALA:H	1:C:311:ARG:CG	2.21	0.54
1:D:114:ALA:HB1	1:D:119:VAL:N	2.22	0.54
1:D:323:ALA:HB1	1:D:331:LEU:HD13	1.90	0.54
1:A:136:LYS:CG	1:A:137:GLU:H	2.04	0.54
1:A:216:LEU:HD23	1:A:216:LEU:C	2.28	0.54
1:B:131:LEU:N	1:B:132:PRO:CD	2.71	0.54
1:C:102:VAL:CG1	1:C:103:TYR:N	2.70	0.54
1:C:142:VAL:HG21	1:C:164:ILE:CD1	2.37	0.54
1:C:196:ILE:HG23	1:C:218:THR:HG23	1.90	0.54
1:C:92:GLN:HB2	1:D:115:ASN:O	2.08	0.54
1:D:242:ASP:O	1:D:246:THR:OG1	2.23	0.54
1:B:137:GLU:O	1:B:138:ASN:HB3	2.08	0.54
1:C:126:ASP:OD2	1:C:129:ASN:HB2	2.08	0.54
1:C:135:ILE:HG23	1:C:135:ILE:O	2.08	0.54
1:C:137:GLU:HG2	1:C:137:GLU:O	2.08	0.54
1:D:136:LYS:HD2	1:D:138:ASN:H	1.72	0.54
1:D:220:ASN:ND2	1:D:220:ASN:C	2.60	0.54
1:B:203:LYS:O	1:B:336:GLY:O	2.26	0.54
1:D:135:ILE:CG2	1:D:135:ILE:O	2.55	0.54
1:A:331:LEU:HD11	1:A:348:MET:HE2	1.90	0.54
1:A:3:GLN:HE21	1:A:11:LYS:HA	1.72	0.54
1:C:135:ILE:O	1:C:135:ILE:CG2	2.56	0.54
1:C:182:LEU:O	1:C:183:SER:CB	2.56	0.54
1:D:136:LYS:HG3	1:D:137:GLU:N	2.12	0.54
1:D:252:THR:O	1:D:256:ARG:HG3	2.08	0.54
1:D:276:GLU:HB3	1:D:277:ASN:HD22	1.74	0.54
1:D:279:VAL:HG11	1:D:311:ARG:HE	1.72	0.54
1:A:7:LYS:HG2	1:D:379:ASP:OD1	2.07	0.54
1:A:75:ALA:CA	1:A:215:VAL:HG12	2.36	0.53
1:B:106:THR:HA	1:B:110:PHE:CD1	2.42	0.53
1:C:136:LYS:O	1:C:137:GLU:CB	2.56	0.53
1:C:326:THR:HG21	1:C:342:LEU:HD13	1.89	0.53
1:C:108:ARG:HB3	1:D:233:ALA:HB1	1.90	0.53
1:A:101:ASP:CB	1:A:148:THR:HB	2.38	0.53
1:C:348:MET:HG2	1:D:40:PRO:O	2.08	0.53
1:A:347:VAL:HG23	1:A:348:MET:HG3	1.90	0.53
1:A:36:LYS:N	1:C:23:GLY:O	2.40	0.53
1:B:344:VAL:H	1:B:348:MET:HE3	1.73	0.53
1:D:70:ALA:HB2	1:D:190:LEU:CD1	2.38	0.53
1:A:114:ALA:CB	1:A:119:VAL:H	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:LEU:HD23	1:A:240:PRO:HB2	1.90	0.53
1:B:96:ALA:CB	1:B:141:LEU:HB3	2.38	0.53
1:B:347:VAL:CG2	1:B:348:MET:H	2.04	0.53
1:D:136:LYS:CA	1:D:139:THR:HG23	2.39	0.53
1:D:354:PRO:O	1:D:356:GLU:N	2.41	0.53
1:A:357:ALA:O	1:A:359:GLU:N	2.38	0.53
1:C:39:SER:O	1:C:40:PRO:C	2.45	0.53
1:D:12:ALA:HA	1:D:67:LEU:HD21	1.91	0.53
1:D:385:LYS:C	1:D:387:ALA:N	2.62	0.53
1:A:104:GLY:O	1:A:107:HIS:HB3	2.08	0.53
1:A:226:ARG:O	1:A:229:PHE:HB3	2.09	0.53
1:D:279:VAL:HB	1:D:311:ARG:O	2.07	0.53
1:C:136:LYS:HG3	1:C:137:GLU:N	2.24	0.53
1:C:202:THR:HG22	3:C:458:HOH:O	2.09	0.53
1:C:307:MET:SD	1:C:335:LEU:HD13	2.49	0.53
1:C:343:GLU:HG2	1:C:348:MET:SD	2.49	0.53
1:D:137:GLU:O	1:D:137:GLU:HG2	2.08	0.53
1:D:162:ASP:HA	1:D:165:LYS:NZ	2.23	0.53
1:B:131:LEU:HG	1:B:135:ILE:HG13	1.90	0.53
1:B:270:PHE:CZ	1:B:385:LYS:HG2	2.44	0.53
1:D:37:GLN:HE21	1:D:43:PRO:HG3	1.74	0.53
1:B:211:VAL:HG23	1:B:245:LEU:HD23	1.90	0.53
1:C:102:VAL:HG11	1:C:106:THR:CG2	2.39	0.53
1:C:114:ALA:CA	1:C:119:VAL:H	2.20	0.53
1:D:221:LYS:HB3	1:D:222:PRO:HD3	1.91	0.53
1:A:261:ALA:HA	1:A:305:GLY:O	2.09	0.52
1:B:1:THR:CG2	1:B:2:LEU:N	2.72	0.52
1:B:351:GLY:O	1:B:353:ILE:N	2.36	0.52
1:C:1:THR:HG21	1:C:14:HIS:CB	2.39	0.52
1:D:346:ALA:O	1:D:350:HIS:O	2.26	0.52
1:B:21:VAL:CG2	1:D:21:VAL:HG21	2.39	0.52
1:B:46:THR:O	1:B:46:THR:CG2	2.56	0.52
1:C:182:LEU:O	1:C:183:SER:OG	2.19	0.52
1:B:1:THR:HG21	1:B:14:HIS:CB	2.40	0.52
1:B:277:ASN:HD22	1:B:277:ASN:H	1.57	0.52
1:C:106:THR:HG22	1:C:110:PHE:CE1	2.44	0.52
1:C:354:PRO:C	1:C:356:GLU:H	2.12	0.52
1:D:179:ASN:ND2	1:D:199:HIS:CE1	2.77	0.52
1:D:74:LEU:HB2	1:D:216:LEU:HD22	1.91	0.52
1:A:22:HIS:HD2	1:C:47:TYR:CD1	2.28	0.52
1:C:13:ILE:O	1:C:13:ILE:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:381:LEU:HG	1:C:385:LYS:HE3	1.92	0.52
1:D:382:GLU:HA	1:D:382:GLU:OE2	2.08	0.52
1:A:265:ASN:HA	1:A:283:TYR:CE2	2.44	0.52
1:A:312:ILE:O	1:A:314:GLY:N	2.37	0.52
1:B:220:ASN:HD21	1:B:222:PRO:HD2	1.71	0.52
1:B:220:ASN:HD22	1:B:222:PRO:HD2	1.70	0.52
1:C:135:ILE:HG21	1:C:168:ALA:HB2	1.89	0.52
1:C:276:GLU:HB3	1:C:277:ASN:HD22	1.74	0.52
1:A:34:THR:O	1:C:24:SER:HA	2.10	0.52
1:C:114:ALA:HB1	1:C:119:VAL:H	1.75	0.52
1:A:333:GLU:HG3	3:B:474:HOH:O	2.10	0.52
1:D:216:LEU:HD23	1:D:216:LEU:C	2.30	0.52
1:D:307:MET:HE1	1:D:369:ARG:NH2	2.25	0.52
1:D:46:THR:O	1:D:46:THR:HG22	2.09	0.52
1:B:114:ALA:HB1	1:B:119:VAL:N	2.24	0.52
1:B:28:PRO:HA	3:D:417:HOH:O	2.09	0.52
1:C:131:LEU:O	1:C:135:ILE:N	2.39	0.52
1:C:95:HIS:HA	1:C:120:GLU:HB2	1.92	0.52
1:D:310:PHE:C	1:D:367:LEU:HD12	2.29	0.52
1:A:102:VAL:HG11	1:A:106:THR:CG2	2.40	0.52
1:A:72:TYR:O	1:A:217:ALA:HA	2.10	0.52
1:B:314:GLY:CA	3:B:419:HOH:O	2.57	0.52
1:B:46:THR:HG22	1:B:46:THR:O	2.10	0.52
1:B:181:PHE:CD1	1:B:335:LEU:HD11	2.45	0.52
1:D:142:VAL:HG21	1:D:164:ILE:HD11	1.92	0.52
1:A:99:ILE:O	1:A:102:VAL:CG2	2.58	0.51
1:C:110:PHE:O	1:C:114:ALA:HB2	2.10	0.51
1:D:135:ILE:HD11	1:D:164:ILE:HA	1.92	0.51
1:A:22:HIS:HD2	1:C:47:TYR:HD1	1.58	0.51
1:A:82:THR:O	1:A:86:ILE:HG13	2.10	0.51
1:B:137:GLU:O	1:B:137:GLU:CG	2.58	0.51
1:B:310:PHE:CE2	1:B:368:VAL:HB	2.45	0.51
1:B:97:VAL:O	1:B:142:VAL:HA	2.11	0.51
1:C:136:LYS:CA	1:C:139:THR:HG23	2.40	0.51
1:A:13:ILE:O	1:A:13:ILE:HG22	2.10	0.51
1:B:354:PRO:O	1:B:356:GLU:N	2.43	0.51
1:C:326:THR:HG21	1:C:342:LEU:CD1	2.40	0.51
1:D:95:HIS:O	1:D:139:THR:HA	2.10	0.51
1:C:221:LYS:HB3	1:C:222:PRO:HD3	1.91	0.51
1:C:53:GLN:NE2	1:C:58:GLU:HG3	2.25	0.51
1:A:67:LEU:HD11	1:A:250:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:ALA:CB	1:B:119:VAL:N	2.71	0.51
1:B:21:VAL:CG2	1:D:21:VAL:CG2	2.89	0.51
1:C:102:VAL:HG11	1:C:106:THR:HG23	1.91	0.51
1:D:102:VAL:HG11	1:D:106:THR:CG2	2.41	0.51
1:D:131:LEU:O	1:D:135:ILE:N	2.42	0.51
1:A:134:LEU:O	1:A:136:LYS:O	2.29	0.51
1:A:1:THR:HG21	1:A:14:HIS:HB3	1.92	0.51
1:B:126:ASP:OD2	1:B:129:ASN:HB2	2.09	0.51
1:B:271:LEU:O	1:B:278:VAL:HG11	2.11	0.51
1:C:220:ASN:HD21	1:C:222:PRO:HD2	1.75	0.51
1:D:106:THR:HG22	1:D:110:PHE:CZ	2.46	0.51
1:D:106:THR:O	1:D:107:HIS:C	2.48	0.51
1:D:345:PRO:HA	1:D:349:THR:HB	1.91	0.51
1:D:3:GLN:HE21	1:D:11:LYS:CG	2.19	0.51
1:A:124:THR:OG1	1:A:134:LEU:CD1	2.58	0.51
1:B:137:GLU:O	1:B:137:GLU:HG2	2.10	0.51
1:D:102:VAL:CG1	1:D:103:TYR:N	2.73	0.51
1:D:91:PRO:HG3	1:D:140:LYS:HE2	1.93	0.51
1:A:348:MET:HE2	1:B:40:PRO:HB3	1.93	0.51
1:A:98:SER:HB3	1:A:143:TRP:HB3	1.93	0.51
1:C:310:PHE:CE1	1:C:312:ILE:HG23	2.43	0.51
1:C:334:SER:HB3	1:D:34:THR:HG21	1.93	0.51
1:B:60:LEU:CD1	1:B:64:VAL:HG23	2.40	0.51
1:C:70:ALA:HA	1:C:219:ASN:HD21	1.75	0.51
1:C:196:ILE:HG23	1:C:218:THR:CG2	2.41	0.50
1:C:311:ARG:CB	1:C:311:ARG:HH11	2.24	0.50
1:A:51:ARG:HH11	1:A:51:ARG:HG2	1.75	0.50
1:D:220:ASN:HD22	1:D:222:PRO:CD	2.23	0.50
1:D:276:GLU:HB3	1:D:277:ASN:ND2	2.27	0.50
1:B:331:LEU:HA	1:B:342:LEU:HD23	1.93	0.50
1:B:46:THR:HB	3:B:455:HOH:O	2.12	0.50
1:D:213:LEU:HD23	1:D:214:GLY:N	2.26	0.50
1:D:343:GLU:HB3	1:D:369:ARG:NH1	2.27	0.50
1:A:294:VAL:O	1:A:297:LYS:HG3	2.11	0.50
1:B:358:ARG:NH1	1:B:358:ARG:HB3	2.25	0.50
1:B:70:ALA:HA	1:B:219:ASN:ND2	2.22	0.50
1:C:230:LEU:O	1:C:234:ILE:HG12	2.11	0.50
1:C:3:GLN:HE21	1:C:11:LYS:HA	1.74	0.50
1:C:51:ARG:HG3	1:C:237:ILE:HD13	1.92	0.50
1:A:151:THR:O	1:A:152:LEU:HB2	2.12	0.50
1:A:221:LYS:HE2	1:A:225:GLU:OE2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LYS:HB2	1:D:376:ASP:HB2	1.92	0.50
1:C:216:LEU:C	1:C:216:LEU:HD23	2.32	0.50
1:C:330:THR:HB	1:C:341:LEU:CD2	2.41	0.50
1:B:265:ASN:HA	1:B:283:TYR:CE2	2.45	0.50
1:C:253:LEU:HD12	1:C:257:VAL:HG23	1.94	0.50
1:D:322:PHE:C	1:D:324:SER:H	2.14	0.50
1:C:369:ARG:CG	1:C:369:ARG:HH11	2.23	0.50
1:C:53:GLN:NE2	1:C:58:GLU:CG	2.75	0.50
1:D:274:ASP:O	1:D:278:VAL:HB	2.12	0.50
1:C:101:ASP:HB3	1:C:148:THR:HB	1.94	0.50
1:D:37:GLN:NE2	1:D:43:PRO:HG3	2.26	0.50
1:A:3:GLN:NE2	1:A:11:LYS:HA	2.26	0.50
1:B:135:ILE:O	1:B:139:THR:CG2	2.60	0.50
1:C:220:ASN:C	1:C:220:ASN:ND2	2.61	0.50
1:D:95:HIS:HB3	1:D:139:THR:N	2.26	0.50
1:D:385:LYS:O	1:D:387:ALA:N	2.45	0.50
1:A:162:ASP:HA	1:A:165:LYS:HZ1	1.75	0.49
1:A:47:TYR:CD1	1:C:22:HIS:HD2	2.30	0.49
1:C:206:ASN:O	1:C:208:HIS:HD2	1.95	0.49
1:C:61:GLU:OE2	1:C:74:LEU:HA	2.12	0.49
1:D:115:ASN:O	1:D:116:ALA:HB3	2.12	0.49
1:D:1:THR:HG22	1:D:2:LEU:N	2.26	0.49
1:A:131:LEU:HD23	1:A:163:LEU:HD23	1.94	0.49
1:A:2:LEU:O	1:A:4:GLU:HG3	2.12	0.49
1:B:311:ARG:HH12	1:B:366:ASP:CG	2.16	0.49
1:B:37:GLN:HE21	1:B:43:PRO:HG3	1.78	0.49
1:A:312:ILE:C	1:A:314:GLY:H	2.16	0.49
1:B:201:ALA:HB3	1:B:213:LEU:O	2.12	0.49
1:B:294:VAL:HA	1:B:297:LYS:CG	2.43	0.49
1:C:253:LEU:HD12	1:C:257:VAL:CG2	2.42	0.49
1:C:382:GLU:HA	1:C:382:GLU:OE2	2.13	0.49
1:C:96:ALA:HB2	1:C:141:LEU:HB3	1.93	0.49
1:D:181:PHE:CE1	1:D:335:LEU:HD11	2.48	0.49
1:C:184:PRO:HD3	1:C:199:HIS:CE1	2.47	0.49
1:D:334:SER:OG	1:D:335:LEU:N	2.44	0.49
1:A:312:ILE:HD11	1:A:319:ALA:HA	1.94	0.49
1:C:126:ASP:OD2	1:C:129:ASN:ND2	2.45	0.49
1:D:106:THR:O	1:D:110:PHE:HB2	2.12	0.49
1:D:76:PHE:HA	1:D:238:PRO:HD3	1.95	0.49
1:C:330:THR:CG2	1:D:36:LYS:HG2	2.43	0.49
1:D:53:GLN:CD	1:D:58:GLU:HB2	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:GLU:HG2	1:A:137:GLU:O	2.12	0.49
1:B:135:ILE:C	1:B:139:THR:HG21	2.33	0.49
1:B:343:GLU:OE2	1:B:345:PRO:HA	2.13	0.49
1:D:321:LYS:O	1:D:322:PHE:C	2.50	0.49
1:A:103:TYR:O	1:A:105:GLY:N	2.45	0.49
1:A:18:HIS:NE2	1:A:27:GLU:HA	2.27	0.49
1:A:52:SER:O	1:A:53:GLN:HB2	2.12	0.49
1:A:13:ILE:O	1:A:13:ILE:CG2	2.61	0.49
1:A:147:PRO:HG2	1:A:182:LEU:HG	1.95	0.49
1:A:280:ALA:HB3	1:A:311:ARG:HD3	1.94	0.49
1:B:93:GLY:HA2	1:B:118:GLY:O	2.13	0.49
1:C:151:THR:O	1:C:152:LEU:HB2	2.11	0.49
1:C:211:VAL:HG13	1:C:242:ASP:HB3	1.95	0.49
1:C:209:SER:O	1:D:33:THR:N	2.45	0.49
1:B:349:THR:HG22	1:B:350:HIS:N	2.28	0.49
1:D:197:VAL:HG23	1:D:217:ALA:HB3	1.94	0.49
1:A:144:ILE:HB	1:A:177:VAL:HG22	1.95	0.48
1:C:101:ASP:OD1	1:C:361:SER:OG	2.22	0.48
1:C:354:PRO:O	1:C:356:GLU:N	2.46	0.48
1:A:203:LYS:HD2	1:A:203:LYS:N	2.28	0.48
1:B:210:ASP:O	1:B:211:VAL:HG23	2.12	0.48
1:B:226:ARG:O	1:B:229:PHE:HB3	2.12	0.48
1:C:265:ASN:HA	1:C:283:TYR:CE2	2.48	0.48
1:A:18:HIS:CD2	1:A:27:GLU:HA	2.48	0.48
1:B:287:LYS:HA	1:B:292:TYR:CD1	2.48	0.48
1:D:307:MET:CE	1:D:335:LEU:HD13	2.43	0.48
1:D:375:GLU:OE2	1:D:380:LEU:HD11	2.13	0.48
1:B:95:HIS:HB3	1:B:139:THR:HA	1.95	0.48
1:A:81:ALA:HA	1:B:234:ILE:O	2.12	0.48
1:C:108:ARG:HH11	1:D:232:ASN:ND2	2.11	0.48
1:C:146:THR:HG21	1:C:157:ILE:HD11	1.95	0.48
1:A:131:LEU:N	1:A:132:PRO:CD	2.77	0.48
1:A:150:PRO:HG3	1:A:345:PRO:HG3	1.96	0.48
1:C:106:THR:O	1:C:107:HIS:C	2.51	0.48
1:C:287:LYS:NZ	3:C:471:HOH:O	2.45	0.48
1:D:354:PRO:C	1:D:356:GLU:N	2.67	0.48
1:A:277:ASN:ND2	1:A:277:ASN:N	2.59	0.48
1:B:379:ASP:OD1	1:C:7:LYS:CG	2.58	0.48
1:C:95:HIS:C	1:C:139:THR:HA	2.33	0.48
1:B:102:VAL:HG12	1:B:103:TYR:N	2.28	0.48
1:B:179:ASN:O	1:B:199:HIS:CE1	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:LEU:HD21	1:B:197:VAL:HG22	1.95	0.48
1:B:230:LEU:O	1:B:234:ILE:HG12	2.14	0.48
1:B:335:LEU:C	1:B:337:GLY:N	2.67	0.48
1:C:124:THR:HG22	1:C:125:ASN:O	2.13	0.48
1:A:23:GLY:HA3	1:C:36:LYS:HB2	1.95	0.48
1:D:106:THR:HA	1:D:110:PHE:CE1	2.48	0.48
1:C:214:GLY:O	1:C:215:VAL:HG13	2.14	0.48
1:A:44:ILE:O	1:C:21:VAL:O	2.32	0.48
1:C:263:SER:O	1:C:267:ILE:HG13	2.13	0.48
1:D:358:ARG:HH11	1:D:358:ARG:HB3	1.79	0.48
1:A:311:ARG:HH11	1:A:311:ARG:HB3	1.78	0.48
1:B:220:ASN:ND2	1:B:220:ASN:C	2.65	0.48
1:B:343:GLU:O	1:B:369:ARG:HB3	2.14	0.48
1:C:335:LEU:HD22	1:C:369:ARG:NH2	2.28	0.48
1:C:44:ILE:HA	3:C:462:HOH:O	2.12	0.48
1:A:54:ASN:HD21	1:A:56:ASN:HB2	1.78	0.48
1:B:196:ILE:HG12	1:B:218:THR:HG21	1.95	0.48
1:C:282:ASN:HD22	1:C:309:SER:HB3	1.78	0.48
1:A:101:ASP:HB3	1:A:148:THR:HB	1.94	0.47
1:A:2:LEU:O	1:A:2:LEU:HD23	2.14	0.47
1:A:369:ARG:HH11	1:A:369:ARG:HG2	1.79	0.47
1:B:323:ALA:O	1:B:331:LEU:HB2	2.14	0.47
1:A:150:PRO:O	1:A:152:LEU:HG	2.14	0.47
1:B:102:VAL:CG1	1:B:103:TYR:N	2.77	0.47
1:B:12:ALA:HA	1:B:67:LEU:HD21	1.95	0.47
1:B:286:LEU:O	1:B:292:TYR:CD1	2.67	0.47
1:C:127:LEU:HD23	1:C:160:VAL:HG21	1.95	0.47
1:C:260:ALA:HB2	3:C:470:HOH:O	2.13	0.47
1:D:321:LYS:HD3	3:D:484:HOH:O	2.14	0.47
1:D:389:LYS:O	1:D:390:GLN:C	2.51	0.47
1:B:3:GLN:NE2	1:B:15:ALA:HB2	2.28	0.47
1:B:342:LEU:C	1:B:342:LEU:HD23	2.35	0.47
1:D:114:ALA:HB2	1:D:119:VAL:HB	1.94	0.47
1:D:189:PRO:HD2	1:D:197:VAL:HG11	1.95	0.47
1:D:325:SER:HB3	1:D:390:GLN:HG3	1.96	0.47
1:A:161:ALA:HB2	1:A:193:GLY:O	2.14	0.47
1:A:208:HIS:CE1	3:D:430:HOH:O	2.66	0.47
1:B:4:GLU:O	1:B:5:SER:HB2	2.13	0.47
1:B:95:HIS:C	1:B:139:THR:HA	2.34	0.47
1:C:150:PRO:HB3	1:C:369:ARG:HD2	1.95	0.47
1:C:220:ASN:HD22	1:C:222:PRO:HD2	1.75	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:ASN:HD21	1:C:56:ASN:HB2	1.80	0.47
1:C:8:PHE:CZ	1:C:67:LEU:HD22	2.48	0.47
1:D:124:THR:HG22	1:D:125:ASN:O	2.14	0.47
1:A:197:VAL:HG23	1:A:217:ALA:O	2.14	0.47
1:A:292:TYR:HE2	1:A:296:LEU:HD11	1.79	0.47
1:B:179:ASN:HD22	1:B:199:HIS:CE1	2.32	0.47
1:B:190:LEU:HD13	1:B:219:ASN:OD1	2.14	0.47
1:B:84:ALA:O	1:B:85:THR:C	2.52	0.47
1:B:92:GLN:HA	1:B:92:GLN:OE1	2.14	0.47
1:C:311:ARG:CB	1:C:311:ARG:NH1	2.77	0.47
1:A:234:ILE:HG13	1:A:236:ALA:H	1.79	0.47
1:C:274:ASP:O	1:C:274:ASP:OD1	2.33	0.47
1:C:3:GLN:C	1:C:4:GLU:HG3	2.35	0.47
1:C:99:ILE:HD11	1:C:144:ILE:HG23	1.96	0.47
1:D:294:VAL:HA	1:D:297:LYS:CG	2.44	0.47
1:D:43:PRO:C	1:D:45:GLY:H	2.17	0.47
1:A:278:VAL:HG11	1:A:281:VAL:CG2	2.44	0.47
1:C:158:GLN:NE2	1:C:158:GLN:HA	2.29	0.47
1:C:37:GLN:NE2	1:C:43:PRO:CG	2.70	0.47
1:D:121:THR:HG22	1:D:123:PHE:CE1	2.50	0.47
1:D:146:THR:CB	1:D:147:PRO:HD3	2.45	0.47
1:D:351:GLY:O	1:D:353:ILE:N	2.39	0.47
1:B:88:GLN:OE1	1:B:234:ILE:HD13	2.14	0.47
1:B:95:HIS:HB3	1:B:139:THR:CA	2.44	0.47
1:C:249:GLY:O	1:C:256:ARG:NH2	2.37	0.47
1:C:270:PHE:HB2	3:C:412:HOH:O	2.14	0.47
1:B:111:THR:O	1:B:114:ALA:HB3	2.15	0.47
1:B:141:LEU:HD12	1:B:174:ILE:HG13	1.97	0.47
1:B:48:GLU:HG3	1:B:49:TYR:N	2.30	0.47
1:C:3:GLN:HE21	1:C:11:LYS:CG	2.24	0.47
1:D:131:LEU:N	1:D:132:PRO:CD	2.78	0.47
1:A:145:GLU:O	1:A:146:THR:C	2.52	0.47
1:A:344:VAL:N	1:A:348:MET:CE	2.78	0.47
1:B:95:HIS:O	1:B:140:LYS:N	2.48	0.47
1:D:91:PRO:HG2	1:D:94:SER:OG	2.15	0.47
1:C:322:PHE:O	1:C:326:THR:HG23	2.14	0.47
1:C:347:VAL:CG2	1:C:348:MET:H	2.14	0.47
1:D:146:THR:HG21	1:D:157:ILE:HD11	1.97	0.47
1:D:203:LYS:O	1:D:336:GLY:O	2.33	0.47
1:A:113:VAL:C	1:A:115:ASN:H	2.18	0.46
1:A:132:PRO:HG2	1:A:133:GLN:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:VAL:HB	1:B:348:MET:HE3	1.97	0.46
1:B:369:ARG:NH1	1:B:369:ARG:HG2	2.28	0.46
1:C:210:ASP:OD2	1:C:210:ASP:N	2.46	0.46
1:D:202:THR:HG23	1:D:211:VAL:O	2.16	0.46
1:D:358:ARG:CB	1:D:358:ARG:NH1	2.77	0.46
1:B:204:TYR:CZ	1:B:336:GLY:CA	2.98	0.46
1:A:347:VAL:CG2	1:A:348:MET:H	2.15	0.46
1:B:135:ILE:HD11	1:B:164:ILE:HA	1.97	0.46
1:B:316:ALA:HB1	3:B:410:HOH:O	2.15	0.46
1:C:131:LEU:N	1:C:132:PRO:CD	2.78	0.46
1:C:321:LYS:CG	1:C:391:ALA:HA	2.20	0.46
1:D:282:ASN:HB2	1:D:309:SER:HB3	1.98	0.46
1:B:42:ASN:HA	1:B:43:PRO:HD3	1.78	0.46
1:B:3:GLN:C	1:B:4:GLU:HG3	2.36	0.46
1:C:162:ASP:HA	1:C:165:LYS:NZ	2.31	0.46
1:C:344:VAL:N	1:C:348:MET:HE1	2.29	0.46
1:C:306:GLY:O	1:C:372:VAL:HG23	2.16	0.46
1:D:264:ALA:O	1:D:308:ILE:HD11	2.15	0.46
1:D:355:LYS:HB2	1:D:358:ARG:NH2	2.31	0.46
1:A:196:ILE:HG23	1:A:218:THR:HG23	1.97	0.46
1:C:317:GLU:O	1:C:318:ALA:C	2.51	0.46
1:C:46:THR:CG2	1:C:46:THR:O	2.63	0.46
1:B:267:ILE:HG22	1:B:267:ILE:O	2.15	0.46
1:C:75:ALA:CA	1:C:215:VAL:HG12	2.42	0.46
1:C:333:GLU:OE1	1:C:343:GLU:HG3	2.15	0.46
1:C:53:GLN:NE2	1:C:58:GLU:HB2	2.31	0.46
1:D:106:THR:CA	1:D:110:PHE:CD1	2.96	0.46
1:A:33:THR:HG23	1:A:49:TYR:CE1	2.51	0.46
1:B:268:ALA:O	1:B:271:LEU:N	2.49	0.46
1:D:11:LYS:HD3	3:D:452:HOH:O	2.16	0.46
1:D:95:HIS:HB2	1:D:138:ASN:HB3	1.96	0.46
1:D:18:HIS:CB	1:D:27:GLU:HG3	2.46	0.46
1:D:213:LEU:HD23	1:D:213:LEU:C	2.35	0.46
1:A:95:HIS:CE1	1:A:139:THR:HG22	2.42	0.46
1:A:206:ASN:ND2	1:A:246:THR:HA	2.26	0.46
1:A:42:ASN:HA	1:A:43:PRO:HD3	1.79	0.46
1:B:144:ILE:O	1:B:177:VAL:HA	2.16	0.46
1:D:33:THR:HG22	1:D:34:THR:N	2.31	0.46
1:A:95:HIS:HB3	1:A:139:THR:HA	1.97	0.46
1:C:70:ALA:HB2	1:C:190:LEU:CD1	2.46	0.46
1:D:87:LEU:HD11	1:D:110:PHE:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:SER:HB2	1:B:242:ASP:OD1	2.16	0.46
1:B:323:ALA:HB1	1:B:331:LEU:CD1	2.32	0.46
1:D:124:THR:OG1	1:D:134:LEU:CD1	2.64	0.46
1:A:111:THR:O	1:A:114:ALA:HB3	2.16	0.45
1:A:124:THR:OG1	1:A:134:LEU:HD11	2.16	0.45
1:A:153:LYS:NZ	1:A:153:LYS:CB	2.79	0.45
1:C:316:ALA:HA	3:C:494:HOH:O	2.16	0.45
1:D:29:ILE:HG22	1:D:31:LEU:HD21	1.98	0.45
1:D:42:ASN:HA	1:D:43:PRO:HD3	1.75	0.45
1:A:347:VAL:CG2	1:A:348:MET:N	2.75	0.45
1:B:114:ALA:O	1:B:115:ASN:C	2.55	0.45
1:C:382:GLU:OE2	1:C:385:LYS:HD2	2.16	0.45
1:D:295:VAL:O	1:D:299:HIS:HB2	2.16	0.45
1:D:39:SER:O	1:D:40:PRO:C	2.54	0.45
1:D:101:ASP:CB	1:D:148:THR:HB	2.46	0.45
1:D:247:HIS:HE1	3:D:437:HOH:O	1.99	0.45
1:D:293:ASP:O	1:D:297:LYS:HG2	2.17	0.45
1:A:159:LYS:NZ	3:A:462:HOH:O	2.49	0.45
1:B:376:ASP:CB	1:C:7:LYS:HB2	2.45	0.45
1:C:312:ILE:C	1:C:314:GLY:H	2.19	0.45
1:C:108:ARG:NH1	1:D:232:ASN:ND2	2.65	0.45
1:A:149:ASN:HB2	1:A:181:PHE:CE2	2.51	0.45
1:A:348:MET:HE2	1:B:40:PRO:CB	2.47	0.45
1:C:136:LYS:CG	1:C:137:GLU:H	2.29	0.45
1:B:376:ASP:HB2	1:C:7:LYS:HB2	1.97	0.45
1:A:343:GLU:HG2	1:A:344:VAL:H	1.82	0.45
1:B:111:THR:O	1:B:114:ALA:N	2.49	0.45
1:B:91:PRO:HG3	1:B:140:LYS:HE2	1.98	0.45
1:C:300:ARG:NH1	3:C:488:HOH:O	2.41	0.45
1:C:33:THR:HG23	1:C:49:TYR:CE1	2.52	0.45
1:D:210:ASP:O	1:D:211:VAL:HG23	2.17	0.45
1:A:23:GLY:C	1:C:35:PHE:HA	2.37	0.45
1:B:109:TYR:O	1:B:110:PHE:C	2.54	0.45
1:B:358:ARG:CZ	1:B:358:ARG:HB2	2.46	0.45
1:D:329:PHE:CE1	1:D:380:LEU:HD22	2.51	0.45
1:A:146:THR:HB	1:A:147:PRO:HD3	1.99	0.45
1:A:31:LEU:O	1:A:32:SER:C	2.55	0.45
1:B:276:GLU:HB3	1:B:277:ASN:HD22	1.81	0.45
1:D:279:VAL:HG11	1:D:311:ARG:NE	2.31	0.45
1:A:18:HIS:HB3	1:A:27:GLU:HG3	1.99	0.45
1:A:277:ASN:HA	1:A:313:LYS:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:THR:O	1:A:46:THR:CG2	2.63	0.45
1:A:53:GLN:HA	1:A:57:ARG:NH2	2.31	0.45
1:B:94:SER:HA	1:B:138:ASN:ND2	2.32	0.45
1:C:34:THR:C	3:C:469:HOH:O	2.55	0.45
1:D:349:THR:O	1:D:351:GLY:N	2.49	0.45
1:A:190:LEU:C	1:A:192:PHE:N	2.70	0.45
1:B:385:LYS:O	1:B:387:ALA:N	2.50	0.45
1:C:166:LYS:HE2	1:C:167:HIS:CE1	2.51	0.45
1:C:71:GLN:H	1:C:219:ASN:HD22	1.62	0.45
1:D:321:LYS:O	1:D:324:SER:N	2.46	0.45
1:D:355:LYS:HB2	1:D:358:ARG:HH21	1.82	0.45
1:A:115:ASN:O	1:A:116:ALA:HB3	2.17	0.44
1:B:136:LYS:NZ	1:B:138:ASN:HA	2.32	0.44
1:C:132:PRO:HB3	1:C:167:HIS:NE2	2.32	0.44
1:C:343:GLU:OE1	1:C:345:PRO:HD3	2.17	0.44
1:D:255:LEU:HA	1:D:255:LEU:HD23	1.75	0.44
1:A:292:TYR:CE2	1:A:296:LEU:HD11	2.53	0.44
1:B:335:LEU:O	1:B:336:GLY:C	2.51	0.44
1:C:272:ALA:HB3	3:C:451:HOH:O	2.17	0.44
1:A:1:THR:HA	1:D:327:ARG:O	2.18	0.44
1:D:344:VAL:N	1:D:348:MET:CE	2.74	0.44
1:A:135:ILE:O	1:A:139:THR:HG21	2.17	0.44
1:B:283:TYR:O	1:B:285:GLY:N	2.50	0.44
1:B:381:LEU:HG	1:B:385:LYS:HE3	1.99	0.44
1:B:248:ARG:HH11	1:C:248:ARG:NH1	2.16	0.44
1:C:72:TYR:O	1:C:217:ALA:HA	2.17	0.44
1:A:20:ASP:OD2	1:A:22:HIS:ND1	2.51	0.44
1:A:330:THR:HG21	1:B:36:LYS:HG2	1.98	0.44
1:B:8:PHE:CE1	1:B:185:TYR:HA	2.53	0.44
1:C:124:THR:HG21	1:C:130:ASP:HB2	2.00	0.44
1:A:102:VAL:CG1	1:A:103:TYR:H	2.30	0.44
1:A:183:SER:O	1:A:184:PRO:C	2.56	0.44
1:A:190:LEU:O	1:A:192:PHE:N	2.50	0.44
1:A:234:ILE:HG13	1:A:235:GLY:N	2.33	0.44
1:A:58:GLU:CD	1:A:62:ARG:HH21	2.21	0.44
1:B:74:LEU:HD12	1:B:216:LEU:HD21	1.98	0.44
1:C:277:ASN:H	1:C:277:ASN:ND2	2.09	0.44
1:C:294:VAL:HA	1:C:297:LYS:HD2	1.99	0.44
1:D:144:ILE:HD11	1:D:160:VAL:HG11	2.00	0.44
1:A:292:TYR:CE2	1:A:296:LEU:HG	2.53	0.44
1:B:95:HIS:CA	1:B:120:GLU:HB2	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:GLN:HA	1:B:6:ASP:OD2	2.18	0.44
1:C:113:VAL:O	1:C:113:VAL:HG12	2.18	0.44
1:C:35:PHE:CZ	1:C:47:TYR:HB3	2.52	0.44
1:C:362:GLY:O	1:C:364:PHE:N	2.50	0.44
1:D:334:SER:O	1:D:335:LEU:HB3	2.17	0.44
1:A:8:PHE:C	1:A:8:PHE:CD2	2.91	0.44
1:C:50:SER:O	1:C:53:GLN:N	2.50	0.44
1:D:17:GLU:HG2	1:D:18:HIS:N	2.33	0.44
1:C:33:THR:HG22	1:C:34:THR:HG23	1.99	0.44
1:C:335:LEU:HD22	1:C:369:ARG:HH21	1.82	0.44
1:D:161:ALA:HB2	1:D:193:GLY:O	2.17	0.44
1:D:322:PHE:C	1:D:324:SER:N	2.71	0.44
1:D:358:ARG:HB2	1:D:358:ARG:NH1	2.32	0.44
1:D:386:GLN:HG2	3:D:436:HOH:O	2.16	0.44
1:A:144:ILE:HD12	1:A:175:LEU:HD11	2.00	0.44
1:A:287:LYS:HA	1:A:292:TYR:CD1	2.53	0.44
1:C:189:PRO:HD2	1:C:197:VAL:HG11	2.00	0.44
1:C:76:PHE:HA	1:C:238:PRO:HD3	2.00	0.44
1:D:376:ASP:HB3	1:D:379:ASP:HB2	2.00	0.44
1:A:114:ALA:CA	1:A:119:VAL:H	2.31	0.43
1:A:330:THR:CG2	1:B:36:LYS:HG2	2.48	0.43
1:B:172:ASP:HB3	3:B:448:HOH:O	2.18	0.43
1:B:22:HIS:ND1	1:B:22:HIS:N	2.66	0.43
1:B:76:PHE:HA	1:B:238:PRO:HD3	2.00	0.43
1:C:216:LEU:O	1:C:216:LEU:HD23	2.17	0.43
1:C:55:PRO:O	1:C:59:ASN:ND2	2.51	0.43
1:A:106:THR:HA	1:A:110:PHE:CE1	2.53	0.43
1:A:75:ALA:CB	1:A:215:VAL:HG12	2.48	0.43
1:B:124:THR:OG1	1:B:134:LEU:HD11	2.17	0.43
1:B:136:LYS:CA	1:B:139:THR:HG23	2.46	0.43
1:B:95:HIS:CE1	1:B:122:SER:OG	2.71	0.43
1:A:95:HIS:C	1:A:139:THR:HA	2.38	0.43
1:A:202:THR:HB	1:A:203:LYS:HD2	1.99	0.43
1:A:79:GLY:O	1:A:82:THR:HB	2.18	0.43
1:C:114:ALA:HB1	1:C:119:VAL:N	2.34	0.43
1:C:168:ALA:O	1:C:171:GLN:HG3	2.18	0.43
1:C:190:LEU:HD21	1:C:197:VAL:HG22	1.99	0.43
1:C:283:TYR:O	1:C:285:GLY:N	2.52	0.43
1:D:95:HIS:CA	1:D:120:GLU:HB2	2.49	0.43
1:D:8:PHE:CE1	1:D:185:TYR:HA	2.53	0.43
1:D:344:VAL:H	1:D:348:MET:HE1	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:344:VAL:O	1:D:345:PRO:C	2.55	0.43
1:D:358:ARG:CB	1:D:358:ARG:HH11	2.32	0.43
1:A:106:THR:CA	1:A:110:PHE:CD1	3.01	0.43
1:A:116:ALA:HB3	1:B:92:GLN:HB2	2.00	0.43
1:A:197:VAL:O	1:A:216:LEU:HA	2.18	0.43
1:C:73:GLY:HA2	1:C:216:LEU:O	2.18	0.43
1:D:232:ASN:HB3	3:D:404:HOH:O	2.18	0.43
1:D:338:ILE:CG2	1:D:339:GLU:N	2.80	0.43
1:D:311:ARG:NH1	1:D:366:ASP:OD1	2.47	0.43
1:A:128:LEU:CD1	1:A:159:LYS:HD3	2.44	0.43
1:A:301:ASP:O	1:A:302:ALA:HB3	2.19	0.43
1:B:197:VAL:O	1:B:216:LEU:HA	2.19	0.43
1:B:338:ILE:CG1	1:B:374:ILE:HD11	2.47	0.43
1:B:74:LEU:O	1:B:215:VAL:HA	2.19	0.43
1:C:335:LEU:HD12	1:C:336:GLY:N	2.33	0.43
1:D:125:ASN:OD1	1:D:126:ASP:N	2.51	0.43
1:D:37:GLN:HA	1:D:43:PRO:HA	2.00	0.43
1:A:144:ILE:CD1	1:A:175:LEU:HD11	2.47	0.43
1:A:220:ASN:C	1:A:220:ASN:ND2	2.71	0.43
1:A:37:GLN:CA	1:A:43:PRO:HA	2.44	0.43
1:A:71:GLN:HB2	1:A:219:ASN:HA	2.01	0.43
1:B:57:ARG:HD3	3:B:433:HOH:O	2.17	0.43
1:C:112:LYS:O	1:C:115:ASN:N	2.51	0.43
1:C:301:ASP:O	1:C:302:ALA:HB3	2.19	0.43
1:C:323:ALA:HA	1:C:342:LEU:HD11	2.00	0.43
1:D:343:GLU:OE1	1:D:345:PRO:HD3	2.17	0.43
1:D:347:VAL:O	1:D:348:MET:C	2.57	0.43
1:B:204:TYR:CZ	1:B:336:GLY:HA3	2.54	0.43
1:B:37:GLN:NE2	1:B:43:PRO:HG3	2.34	0.43
1:C:3:GLN:NE2	1:C:11:LYS:HA	2.33	0.43
1:C:124:THR:OG1	1:C:134:LEU:CD1	2.67	0.43
1:C:146:THR:HG1	1:C:147:PRO:HD3	1.81	0.43
1:C:196:ILE:HD11	1:C:223:LEU:HD21	2.00	0.43
1:D:332:ALA:O	1:D:343:GLU:HB2	2.19	0.43
1:A:195:ASP:O	1:A:218:THR:HG22	2.18	0.43
1:A:274:ASP:O	1:A:276:GLU:N	2.52	0.43
1:A:344:VAL:H	1:A:348:MET:HE1	1.81	0.43
1:B:32:SER:HB3	1:D:26:ILE:HB	1.99	0.43
1:C:271:LEU:O	1:C:278:VAL:HG11	2.19	0.43
1:C:48:GLU:HG3	1:C:49:TYR:N	2.34	0.43
1:C:53:GLN:NE2	1:C:58:GLU:OE2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:ALA:HB3	3:C:432:HOH:O	2.18	0.43
1:D:311:ARG:HB3	1:D:311:ARG:HH11	1.83	0.43
1:B:190:LEU:C	1:B:192:PHE:H	2.20	0.43
1:C:348:MET:CG	1:D:40:PRO:O	2.66	0.43
1:A:108:ARG:HB3	1:B:233:ALA:HB1	2.01	0.43
1:A:120:GLU:OE1	1:A:137:GLU:HG2	2.19	0.43
1:B:317:GLU:O	1:B:320:SER:N	2.52	0.43
1:B:7:LYS:HB3	3:B:449:HOH:O	2.19	0.43
1:C:190:LEU:CD2	1:C:197:VAL:HG22	2.49	0.43
1:C:348:MET:HE2	1:D:40:PRO:CB	2.44	0.43
1:D:323:ALA:O	1:D:331:LEU:HB2	2.19	0.43
1:B:115:ASN:O	1:B:117:HIS:N	2.50	0.42
1:A:348:MET:CG	1:B:40:PRO:O	2.46	0.42
1:B:74:LEU:HB2	1:B:216:LEU:CD2	2.46	0.42
1:D:136:LYS:CD	1:D:138:ASN:H	2.32	0.42
1:A:23:GLY:CA	1:C:36:LYS:HB2	2.48	0.42
1:A:329:PHE:CD2	1:A:340:SER:HB3	2.54	0.42
1:B:136:LYS:O	1:B:137:GLU:CB	2.68	0.42
1:C:195:ASP:O	1:C:218:THR:HG22	2.18	0.42
1:C:283:TYR:C	1:C:285:GLY:H	2.23	0.42
1:C:331:LEU:HD11	1:C:348:MET:CE	2.49	0.42
1:D:359:GLU:OE1	1:D:364:PHE:CD2	2.72	0.42
1:D:99:ILE:O	1:D:102:VAL:CG2	2.64	0.42
1:A:106:THR:O	1:A:107:HIS:C	2.58	0.42
1:A:72:TYR:HD1	1:A:218:THR:O	2.02	0.42
1:A:294:VAL:HA	1:A:297:LYS:CG	2.49	0.42
1:A:323:ALA:HA	1:A:342:LEU:HD11	2.01	0.42
1:B:106:THR:O	1:B:107:HIS:C	2.57	0.42
1:B:75:ALA:CA	1:B:215:VAL:HG12	2.49	0.42
1:B:294:VAL:HA	1:B:297:LYS:HG3	2.01	0.42
1:B:12:ALA:CA	1:B:67:LEU:HD21	2.50	0.42
1:C:145:GLU:O	1:C:146:THR:C	2.56	0.42
1:C:173:VAL:O	1:C:173:VAL:HG12	2.20	0.42
1:C:271:LEU:HD21	1:C:384:ILE:HG21	2.01	0.42
1:D:51:ARG:HG3	1:D:237:ILE:CD1	2.44	0.42
1:A:95:HIS:HB3	1:A:139:THR:CA	2.49	0.42
1:B:123:PHE:N	1:B:123:PHE:CD1	2.88	0.42
1:B:190:LEU:CD2	1:B:197:VAL:HG22	2.49	0.42
2:B:400:PLP:H6	3:B:409:HOH:O	2.20	0.42
1:C:121:THR:HB	3:C:426:HOH:O	2.19	0.42
1:D:364:PHE:HD2	1:D:364:PHE:HA	1.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:SER:HB2	1:B:34:THR:HG23	2.01	0.42
1:A:338:ILE:HG21	1:A:338:ILE:HD13	1.86	0.42
1:B:17:GLU:OE1	1:D:36:LYS:NZ	2.50	0.42
1:B:96:ALA:HB1	1:B:141:LEU:HB3	2.01	0.42
1:C:287:LYS:HA	1:C:292:TYR:CD1	2.55	0.42
1:D:160:VAL:O	1:D:164:ILE:HG13	2.19	0.42
1:D:91:PRO:O	1:D:94:SER:OG	2.33	0.42
1:A:136:LYS:CG	1:A:137:GLU:N	2.73	0.42
1:A:312:ILE:HD12	1:A:318:ALA:HB1	2.01	0.42
1:B:134:LEU:C	1:B:136:LYS:N	2.72	0.42
1:D:104:GLY:O	1:D:107:HIS:HB3	2.20	0.42
1:D:136:LYS:HZ1	1:D:138:ASN:HA	1.84	0.42
1:D:204:TYR:CZ	1:D:336:GLY:CA	3.03	0.42
1:A:146:THR:CB	1:A:147:PRO:CD	2.98	0.42
1:A:182:LEU:HD22	1:A:186:ILE:HG21	2.01	0.42
1:A:18:HIS:CB	1:A:27:GLU:HG3	2.50	0.42
1:A:88:GLN:HG3	1:A:230:LEU:HD22	2.01	0.42
1:C:331:LEU:O	1:C:332:ALA:HB2	2.20	0.42
1:C:375:GLU:HB2	1:C:380:LEU:HD11	2.01	0.42
1:C:389:LYS:O	1:C:390:GLN:C	2.57	0.42
1:C:54:ASN:ND2	1:C:56:ASN:H	2.17	0.42
1:D:105:GLY:O	1:D:106:THR:C	2.57	0.42
1:A:21:VAL:O	1:C:44:ILE:O	2.38	0.42
1:A:18:HIS:CG	1:A:27:GLU:HG3	2.54	0.42
1:A:354:PRO:C	1:A:356:GLU:N	2.73	0.42
1:B:113:VAL:C	1:B:115:ASN:H	2.23	0.42
1:B:203:LYS:HD2	1:B:203:LYS:N	2.34	0.42
1:B:310:PHE:HE1	1:B:312:ILE:HG23	1.85	0.42
1:B:344:VAL:HB	1:B:347:VAL:HG22	2.02	0.42
1:C:150:PRO:HB3	1:C:369:ARG:CD	2.50	0.42
1:D:21:VAL:CG1	1:D:21:VAL:O	2.67	0.42
1:B:47:TYR:HE1	1:D:22:HIS:HD2	1.67	0.42
1:A:274:ASP:O	1:A:275:LYS:C	2.58	0.42
1:C:72:TYR:HD1	1:C:218:THR:O	2.03	0.42
1:C:26:ILE:HD13	1:C:26:ILE:HA	1.81	0.42
1:D:289:HIS:CD2	1:D:291:ASN:H	2.38	0.42
1:C:331:LEU:HD21	1:D:40:PRO:CA	2.49	0.42
1:A:137:GLU:CG	1:A:137:GLU:O	2.68	0.42
1:A:98:SER:HA	1:A:143:TRP:O	2.20	0.42
1:A:228:GLN:O	1:A:231:GLN:HB3	2.20	0.42
1:B:135:ILE:CG2	1:B:168:ALA:HB2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:ILE:HG21	1:B:168:ALA:HB2	2.02	0.42
1:C:333:GLU:O	1:C:334:SER:HB3	2.20	0.42
1:D:311:ARG:NH1	1:D:364:PHE:CD1	2.88	0.42
1:B:248:ARG:NH1	1:C:248:ARG:HH11	2.18	0.41
1:C:88:GLN:HG3	1:C:230:LEU:HD13	2.02	0.41
1:D:168:ALA:O	1:D:171:GLN:HG2	2.19	0.41
1:A:114:ALA:O	1:A:115:ASN:C	2.59	0.41
1:A:311:ARG:CB	1:A:311:ARG:HH11	2.32	0.41
1:B:334:SER:C	1:B:335:LEU:HD23	2.41	0.41
1:C:42:ASN:HA	1:C:43:PRO:HD3	1.71	0.41
1:D:340:SER:C	1:D:341:LEU:HD23	2.40	0.41
1:A:286:LEU:O	1:A:289:HIS:N	2.49	0.41
1:A:70:ALA:HB2	1:A:190:LEU:HD12	2.02	0.41
1:B:385:LYS:C	1:B:387:ALA:N	2.72	0.41
1:B:91:PRO:O	1:B:92:GLN:C	2.59	0.41
1:C:226:ARG:O	1:C:229:PHE:HB3	2.20	0.41
1:D:343:GLU:HG2	1:D:344:VAL:N	2.36	0.41
1:A:154:VAL:HB	1:A:291:ASN:HB2	2.02	0.41
1:A:293:ASP:O	1:A:297:LYS:HG2	2.20	0.41
1:A:317:GLU:O	1:A:318:ALA:C	2.58	0.41
1:A:37:GLN:CB	1:A:43:PRO:HA	2.51	0.41
1:B:8:PHE:CD2	1:B:8:PHE:C	2.94	0.41
1:C:250:LEU:C	1:C:250:LEU:HD23	2.41	0.41
1:A:274:ASP:OD1	1:A:277:ASN:N	2.53	0.41
1:A:264:ALA:CA	1:A:308:ILE:HD11	2.50	0.41
1:A:30:SER:HB2	1:A:55:PRO:HG2	2.02	0.41
1:A:53:GLN:OE1	1:A:58:GLU:HB2	2.20	0.41
1:B:101:ASP:CB	1:B:148:THR:HB	2.51	0.41
1:B:203:LYS:HG2	1:B:335:LEU:HG	2.01	0.41
1:C:114:ALA:CB	1:C:119:VAL:N	2.78	0.41
1:C:156:ASP:HB3	1:C:159:LYS:HB2	2.01	0.41
1:C:1:THR:CG2	1:C:2:LEU:N	2.83	0.41
1:C:386:GLN:N	3:C:472:HOH:O	2.53	0.41
1:D:120:GLU:HA	3:D:424:HOH:O	2.21	0.41
1:D:121:THR:CG2	1:D:123:PHE:CE1	3.04	0.41
1:C:331:LEU:HD21	1:D:40:PRO:CD	2.51	0.41
1:A:33:THR:HG23	1:A:49:TYR:HE1	1.85	0.41
1:B:144:ILE:HB	1:B:177:VAL:HG22	2.02	0.41
1:C:182:LEU:HD23	1:C:182:LEU:HA	1.90	0.41
1:D:130:ASP:O	1:D:134:LEU:HG	2.20	0.41
1:A:181:PHE:CD1	1:A:181:PHE:N	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ILE:HD13	1:A:189:PRO:HB3	2.02	0.41
1:A:344:VAL:N	1:A:348:MET:HE1	2.34	0.41
1:A:380:LEU:O	1:A:384:ILE:HG12	2.20	0.41
1:B:149:ASN:HA	1:B:150:PRO:HA	1.81	0.41
1:B:172:ASP:CB	3:B:448:HOH:O	2.67	0.41
1:B:175:LEU:HD23	1:B:193:GLY:O	2.21	0.41
1:B:189:PRO:HB2	1:B:197:VAL:HG13	2.01	0.41
1:B:242:ASP:O	1:B:246:THR:OG1	2.25	0.41
1:B:358:ARG:NH1	1:B:358:ARG:HB2	2.35	0.41
1:B:94:SER:O	1:B:120:GLU:N	2.45	0.41
1:C:115:ASN:OD1	1:D:88:GLN:HA	2.20	0.41
1:C:294:VAL:HA	1:C:297:LYS:HG3	2.02	0.41
1:C:33:THR:HG22	1:C:34:THR:N	2.35	0.41
1:D:134:LEU:O	1:D:136:LYS:O	2.39	0.41
1:A:258:ARG:O	1:A:262:LEU:HG	2.21	0.41
1:A:6:ASP:OD1	1:D:327:ARG:NH2	2.43	0.41
1:A:95:HIS:O	1:A:140:LYS:N	2.47	0.41
1:B:143:TRP:CE3	1:B:176:VAL:HG11	2.56	0.41
1:B:358:ARG:O	1:B:359:GLU:HG2	2.21	0.41
1:A:348:MET:SD	1:B:40:PRO:HA	2.60	0.41
1:C:135:ILE:C	1:C:139:THR:HG21	2.40	0.41
1:C:280:ALA:CB	1:C:311:ARG:HD3	2.48	0.41
1:D:100:GLY:O	1:D:102:VAL:N	2.54	0.41
1:D:221:LYS:HE2	1:D:225:GLU:OE2	2.20	0.41
1:B:345:PRO:O	1:B:350:HIS:N	2.54	0.41
1:C:332:ALA:HA	1:D:37:GLN:HG3	2.02	0.41
1:C:386:GLN:O	1:C:386:GLN:CD	2.59	0.41
1:D:228:GLN:O	1:D:231:GLN:HB3	2.21	0.41
1:A:357:ALA:C	1:A:359:GLU:H	2.22	0.41
1:A:35:PHE:CD2	1:C:22:HIS:HB3	2.56	0.41
1:B:72:TYR:CD2	1:B:224:TYR:CD2	3.08	0.41
1:C:220:ASN:ND2	1:C:223:LEU:H	2.19	0.41
1:D:265:ASN:HA	1:D:283:TYR:CE2	2.56	0.41
1:D:335:LEU:CG	1:D:336:GLY:N	2.83	0.41
1:A:211:VAL:CG2	1:A:245:LEU:HD23	2.51	0.41
1:A:355:LYS:O	1:A:356:GLU:C	2.60	0.41
1:B:146:THR:CB	1:B:147:PRO:CD	2.99	0.41
1:B:208:HIS:CE1	1:B:338:ILE:CD1	3.03	0.41
1:D:106:THR:OG1	1:D:107:HIS:N	2.53	0.41
1:D:123:PHE:H	1:D:123:PHE:HD1	1.68	0.41
1:A:99:ILE:HG22	1:A:100:GLY:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LEU:O	1:A:135:ILE:N	2.49	0.40
1:A:57:ARG:O	1:A:60:LEU:HB3	2.21	0.40
1:B:187:SER:C	1:B:188:ASN:ND2	2.74	0.40
1:B:330:THR:HB	1:B:341:LEU:CD2	2.50	0.40
1:B:343:GLU:CG	1:B:344:VAL:N	2.84	0.40
1:C:208:HIS:CE1	1:C:338:ILE:HD12	2.57	0.40
1:C:355:LYS:HA	1:C:358:ARG:CZ	2.52	0.40
1:D:301:ASP:O	1:D:302:ALA:HB3	2.20	0.40
1:D:329:PHE:CZ	1:D:384:ILE:HD11	2.56	0.40
1:A:360:ALA:C	1:A:362:GLY:N	2.74	0.40
1:A:369:ARG:NH1	1:A:369:ARG:HG2	2.36	0.40
1:A:53:GLN:NE2	1:A:58:GLU:HG3	2.36	0.40
1:B:208:HIS:CD2	1:B:208:HIS:N	2.90	0.40
1:B:53:GLN:HA	1:B:57:ARG:NH2	2.36	0.40
1:B:95:HIS:NE2	1:B:122:SER:OG	2.55	0.40
1:C:125:ASN:OD1	1:C:126:ASP:N	2.55	0.40
1:C:190:LEU:C	1:C:192:PHE:H	2.24	0.40
1:C:83:THR:O	1:C:86:ILE:HB	2.20	0.40
1:A:89:SER:HA	1:A:230:LEU:HD11	2.03	0.40
1:B:139:THR:C	1:B:140:LYS:HG2	2.42	0.40
1:C:260:ALA:CB	3:C:470:HOH:O	2.68	0.40
1:D:137:GLU:CG	1:D:137:GLU:O	2.68	0.40
1:A:300:ARG:C	1:A:302:ALA:H	2.23	0.40
1:B:136:LYS:HD2	1:B:136:LYS:HA	1.90	0.40
1:C:72:TYR:HB3	1:C:224:TYR:CD1	2.57	0.40
1:C:349:THR:CG2	1:C:350:HIS:N	2.76	0.40
1:D:184:PRO:HD3	1:D:199:HIS:CE1	2.55	0.40
1:A:101:ASP:HB2	1:A:148:THR:HB	2.01	0.40
1:A:229:PHE:O	1:A:230:LEU:C	2.60	0.40
1:A:81:ALA:CA	1:B:234:ILE:O	2.69	0.40
1:B:254:HIS:H	1:B:254:HIS:CD2	2.39	0.40
1:C:112:LYS:C	1:C:114:ALA:N	2.75	0.40
1:D:101:ASP:HB2	1:D:148:THR:HB	2.04	0.40
1:D:154:VAL:HG12	1:D:294:VAL:CG1	2.51	0.40
1:D:52:SER:O	1:D:53:GLN:HB2	2.21	0.40
1:D:99:ILE:HA	1:D:124:THR:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	391/393 (100%)	304 (78%)	63 (16%)	24 (6%)	2	2
1	B	391/393 (100%)	294 (75%)	63 (16%)	34 (9%)	1	1
1	C	391/393 (100%)	310 (79%)	51 (13%)	30 (8%)	1	1
1	D	391/393 (100%)	302 (77%)	57 (15%)	32 (8%)	1	1
All	All	1564/1572 (100%)	1210 (77%)	234 (15%)	120 (8%)	1	1

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	PRO
1	A	46	THR
1	A	135	ILE
1	A	137	GLU
1	A	138	ASN
1	A	316	ALA
1	B	46	THR
1	B	101	ASP
1	B	137	GLU
1	B	168	ALA
1	B	316	ALA
1	B	336	GLY
1	B	350	HIS
1	C	43	PRO
1	C	46	THR
1	C	101	ASP
1	C	135	ILE
1	C	137	GLU
1	C	276	GLU
1	C	279	VAL
1	C	316	ALA
1	C	350	HIS

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Mol	Chain	Res	Type
1	C	363	VAL
1	D	46	THR
1	D	108	ARG
1	D	137	GLU
1	D	138	ASN
1	D	168	ALA
1	D	316	ALA
1	D	347	VAL
1	D	350	HIS
1	D	363	VAL
1	A	53	GLN
1	A	101	ASP
1	A	118	GLY
1	A	191	ASN
1	A	279	VAL
1	A	313	LYS
1	A	363	VAL
1	B	108	ARG
1	B	135	ILE
1	B	138	ASN
1	B	209	SER
1	B	279	VAL
1	B	335	LEU
1	B	347	VAL
1	B	352	GLY
1	B	358	ARG
1	B	363	VAL
1	C	53	GLN
1	C	108	ARG
1	C	138	ASN
1	C	146	THR
1	C	203	LYS
1	C	332	ALA
1	C	352	GLY
1	D	101	ASP
1	D	117	HIS
1	D	135	ILE
1	D	323	ALA
1	D	335	LEU
1	D	336	GLY
1	D	355	LYS
1	D	359	GLU

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Mol	Chain	Res	Type
1	D	386	GLN
1	A	146	THR
1	A	168	ALA
1	A	287	LYS
1	A	358	ARG
1	B	43	PRO
1	B	92	GLN
1	B	172	ASP
1	B	332	ALA
1	B	386	GLN
1	C	349	THR
1	C	386	GLN
1	D	334	SER
1	D	352	GLY
1	A	107	HIS
1	A	108	ARG
1	A	203	LYS
1	A	276	GLU
1	A	301	ASP
1	A	359	GLU
1	B	107	HIS
1	B	115	ASN
1	B	276	GLU
1	C	126	ASP
1	C	163	LEU
1	C	168	ALA
1	C	313	LYS
1	D	115	ASN
1	D	128	LEU
1	D	301	ASP
1	D	332	ALA
1	A	275	LYS
1	B	146	THR
1	B	167	HIS
1	B	301	ASP
1	B	355	LYS
1	B	359	GLU
1	C	50	SER
1	C	183	SER
1	D	50	SER
1	D	276	GLU
1	D	349	THR

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Mol	Chain	Res	Type
1	D	358	ARG
1	B	53	GLN
1	B	334	SER
1	C	193	GLY
1	C	205	ILE
1	C	284	PRO
1	C	347	VAL
1	D	348	MET
1	B	284	PRO
1	C	118	GLY
1	D	118	GLY
1	D	93	GLY
1	D	279	VAL
1	B	193	GLY

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	318/324 (98%)	295 (93%)	23 (7%)	17	33
1	B	318/324 (98%)	288 (91%)	30 (9%)	10	19
1	C	318/324 (98%)	297 (93%)	21 (7%)	19	38
1	D	318/324 (98%)	299 (94%)	19 (6%)	22	44
All	All	1272/1296 (98%)	1179 (93%)	93 (7%)	16	33

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	THR
1	A	40	PRO
1	A	54	ASN
1	A	103	TYR
1	A	117	HIS
1	A	135	ILE
1	A	139	THR

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Mol	Chain	Res	Type
1	A	150	PRO
1	A	197	VAL
1	A	216	LEU
1	A	220	ASN
1	A	227	LEU
1	A	239	SER
1	A	247	HIS
1	A	250	LEU
1	A	277	ASN
1	A	290	PRO
1	A	311	ARG
1	A	312	ILE
1	A	335	LEU
1	A	339	GLU
1	A	342	LEU
1	A	343	GLU
1	B	21	VAL
1	B	33	THR
1	B	34	THR
1	B	60	LEU
1	B	77	SER
1	B	103	TYR
1	B	117	HIS
1	B	123	PHE
1	B	130	ASP
1	B	134	LEU
1	B	135	ILE
1	B	139	THR
1	B	146	THR
1	B	150	PRO
1	B	171	GLN
1	B	197	VAL
1	B	216	LEU
1	B	220	ASN
1	B	227	LEU
1	B	239	SER
1	B	247	HIS
1	B	250	LEU
1	B	277	ASN
1	B	290	PRO
1	B	312	ILE
1	B	320	SER

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Mol	Chain	Res	Type
1	B	335	LEU
1	B	339	GLU
1	B	342	LEU
1	B	343	GLU
1	C	34	THR
1	C	103	TYR
1	C	117	HIS
1	C	135	ILE
1	C	139	THR
1	C	197	VAL
1	C	216	LEU
1	C	220	ASN
1	C	227	LEU
1	C	247	HIS
1	C	250	LEU
1	C	277	ASN
1	C	290	PRO
1	C	311	ARG
1	C	312	ILE
1	C	320	SER
1	C	339	GLU
1	C	342	LEU
1	C	343	GLU
1	C	354	PRO
1	C	369	ARG
1	D	33	THR
1	D	34	THR
1	D	103	TYR
1	D	117	HIS
1	D	135	ILE
1	D	139	THR
1	D	150	PRO
1	D	197	VAL
1	D	216	LEU
1	D	220	ASN
1	D	227	LEU
1	D	252	THR
1	D	277	ASN
1	D	312	ILE
1	D	335	LEU
1	D	342	LEU
1	D	343	GLU

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Mol	Chain	Res	Type
1	D	354	PRO
1	D	364	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	37	GLN
1	A	54	ASN
1	A	158	GLN
1	A	179	ASN
1	A	188	ASN
1	A	208	HIS
1	A	219	ASN
1	A	220	ASN
1	A	231	GLN
1	A	254	HIS
1	A	277	ASN
1	A	289	HIS
1	A	350	HIS
1	B	3	GLN
1	B	37	GLN
1	B	179	ASN
1	B	188	ASN
1	B	206	ASN
1	B	208	HIS
1	B	219	ASN
1	B	220	ASN
1	B	231	GLN
1	B	254	HIS
1	B	277	ASN
1	B	350	HIS
1	C	3	GLN
1	C	37	GLN
1	C	53	GLN
1	C	54	ASN
1	C	69	ASN
1	C	115	ASN
1	C	129	ASN
1	C	158	GLN
1	C	188	ASN
1	C	191	ASN

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Mol	Chain	Res	Type
1	C	206	ASN
1	C	208	HIS
1	C	219	ASN
1	C	220	ASN
1	C	231	GLN
1	C	277	ASN
1	C	282	ASN
1	C	350	HIS
1	D	3	GLN
1	D	22	HIS
1	D	37	GLN
1	D	179	ASN
1	D	188	ASN
1	D	208	HIS
1	D	219	ASN
1	D	220	ASN
1	D	231	GLN
1	D	247	HIS
1	D	254	HIS
1	D	277	ASN
1	D	282	ASN
1	D	289	HIS
1	D	291	ASN
1	D	350	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	PLP	A	400	1	15,15,16	4.08	4 (26%)	20,22,23	2.44	8 (40%)
2	PLP	B	400	1	15,15,16	4.28	6 (40%)	20,22,23	2.60	6 (30%)
2	PLP	C	400	1	15,15,16	4.21	4 (26%)	20,22,23	2.62	10 (50%)
2	PLP	D	400	1	15,15,16	4.08	6 (40%)	20,22,23	2.49	9 (45%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLP	A	400	1	-	0/6/6/8	0/1/1/1
2	PLP	B	400	1	-	0/6/6/8	0/1/1/1
2	PLP	C	400	1	-	0/6/6/8	0/1/1/1
2	PLP	D	400	1	-	0/6/6/8	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	400	PLP	P-O4P	-2.58	1.51	1.60
2	D	400	PLP	P-O3P	-2.56	1.44	1.54
2	B	400	PLP	C4A-C4	-2.48	1.46	1.51
2	A	400	PLP	P-O3P	-2.16	1.45	1.54
2	B	400	PLP	P-O3P	-2.05	1.46	1.54
2	D	400	PLP	C3-C4	2.06	1.44	1.40
2	A	400	PLP	C2-N1	2.15	1.38	1.33
2	B	400	PLP	C5A-C5	2.39	1.57	1.50
2	D	400	PLP	C6-N1	2.42	1.39	1.34
2	B	400	PLP	C2-N1	2.59	1.39	1.33
2	C	400	PLP	C2-N1	2.64	1.39	1.33
2	D	400	PLP	C2-N1	3.40	1.40	1.33
2	A	400	PLP	C5-C4	7.76	1.49	1.40
2	C	400	PLP	C5-C4	7.89	1.49	1.40
2	B	400	PLP	C5-C4	9.70	1.51	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	400	PLP	C3-C2	10.14	1.47	1.40
2	D	400	PLP	C5-C4	10.43	1.52	1.40
2	B	400	PLP	C3-C2	12.20	1.49	1.40
2	A	400	PLP	C3-C2	12.86	1.49	1.40
2	C	400	PLP	C3-C2	13.28	1.50	1.40

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	400	PLP	O2P-P-O4P	-3.80	96.63	106.73
2	B	400	PLP	C3-C2-N1	-3.61	116.01	120.75
2	A	400	PLP	C3-C2-N1	-3.33	116.38	120.75
2	C	400	PLP	C3-C2-N1	-3.23	116.51	120.75
2	D	400	PLP	C3-C2-N1	-3.10	116.68	120.75
2	D	400	PLP	O3-C3-C2	-3.07	111.35	117.78
2	B	400	PLP	C5-C6-N1	-2.93	118.91	123.87
2	C	400	PLP	C5-C6-N1	-2.85	119.04	123.87
2	D	400	PLP	C5-C6-N1	-2.84	119.06	123.87
2	A	400	PLP	O3-C3-C2	-2.80	111.92	117.78
2	A	400	PLP	C5-C6-N1	-2.46	119.70	123.87
2	B	400	PLP	C2A-C2-N1	-2.27	113.37	117.89
2	C	400	PLP	O3-C3-C2	-2.21	113.15	117.78
2	C	400	PLP	O3P-P-O1P	2.07	118.62	110.50
2	A	400	PLP	O4P-C5A-C5	2.17	113.68	109.32
2	D	400	PLP	O3P-P-O2P	2.18	116.41	107.61
2	D	400	PLP	C6-C5-C4	2.36	120.15	118.18
2	C	400	PLP	O3P-P-O2P	2.62	118.20	107.61
2	D	400	PLP	O4P-C5A-C5	2.68	114.72	109.32
2	B	400	PLP	O3-C3-C4	2.88	125.96	118.14
2	C	400	PLP	O3-C3-C4	3.11	126.60	118.14
2	A	400	PLP	C6-C5-C4	3.19	120.84	118.18
2	A	400	PLP	C6-N1-C2	3.20	125.42	119.26
2	C	400	PLP	C6-N1-C2	3.26	125.55	119.26
2	C	400	PLP	C6-C5-C4	3.30	120.94	118.18
2	A	400	PLP	O3-C3-C4	3.42	127.43	118.14
2	D	400	PLP	C6-N1-C2	3.50	126.01	119.26
2	D	400	PLP	O3-C3-C4	3.68	128.13	118.14
2	B	400	PLP	C6-N1-C2	3.84	126.65	119.26
2	D	400	PLP	C2A-C2-C3	6.24	128.40	120.96
2	A	400	PLP	C2A-C2-C3	6.39	128.59	120.96
2	C	400	PLP	C2A-C2-C3	6.75	129.01	120.96
2	B	400	PLP	C2A-C2-C3	8.06	130.57	120.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	400	PLP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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	393/393 (100%)	0.61	47 (11%) 5 3	19, 51, 70, 70	0
1	B	393/393 (100%)	0.83	58 (14%) 3 1	20, 54, 70, 70	0
1	C	393/393 (100%)	0.88	66 (16%) 2 1	24, 56, 70, 70	0
1	D	393/393 (100%)	0.75	53 (13%) 3 2	18, 51, 70, 70	0
All	All	1572/1572 (100%)	0.77	224 (14%) 3 1	18, 53, 70, 70	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	VAL	13.1
1	C	39	SER	13.0
1	D	103	TYR	10.9
1	B	117	HIS	10.8
1	D	362	GLY	10.5
1	D	115	ASN	9.7
1	C	38	SER	9.6
1	C	116	ALA	9.4
1	C	103	TYR	9.4
1	A	46	THR	9.2
1	B	118	GLY	9.0
1	A	33	THR	9.0
1	D	118	GLY	8.8
1	A	352	GLY	8.8
1	D	393	ASN	8.8
1	D	116	ALA	8.7
1	B	346	ALA	8.5
1	D	364	PHE	8.3
1	B	391	ALA	8.2
1	B	324	SER	8.1
1	A	45	GLY	7.8

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Mol	Chain	Res	Type	RSRZ
1	B	353	ILE	7.7
1	B	323	ALA	7.7
1	B	354	PRO	7.6
1	C	41	ALA	7.6
1	C	110	PHE	7.6
1	B	320	SER	7.4
1	A	313	LYS	7.2
1	D	349	THR	7.2
1	B	351	GLY	7.2
1	A	116	ALA	7.1
1	B	316	ALA	7.1
1	A	25	VAL	7.0
1	C	115	ASN	7.0
1	A	42	ASN	6.9
1	A	103	TYR	6.9
1	D	350	HIS	6.9
1	D	356	GLU	6.7
1	C	40	PRO	6.7
1	D	101	ASP	6.7
1	B	349	THR	6.6
1	C	101	ASP	6.6
1	B	110	PHE	6.6
1	B	101	ASP	6.5
1	C	49	TYR	6.5
1	D	360	ALA	6.4
1	B	170	GLY	6.4
1	D	41	ALA	6.4
1	A	43	PRO	6.4
1	B	115	ASN	6.2
1	D	353	ILE	6.2
1	A	41	ALA	6.1
1	C	44	ILE	6.1
1	D	114	ALA	6.1
1	C	102	VAL	6.1
1	D	117	HIS	5.9
1	A	117	HIS	5.9
1	B	393	ASN	5.9
1	B	352	GLY	5.8
1	C	118	GLY	5.8
1	C	19	VAL	5.8
1	D	336	GLY	5.8
1	A	105	GLY	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	392	THR	5.7
1	C	393	ASN	5.6
1	D	317	GLU	5.6
1	C	36	LYS	5.5
1	B	357	ALA	5.5
1	C	43	PRO	5.4
1	D	391	ALA	5.4
1	C	50	SER	5.4
1	B	103	TYR	5.4
1	D	319	ALA	5.3
1	C	124	THR	5.3
1	C	37	GLN	5.2
1	D	354	PRO	5.2
1	B	345	PRO	5.2
1	B	350	HIS	5.2
1	D	352	GLY	5.2
1	D	344	VAL	5.2
1	D	102	VAL	5.2
1	B	361	SER	5.1
1	A	102	VAL	5.1
1	B	161	ALA	5.1
1	D	320	SER	5.0
1	B	116	ALA	5.0
1	C	117	HIS	5.0
1	C	46	THR	5.0
1	C	23	GLY	5.0
1	B	319	ALA	4.9
1	D	42	ASN	4.8
1	C	32	SER	4.8
1	C	42	ASN	4.8
1	B	102	VAL	4.7
1	C	33	THR	4.7
1	C	353	ILE	4.6
1	C	123	PHE	4.6
1	D	361	SER	4.5
1	C	352	GLY	4.5
1	C	45	GLY	4.4
1	A	19	VAL	4.4
1	A	38	SER	4.4
1	A	44	ILE	4.2
1	B	355	LYS	4.2
1	C	21	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	35	PHE	4.1
1	A	118	GLY	4.1
1	A	35	PHE	4.1
1	D	1	THR	4.1
1	A	115	ASN	4.0
1	C	133	GLN	4.0
1	D	100	GLY	4.0
1	A	26	ILE	4.0
1	A	37	GLN	3.9
1	A	39	SER	3.9
1	B	358	ARG	3.8
1	C	52	SER	3.8
1	B	124	THR	3.8
1	B	344	VAL	3.8
1	D	48	GLU	3.8
1	B	43	PRO	3.8
1	B	390	GLN	3.8
1	D	357	ALA	3.8
1	B	276	GLU	3.7
1	C	20	ASP	3.7
1	C	22	HIS	3.6
1	D	363	VAL	3.6
1	D	345	PRO	3.6
1	C	25	VAL	3.6
1	C	24	SER	3.5
1	A	36	LYS	3.5
1	D	390	GLN	3.5
1	C	275	LYS	3.5
1	C	170	GLY	3.5
1	C	47	TYR	3.5
1	D	359	GLU	3.5
1	B	317	GLU	3.4
1	C	18	HIS	3.4
1	C	2	LEU	3.4
1	A	101	ASP	3.4
1	B	280	ALA	3.4
1	C	391	ALA	3.4
1	B	348	MET	3.4
1	A	393	ASN	3.4
1	D	365	ASP	3.4
1	C	114	ALA	3.4
1	C	53	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	18	HIS	3.3
1	A	110	PHE	3.3
1	B	107	HIS	3.3
1	A	137	GLU	3.3
1	B	1	THR	3.3
1	A	34	THR	3.3
1	C	318	ALA	3.2
1	A	58	GLU	3.2
1	C	3	GLN	3.2
1	B	360	ALA	3.2
1	A	3	GLN	3.2
1	D	110	PHE	3.1
1	D	323	ALA	3.1
1	C	1	THR	3.1
1	A	52	SER	3.1
1	B	392	THR	3.0
1	C	319	ALA	3.0
1	B	171	GLN	3.0
1	B	168	ALA	3.0
1	C	107	HIS	3.0
1	B	362	GLY	3.0
1	A	20	ASP	2.9
1	D	123	PHE	2.9
1	D	316	ALA	2.9
1	C	392	THR	2.9
1	A	47	TYR	2.9
1	A	32	SER	2.9
1	A	123	PHE	2.9
1	A	2	LEU	2.9
1	C	356	GLU	2.9
1	D	124	THR	2.9
1	D	351	GLY	2.8
1	A	1	THR	2.8
1	B	131	LEU	2.8
1	D	387	ALA	2.7
1	C	105	GLY	2.7
1	A	120	GLU	2.7
1	B	100	GLY	2.7
1	B	266	LYS	2.6
1	D	107	HIS	2.6
1	D	277	ASN	2.6
1	A	22	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	132	PRO	2.5
1	D	347	VAL	2.5
1	B	169	ALA	2.5
1	A	107	HIS	2.5
1	B	343	GLU	2.5
1	A	51	ARG	2.5
1	C	88	GLN	2.5
1	B	2	LEU	2.4
1	C	4	GLU	2.4
1	D	3	GLN	2.4
1	D	369	ARG	2.4
1	C	344	VAL	2.4
1	B	99	ILE	2.4
1	C	363	VAL	2.4
1	B	135	ILE	2.3
1	B	368	VAL	2.3
1	B	3	GLN	2.3
1	B	4	GLU	2.2
1	C	113	VAL	2.2
1	D	22	HIS	2.2
1	C	106	THR	2.2
1	A	312	ILE	2.2
1	D	197	VAL	2.2
1	A	106	THR	2.2
1	A	370	ILE	2.2
1	C	138	ASN	2.2
1	B	363	VAL	2.2
1	C	313	LYS	2.2
1	B	120	GLU	2.1
1	D	146	THR	2.1
1	C	108	ARG	2.1
1	B	109	TYR	2.1
1	C	360	ALA	2.1
1	C	272	ALA	2.0
1	C	28	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	PLP	B	400	15/16	0.86	0.34	1.22	51,64,70,70	0
2	PLP	D	400	15/16	0.82	0.41	0.75	47,62,68,70	0
2	PLP	C	400	15/16	0.88	0.28	0.32	35,59,70,70	0
2	PLP	A	400	15/16	0.89	0.23	0.31	38,56,66,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.