



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:06 AM UTC

PDB ID : 1GXD / pdb_00001gxd
Title : proMMP-2/TIMP-2 complex
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Deposited on : 2002-04-02
Resolution : 3.10 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
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

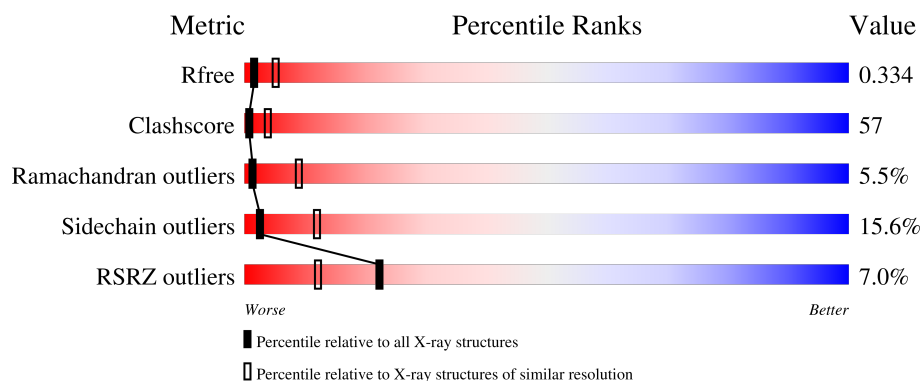
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	631	6% 39% 48% 10% ..
1	B	631	5% 37% 46% 13% ..
2	C	194	13% 25% 52% 20% ..
2	D	194	10% 31% 56% 10% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12945 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 72 KDA TYPE IV COLLAGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	624	Total	C	N	O	S	0	0	0
			4963	3186	817	933	27			
1	B	623	Total	C	N	O	S	0	0	0
			4958	3183	816	932	27			

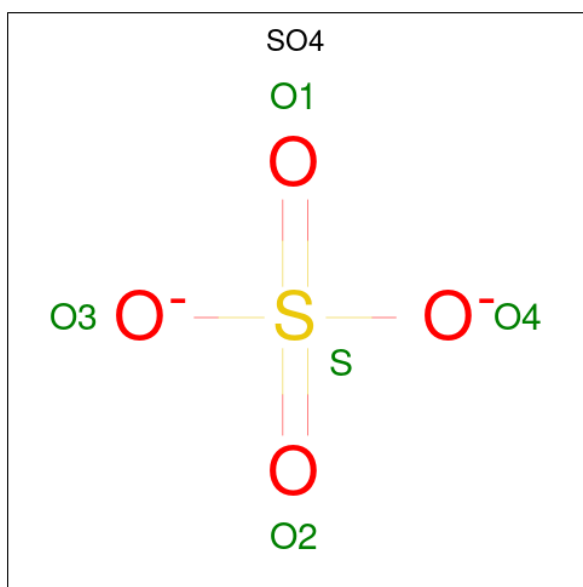
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	375	ALA	GLU	engineered mutation	UNP P08253
B	375	ALA	GLU	engineered mutation	UNP P08253

- Molecule 2 is a protein called METALLOPROTEINASE INHIBITOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	192	Total	C	N	O	S	0	0	0
			1504	952	254	281	17			
2	D	192	Total	C	N	O	S	0	0	0
			1504	952	254	281	17			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Zn	0	0
			2	2		
4	B	2	Total	Zn	0	0
			2	2		

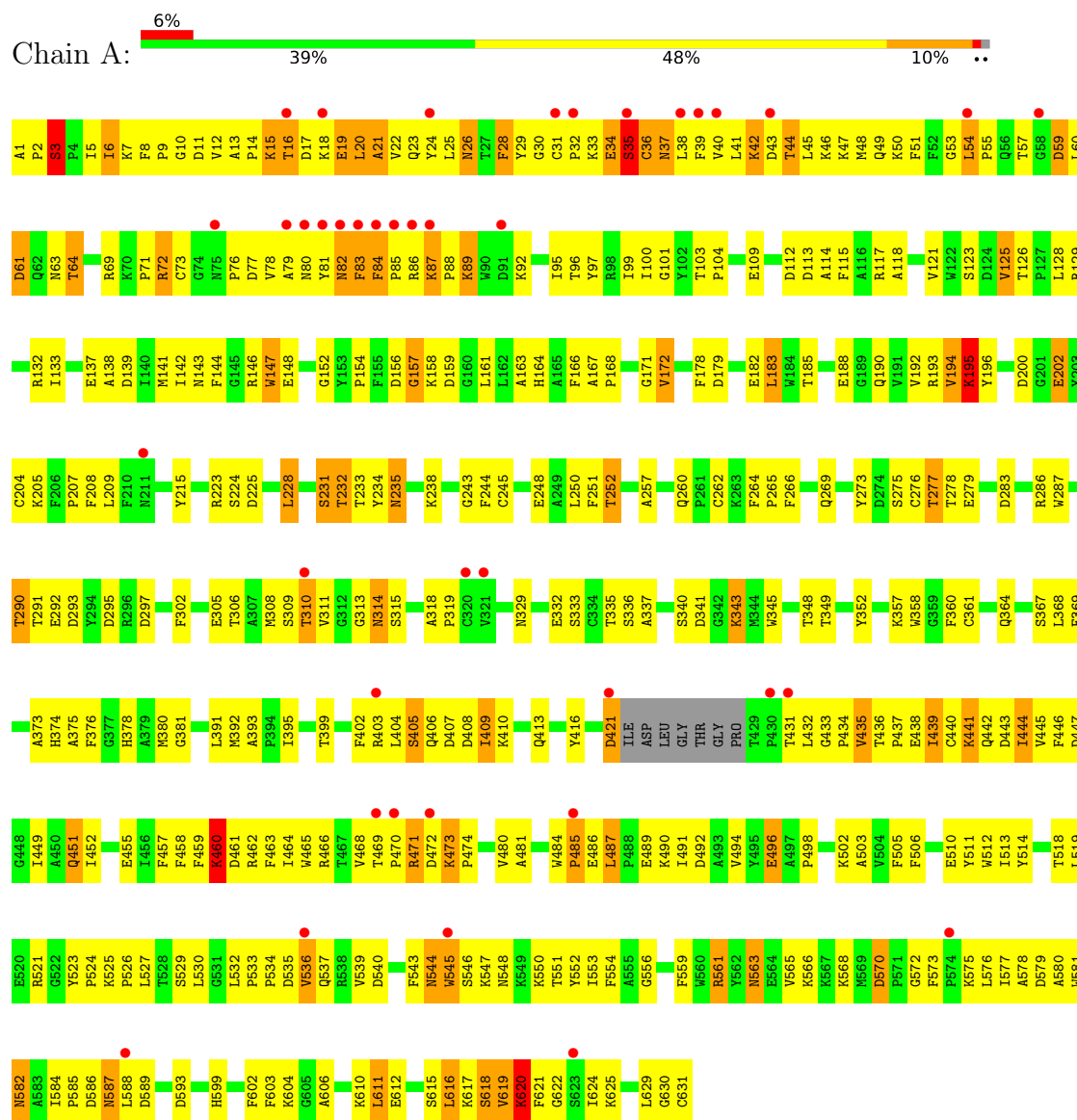
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		

3 Residue-property plots

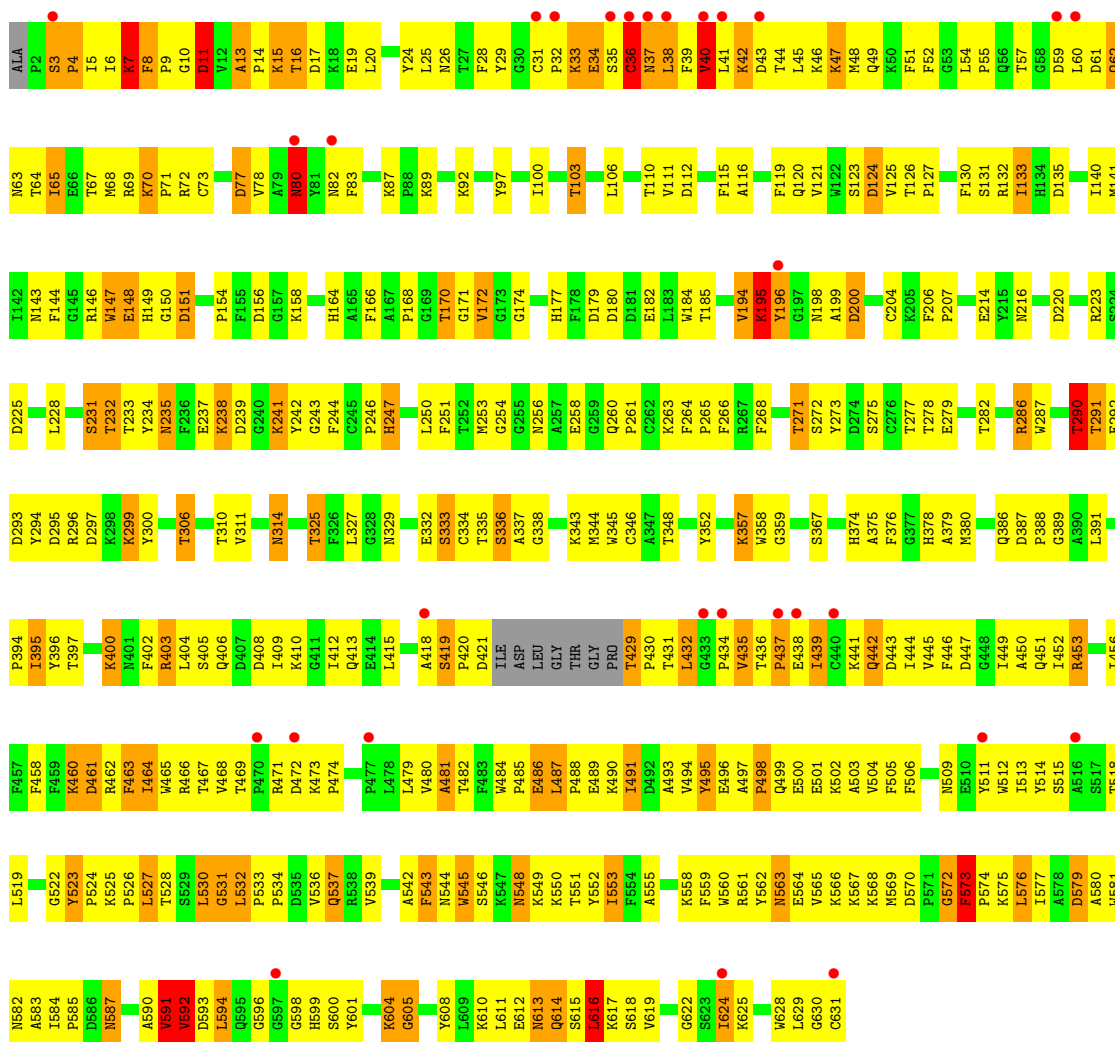
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 72 KDA TYPE IV COLLAGENASE

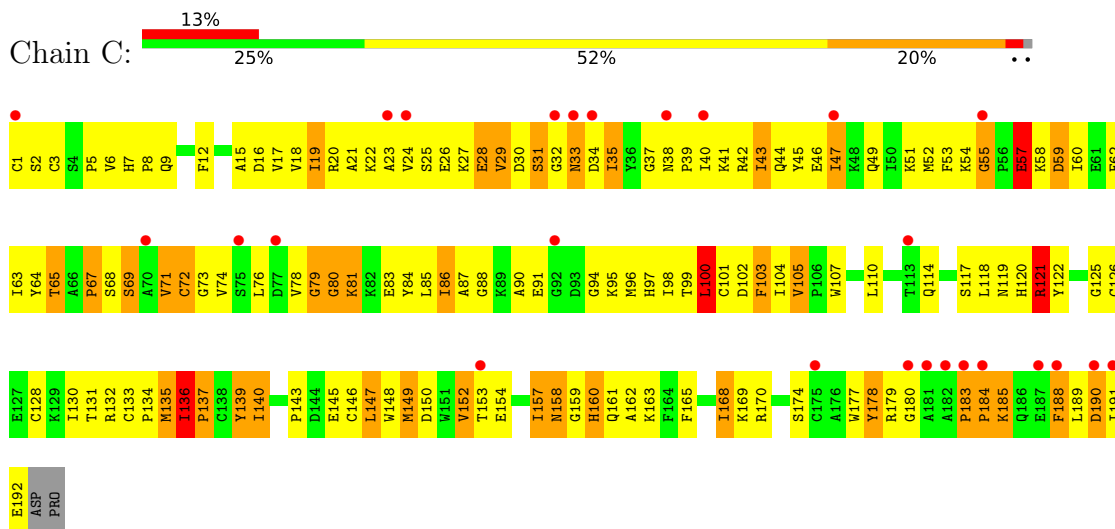


• Molecule 1: 72 KDA TYPE IV COLLAGENASE



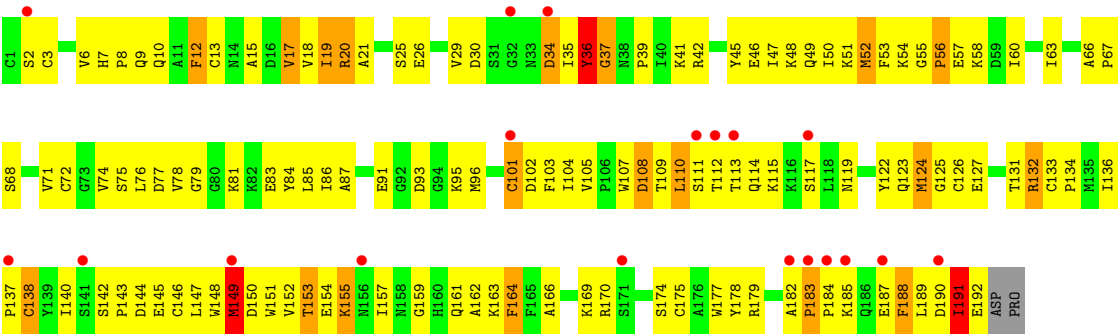


- Molecule 2: METALLOPROTEINASE INHIBITOR 2



- Molecule 2: METALLOPROTEINASE INHIBITOR 2





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	75.70Å 374.57Å 191.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 3.10 8.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (8.00-3.10) 88.0 (8.00-3.10)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 3.10Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.275 , 0.333 0.283 , 0.334	Depositor DCC
R_{free} test set	2343 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	84.8	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 73.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	12945	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: ZN, SO4, CA

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	0.51	1/5118 (0.0%)	1.05	23/6939 (0.3%)
1	B	0.58	1/5113 (0.0%)	1.08	22/6931 (0.3%)
2	C	0.42	1/1540 (0.1%)	1.04	9/2079 (0.4%)
2	D	0.44	1/1540 (0.1%)	1.04	7/2079 (0.3%)
All	All	0.52	4/13311 (0.0%)	1.06	61/18028 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	149	MET	CA-CB	-10.79	1.38	1.53
1	B	8	PHE	N-CA	5.48	1.53	1.46
1	A	620	LYS	N-CA	5.20	1.52	1.46
2	C	183	PRO	CA-C	5.09	1.56	1.52

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	149	MET	N-CA-CB	20.45	143.28	111.39
1	A	573	PHE	N-CA-C	-16.21	89.31	110.39
1	B	573	PHE	N-CA-C	-11.22	85.02	109.81
1	B	439	ILE	N-CA-C	9.55	119.39	110.42
2	C	183	PRO	N-CA-C	8.43	120.99	110.70
1	A	361	CYS	N-CA-C	-8.09	99.46	109.65
1	A	50	LYS	N-CA-C	-7.67	102.60	110.97
2	C	185	LYS	N-CA-C	7.65	120.50	108.79
1	B	537	GLN	N-CA-C	7.12	118.69	111.07
1	B	37	ASN	N-CA-C	-7.04	103.65	111.82
1	A	202	GLU	N-CA-C	6.65	118.59	110.41
2	C	184	PRO	N-CA-C	6.54	125.95	112.47
1	B	156	ASP	N-CA-C	6.54	119.28	108.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	77	ASP	N-CA-C	-6.53	105.85	113.88
1	B	576	LEU	N-CA-C	-6.45	97.75	108.34
1	A	471	ARG	N-CA-C	-6.31	104.63	112.90
1	A	83	PHE	CA-C-N	6.26	137.06	121.80
1	A	83	PHE	C-N-CA	6.26	137.06	121.80
2	C	57	GLU	N-CA-C	6.19	119.00	111.82
1	B	46	LYS	N-CA-C	-6.17	97.66	110.80
2	C	136	ILE	N-CA-C	-6.03	95.85	108.88
1	A	278	THR	N-CA-C	-5.98	104.51	112.94
1	A	290	THR	N-CA-C	-5.95	104.69	113.61
1	B	150	GLY	N-CA-C	5.91	122.92	115.42
1	A	35	SER	N-CA-C	-5.86	101.23	109.96
1	B	156	ASP	N-CA-CB	-5.84	102.29	111.23
2	D	149	MET	CB-CA-C	-5.84	102.05	111.28
1	B	290	THR	N-CA-C	-5.83	105.05	114.09
2	C	55	GLY	N-CA-C	5.72	124.01	112.34
2	D	19	ILE	N-CA-C	5.69	116.90	108.65
1	B	573	PHE	CB-CA-C	5.64	121.27	110.17
2	C	47	ILE	N-CA-C	5.63	117.78	108.99
2	D	108	ASP	N-CA-C	-5.59	102.74	110.35
2	D	175	CYS	N-CA-C	5.58	117.73	109.69
1	B	545	TRP	N-CA-C	5.54	117.61	109.24
1	B	463	PHE	N-CA-C	5.50	116.77	108.46
1	A	84	PHE	N-CA-C	-5.47	97.72	109.81
1	B	523	TYR	N-CA-C	-5.46	103.16	109.93
1	B	336	SER	N-CA-C	-5.46	105.99	113.30
1	A	465	TRP	N-CA-C	-5.40	100.90	109.59
1	A	523	TYR	N-CA-C	-5.32	102.73	110.08
1	A	13	ALA	N-CA-C	5.30	119.46	110.02
1	B	220	ASP	N-CA-C	-5.30	106.04	112.88
2	C	137	PRO	N-CD-CG	-5.27	97.48	103.80
2	D	138	CYS	N-CA-C	5.24	116.95	109.14
1	B	265	PRO	N-CD-CG	-5.24	97.52	103.80
1	A	582	ASN	N-CA-C	5.23	116.44	108.12
1	A	195	LYS	CA-C-N	-5.22	115.26	122.16
1	A	195	LYS	C-N-CA	-5.22	115.26	122.16
1	A	95	ILE	N-CA-C	5.22	115.37	107.75
1	A	275	SER	N-CA-C	-5.21	101.55	108.74
2	C	59	ASP	N-CA-C	5.21	117.65	110.35
1	A	463	PHE	N-CA-C	5.20	117.29	109.23
1	B	271	THR	N-CA-C	5.20	117.65	108.75
1	B	47	LYS	N-CA-C	-5.20	105.51	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3	SER	CA-C-N	5.17	125.42	119.83
1	A	3	SER	C-N-CA	5.17	125.42	119.83
1	A	83	PHE	N-CA-C	5.13	121.72	110.80
1	B	195	LYS	N-CA-C	5.10	121.67	110.80
1	B	36	CYS	N-CA-C	5.05	116.19	108.42
2	D	188	PHE	N-CA-C	-5.03	102.85	110.24

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	4963	0	4674	481	0
1	B	4958	0	4667	553	0
2	C	1504	0	1470	284	3
2	D	1504	0	1470	179	3
3	A	5	0	0	1	0
3	B	5	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	12945	0	12281	1437	3

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 57.

All (1437) 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:429:THR:CG2	1:B:430:PRO:HD2	1.18	1.59
1:A:409:ILE:HG13	1:A:432:LEU:CD1	1.16	1.58
1:A:409:ILE:CD1	1:A:432:LEU:HD21	1.10	1.58
1:A:409:ILE:CG1	1:A:432:LEU:HD11	1.14	1.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:429:THR:HG23	1:B:430:PRO:CD	1.06	1.49
1:A:409:ILE:HG13	1:A:432:LEU:CG	1.41	1.46
1:A:406:GLN:CA	1:A:432:LEU:HD12	1.41	1.45
2:D:183:PRO:HB2	2:D:184:PRO:CD	1.50	1.38
1:A:406:GLN:HA	1:A:432:LEU:CD1	1.58	1.34
1:B:429:THR:CG2	1:B:430:PRO:CD	1.82	1.33
1:A:409:ILE:CD1	1:A:432:LEU:CD2	2.06	1.31
2:D:36:TYR:O	2:D:36:TYR:CD1	1.84	1.30
1:B:630:GLY:O	1:B:631:CYS:N	1.66	1.29
2:C:86:ILE:CD1	2:C:104:ILE:HG23	1.64	1.27
1:A:618:SER:O	1:A:619:VAL:HG23	1.31	1.26
1:A:53:GLY:O	1:A:55:PRO:HD3	1.24	1.26
1:B:498:PRO:HG2	1:B:564:GLU:CG	1.68	1.23
1:A:618:SER:O	1:A:619:VAL:CG2	1.85	1.23
1:B:196:TYR:CD2	1:B:244:PHE:CD1	2.28	1.21
1:B:572:GLY:C	1:B:573:PHE:O	1.70	1.21
2:D:149:MET:HB2	2:D:152:VAL:CG1	1.72	1.20
2:C:29:VAL:HG22	2:C:43:ILE:CA	1.72	1.19
2:C:79:GLY:O	2:C:81:LYS:HG3	1.42	1.19
1:B:3:SER:HB2	1:B:4:PRO:CD	1.73	1.19
1:B:60:LEU:O	1:B:60:LEU:HD13	1.43	1.18
1:B:559:PHE:HZ	2:D:188:PHE:CZ	1.62	1.18
1:A:20:LEU:HD23	1:A:21:ALA:H	1.06	1.17
2:D:182:ALA:CB	2:D:185:LYS:HE3	1.73	1.17
1:B:497:ALA:HB3	1:B:500:GLU:O	1.44	1.16
2:C:29:VAL:CG2	2:C:43:ILE:HA	1.75	1.15
2:C:86:ILE:HG23	2:C:104:ILE:HG12	1.17	1.15
1:B:61:ASP:HA	1:B:64:THR:HG22	1.27	1.15
1:A:630:GLY:C	1:A:631:CYS:N	2.05	1.15
1:B:419:SER:CB	1:B:420:PRO:HD3	1.77	1.15
1:A:25:LEU:O	1:A:29:TYR:HB2	1.45	1.14
2:C:29:VAL:HG13	2:C:42:ARG:C	1.72	1.14
2:C:27:LYS:HB2	2:C:44:GLN:HG2	1.29	1.14
1:B:37:ASN:HB3	1:B:43:ASP:OD2	1.46	1.13
1:B:622:GLY:HA2	2:D:137:PRO:HB3	1.21	1.13
1:A:580:ALA:HB3	2:C:188:PHE:CE2	1.84	1.12
2:D:149:MET:CB	2:D:152:VAL:CG1	2.26	1.12
1:B:419:SER:CB	1:B:420:PRO:CD	2.27	1.12
2:C:136:ILE:HD11	2:C:152:VAL:CG2	1.79	1.11
1:B:34:GLU:OE1	1:B:34:GLU:HA	1.45	1.11
1:B:453:ARG:O	1:B:453:ARG:HD3	1.49	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:LYS:HG3	1:B:515:SER:HB2	1.33	1.10
1:B:530:LEU:O	1:B:532:LEU:N	1.83	1.10
1:A:45:LEU:HD23	1:A:59:ASP:HA	1.21	1.10
1:A:409:ILE:CG1	1:A:432:LEU:HD21	1.81	1.10
1:B:473:LYS:HG2	1:B:474:PRO:HD2	1.20	1.10
2:C:86:ILE:HD11	2:C:104:ILE:HG23	1.30	1.10
2:D:149:MET:HB2	2:D:152:VAL:HG13	1.31	1.10
1:A:1:ALA:HB3	1:A:2:PRO:HD3	1.27	1.09
1:A:409:ILE:HG12	1:A:432:LEU:HD11	1.13	1.09
1:A:36:CYS:HB3	1:A:38:LEU:CD1	1.81	1.09
1:B:612:GLU:HB2	1:B:618:SER:HB3	1.31	1.09
1:B:357:LYS:HB3	1:B:357:LYS:HZ2	1.02	1.09
1:B:429:THR:HG22	1:B:430:PRO:HD2	1.14	1.09
2:D:183:PRO:HB2	2:D:184:PRO:HD3	1.13	1.08
1:A:37:ASN:O	1:A:41:LEU:HB2	1.52	1.08
1:B:357:LYS:HB3	1:B:357:LYS:NZ	1.63	1.08
1:B:559:PHE:CZ	2:D:188:PHE:CZ	2.40	1.08
1:B:419:SER:HB3	1:B:420:PRO:CD	1.81	1.08
1:A:630:GLY:O	1:A:631:CYS:N	1.87	1.08
1:A:409:ILE:HD12	1:A:432:LEU:HD21	1.12	1.07
1:A:409:ILE:HD11	1:A:432:LEU:CD2	1.77	1.06
1:B:196:TYR:HE1	1:B:251:PHE:CZ	1.74	1.06
2:C:60:ILE:HA	2:C:94:GLY:HA2	1.31	1.06
1:A:409:ILE:HD11	1:A:432:LEU:HD21	1.06	1.06
1:A:409:ILE:CG1	1:A:432:LEU:CD1	1.93	1.05
1:B:498:PRO:HG2	1:B:564:GLU:HG2	1.37	1.05
1:B:563:ASN:O	1:B:563:ASN:ND2	1.90	1.04
1:A:45:LEU:CD2	1:A:59:ASP:HA	1.86	1.04
1:B:406:GLN:NE2	1:B:432:LEU:O	1.90	1.04
1:B:497:ALA:CB	1:B:500:GLU:O	2.04	1.04
1:B:438:GLU:OE2	1:B:441:LYS:HD2	1.56	1.04
1:A:630:GLY:O	1:A:631:CYS:CA	2.05	1.04
1:B:403:ARG:HG2	1:B:403:ARG:HH11	1.23	1.04
1:B:5:ILE:HD12	1:B:327:LEU:HD13	1.35	1.03
1:B:630:GLY:C	1:B:631:CYS:N	2.14	1.03
2:C:29:VAL:HG13	2:C:42:ARG:O	1.56	1.03
1:A:577:ILE:HG23	1:A:581:TRP:HB2	1.40	1.03
1:B:498:PRO:HG2	1:B:564:GLU:HG3	1.34	1.03
1:B:196:TYR:CE1	1:B:251:PHE:CZ	2.47	1.02
1:B:196:TYR:CE1	1:B:251:PHE:CE1	2.46	1.02
1:B:511:TYR:CE2	1:B:523:TYR:HE2	1.78	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:TYR:HD2	1:A:86:ARG:CZ	1.71	1.02
2:C:41:LYS:O	2:C:67:PRO:HG3	1.61	1.01
2:D:190:ASP:O	2:D:192:GLU:HG2	1.58	1.01
1:A:545:TRP:HZ3	1:A:547:LYS:HE2	1.23	1.01
1:B:498:PRO:CG	1:B:564:GLU:HG3	1.90	1.00
1:A:409:ILE:CG1	1:A:432:LEU:CD2	2.39	1.00
1:B:511:TYR:CE2	1:B:523:TYR:CE2	2.48	1.00
1:B:143:ASN:HD22	1:B:144:PHE:H	1.02	1.00
1:B:286:ARG:HG3	1:B:286:ARG:HH11	1.20	1.00
1:B:462:ARG:O	1:B:463:PHE:CG	2.15	1.00
1:B:143:ASN:ND2	1:B:144:PHE:H	1.60	0.99
2:D:17:VAL:HA	2:D:54:LYS:O	1.62	0.99
2:D:183:PRO:CB	2:D:184:PRO:CD	2.40	0.99
1:B:196:TYR:CE2	1:B:244:PHE:CG	2.51	0.99
2:C:47:ILE:HG21	2:C:63:ILE:HG12	1.44	0.99
2:C:86:ILE:CG2	2:C:104:ILE:HG12	1.92	0.99
1:B:419:SER:HB3	1:B:420:PRO:HD3	0.99	0.98
1:A:409:ILE:HG13	1:A:432:LEU:CD2	1.93	0.97
2:D:146:CYS:HB3	2:D:177:TRP:CZ2	1.99	0.97
1:A:20:LEU:HD23	1:A:21:ALA:N	1.80	0.97
2:C:86:ILE:CD1	2:C:104:ILE:CG2	2.42	0.97
1:B:5:ILE:HD12	1:B:327:LEU:CD1	1.95	0.97
1:A:527:LEU:HB2	1:A:536:VAL:CG1	1.95	0.96
2:C:27:LYS:HB2	2:C:44:GLN:CG	1.95	0.96
1:A:84:PHE:CE1	1:A:85:PRO:O	2.19	0.96
1:A:406:GLN:CA	1:A:432:LEU:CD1	2.28	0.96
2:D:182:ALA:HB1	2:D:185:LYS:HE3	1.43	0.96
1:A:28:PHE:CE2	1:A:72:ARG:HD2	2.01	0.96
2:C:136:ILE:CD1	2:C:152:VAL:CG2	2.43	0.95
1:A:143:ASN:ND2	1:A:144:PHE:H	1.64	0.95
1:A:630:GLY:O	1:A:631:CYS:HA	1.65	0.95
1:B:622:GLY:CA	2:D:137:PRO:HB3	1.96	0.94
1:A:471:ARG:O	1:A:630:GLY:HA2	1.67	0.94
1:A:53:GLY:O	1:A:55:PRO:CD	2.16	0.94
2:D:60:ILE:HG21	2:D:96:MET:HE3	1.46	0.94
1:B:3:SER:HB2	1:B:4:PRO:HD2	1.48	0.94
1:B:73:CYS:HG	4:B:1634:ZN:ZN	0.70	0.94
1:B:562:TYR:HE2	1:B:564:GLU:OE2	1.50	0.94
2:C:86:ILE:HG23	2:C:104:ILE:CG1	1.97	0.94
1:A:143:ASN:HD22	1:A:144:PHE:H	1.05	0.93
1:B:194:VAL:CG1	1:B:243:GLY:HA3	1.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:559:PHE:CZ	2:D:188:PHE:CE2	2.56	0.93
1:B:61:ASP:HA	1:B:64:THR:CG2	1.97	0.93
2:C:29:VAL:HG21	2:C:43:ILE:HD13	1.49	0.93
1:A:409:ILE:CG1	1:A:432:LEU:CG	2.33	0.93
2:D:183:PRO:HB2	2:D:184:PRO:HD2	1.50	0.92
1:B:429:THR:HG23	1:B:430:PRO:HD3	0.93	0.92
1:B:25:LEU:O	1:B:29:TYR:O	1.88	0.92
1:B:41:LEU:HD12	1:B:43:ASP:OD2	1.70	0.92
1:A:42:LYS:O	1:A:46:LYS:HE3	1.68	0.92
1:B:196:TYR:CZ	1:B:244:PHE:CB	2.52	0.92
1:B:196:TYR:CZ	1:B:244:PHE:HB2	2.05	0.91
1:B:314:ASN:HD21	1:B:358:TRP:H	1.17	0.91
2:C:43:ILE:HB	2:C:65:THR:HG23	1.51	0.91
2:D:36:TYR:O	2:D:36:TYR:HD1	1.36	0.91
1:B:511:TYR:HE2	1:B:523:TYR:HE2	1.08	0.90
2:C:32:GLY:O	2:C:39:PRO:HA	1.71	0.90
2:D:20:ARG:NH2	2:D:83:GLU:CD	2.30	0.90
2:D:183:PRO:CB	2:D:184:PRO:HD3	1.99	0.90
2:D:102:ASP:O	2:D:104:ILE:HG13	1.72	0.90
2:D:149:MET:HB3	2:D:152:VAL:CG1	2.00	0.90
2:D:68:SER:O	2:D:71:VAL:HG22	1.71	0.90
2:D:149:MET:CB	2:D:152:VAL:HG12	2.00	0.90
1:A:60:LEU:HG	1:A:60:LEU:O	1.71	0.90
1:B:357:LYS:NZ	1:B:357:LYS:CB	2.35	0.90
2:D:35:ILE:O	2:D:35:ILE:HG22	1.71	0.90
1:A:53:GLY:C	1:A:55:PRO:HD3	1.97	0.89
1:B:473:LYS:HG2	1:B:474:PRO:CD	2.02	0.89
2:D:140:ILE:O	2:D:140:ILE:HG13	1.70	0.89
1:A:36:CYS:HB3	1:A:38:LEU:HD12	1.51	0.89
1:B:61:ASP:CA	1:B:64:THR:HG22	2.02	0.89
1:B:543:PHE:CE2	1:B:545:TRP:HD1	1.89	0.89
1:A:59:ASP:HB2	1:A:61:ASP:OD1	1.73	0.89
1:B:511:TYR:HE2	1:B:523:TYR:CE2	1.89	0.89
2:C:47:ILE:HG21	2:C:63:ILE:CG1	2.03	0.89
1:A:26:ASN:HB2	1:A:31:CYS:H	1.37	0.88
1:B:391:LEU:HD22	1:B:402:PHE:CZ	2.08	0.88
2:C:27:LYS:O	2:C:44:GLN:HB3	1.71	0.88
1:A:403:ARG:HH11	1:A:403:ARG:HG2	1.38	0.88
1:B:196:TYR:CE1	1:B:244:PHE:HB2	2.08	0.88
2:C:34:ASP:OD1	2:C:35:ILE:N	2.06	0.88
1:B:235:ASN:ND2	1:B:238:LYS:H	1.68	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:149:MET:HB2	2:D:152:VAL:HG12	1.54	0.88
1:B:559:PHE:HZ	2:D:188:PHE:CE2	1.90	0.88
1:A:457:PHE:HA	1:A:466:ARG:HB3	1.56	0.88
1:A:618:SER:C	1:A:619:VAL:HG23	1.99	0.88
1:B:194:VAL:HG11	1:B:243:GLY:HA3	1.55	0.88
1:B:580:ALA:HB2	2:D:188:PHE:CZ	2.08	0.88
1:B:57:THR:CG2	1:B:60:LEU:HB2	2.04	0.88
1:B:41:LEU:HB3	1:B:43:ASP:OD1	1.73	0.87
2:D:187:GLU:OE2	2:D:189:LEU:HD13	1.73	0.87
1:A:617:LYS:NZ	2:C:174:SER:HB2	1.90	0.87
2:D:182:ALA:HB3	2:D:185:LYS:HE3	1.56	0.87
1:A:45:LEU:HD23	1:A:59:ASP:CA	2.04	0.87
1:B:473:LYS:CG	1:B:474:PRO:HD2	2.02	0.86
1:A:464:ILE:HG23	1:A:480:VAL:HG12	1.57	0.86
1:A:81:TYR:CD2	1:A:86:ARG:CZ	2.58	0.86
1:B:3:SER:HB2	1:B:4:PRO:HD3	1.57	0.86
1:A:26:ASN:HB3	1:A:31:CYS:O	1.74	0.86
2:D:20:ARG:NH2	2:D:83:GLU:OE2	2.08	0.86
1:B:196:TYR:CZ	1:B:251:PHE:CE1	2.64	0.86
2:D:36:TYR:CD1	2:D:36:TYR:C	2.52	0.86
1:A:1:ALA:CB	1:A:2:PRO:HD3	2.06	0.86
2:C:86:ILE:HD11	2:C:104:ILE:CG2	2.05	0.86
2:C:69:SER:HA	2:C:73:GLY:HA3	1.57	0.85
2:D:131:THR:HG22	2:D:132:ARG:H	1.40	0.85
2:C:149:MET:O	2:C:152:VAL:HG12	1.76	0.85
1:B:543:PHE:CE2	1:B:545:TRP:CD1	2.65	0.85
2:D:20:ARG:HH22	2:D:83:GLU:CD	1.82	0.85
1:A:10:GLY:HA2	1:B:296:ARG:NH1	1.90	0.85
1:A:38:LEU:O	1:A:41:LEU:O	1.93	0.85
1:B:123:SER:O	1:B:125:VAL:N	2.09	0.84
1:B:391:LEU:HD22	1:B:402:PHE:HZ	1.39	0.84
1:B:143:ASN:HD22	1:B:144:PHE:N	1.75	0.84
1:A:618:SER:O	1:A:619:VAL:HG22	1.76	0.84
1:A:580:ALA:HB3	2:C:188:PHE:CD2	2.12	0.84
1:B:3:SER:CB	1:B:4:PRO:CD	2.55	0.84
1:B:126:THR:HB	1:B:127:PRO:HD2	1.60	0.84
1:A:54:LEU:H	1:A:54:LEU:HD23	1.42	0.84
1:B:498:PRO:CD	1:B:564:GLU:HG3	2.06	0.84
2:C:18:VAL:HG13	2:C:87:ALA:HB2	1.60	0.84
2:C:27:LYS:CB	2:C:44:GLN:HG2	2.07	0.84
1:B:543:PHE:HE2	1:B:545:TRP:CD1	1.95	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:562:TYR:CE2	1:B:564:GLU:CD	2.57	0.83
1:A:72:ARG:HD3	1:A:73:CYS:O	1.79	0.83
2:D:149:MET:CB	2:D:152:VAL:HG13	1.99	0.83
2:C:25:SER:OG	2:C:46:GLU:OE1	1.95	0.83
1:B:60:LEU:HD11	1:B:63:ASN:HB3	1.59	0.83
2:C:69:SER:HA	2:C:73:GLY:CA	2.07	0.83
1:A:545:TRP:CZ3	1:A:547:LYS:HE2	2.13	0.83
1:B:462:ARG:O	1:B:463:PHE:CD1	2.31	0.82
2:D:140:ILE:CG2	2:D:147:LEU:HB2	2.09	0.82
1:B:515:SER:O	1:B:518:THR:HG22	1.77	0.82
2:D:131:THR:OG1	2:D:145:GLU:OE1	1.96	0.82
1:A:406:GLN:N	1:A:432:LEU:CD1	2.42	0.82
1:A:439:ILE:HG22	1:A:440:CYS:N	1.94	0.82
1:A:527:LEU:HB2	1:A:536:VAL:HG12	1.59	0.82
1:B:54:LEU:HB3	1:B:55:PRO:CD	2.09	0.82
1:B:453:ARG:O	1:B:453:ARG:CD	2.27	0.82
2:C:133:CYS:HB3	2:C:149:MET:HB3	1.62	0.82
1:A:84:PHE:CD1	1:A:85:PRO:O	2.32	0.82
1:B:54:LEU:HB3	1:B:55:PRO:HD2	1.62	0.82
1:B:196:TYR:OH	1:B:251:PHE:CE1	2.32	0.82
1:B:310:THR:HG21	1:B:359:GLY:HA3	1.62	0.82
2:C:86:ILE:CG1	2:C:104:ILE:HG23	2.10	0.82
2:D:150:ASP:CG	2:D:151:TRP:N	2.36	0.82
2:C:136:ILE:CD1	2:C:152:VAL:HG21	2.10	0.81
1:B:306:THR:O	1:B:306:THR:HG22	1.79	0.81
1:B:469:THR:CG2	1:B:471:ARG:HD3	2.10	0.81
1:B:493:ALA:HB3	1:B:506:PHE:HB2	1.62	0.81
1:B:462:ARG:C	1:B:463:PHE:CD1	2.58	0.81
1:A:409:ILE:CB	1:A:432:LEU:HD11	2.10	0.81
1:B:196:TYR:OH	1:B:251:PHE:HE1	1.63	0.81
2:C:46:GLU:HA	2:C:62:PHE:HD1	1.44	0.81
1:B:34:GLU:OE1	1:B:34:GLU:CA	2.25	0.81
2:D:150:ASP:CG	2:D:151:TRP:H	1.88	0.81
1:A:156:ASP:O	1:A:157:GLY:O	1.98	0.81
2:D:47:ILE:HG12	2:D:63:ILE:HG13	1.62	0.81
1:A:84:PHE:CD1	1:A:84:PHE:C	2.59	0.80
1:A:25:LEU:HD11	1:A:45:LEU:HD13	1.62	0.80
2:C:143:PRO:O	2:C:174:SER:HB3	1.81	0.80
1:A:471:ARG:O	1:A:630:GLY:CA	2.30	0.80
1:B:196:TYR:CE2	1:B:244:PHE:CB	2.65	0.80
2:C:60:ILE:HA	2:C:94:GLY:CA	2.09	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:ASN:HD22	1:A:144:PHE:N	1.79	0.80
1:B:13:ALA:O	1:B:15:LYS:HG3	1.82	0.80
1:B:419:SER:HB2	1:B:420:PRO:CD	2.09	0.80
2:C:165:PHE:CD2	2:C:177:TRP:HB3	2.17	0.80
1:A:617:LYS:HZ3	2:C:174:SER:HB2	1.45	0.79
1:B:563:ASN:HD22	1:B:563:ASN:C	1.89	0.79
1:A:128:LEU:O	1:A:129:ARG:HD3	1.81	0.79
1:A:617:LYS:HE2	2:C:170:ARG:HG3	1.65	0.79
2:C:136:ILE:HD11	2:C:152:VAL:HG23	1.63	0.79
2:C:47:ILE:HD11	2:C:60:ILE:O	1.82	0.79
1:B:37:ASN:CB	1:B:43:ASP:OD2	2.28	0.79
1:A:84:PHE:HB2	1:A:167:ALA:HB3	1.64	0.79
1:A:406:GLN:HA	1:A:406:GLN:HE21	1.48	0.79
1:A:223:ARG:NH2	1:A:225:ASP:OD2	2.16	0.79
2:C:7:HIS:CE1	2:C:162:ALA:HA	2.17	0.79
2:D:154:GLU:O	2:D:155:LYS:HB2	1.82	0.78
1:B:268:PHE:O	1:B:295:ASP:OD2	2.01	0.78
1:B:562:TYR:HE2	1:B:564:GLU:CD	1.91	0.78
1:B:573:PHE:CD1	1:B:575:LYS:HE2	2.18	0.78
2:C:136:ILE:HD13	2:C:152:VAL:HG21	1.63	0.78
1:A:409:ILE:HG13	1:A:432:LEU:HG	1.64	0.78
1:B:133:ILE:HG12	1:B:133:ILE:O	1.80	0.78
2:C:29:VAL:CG1	2:C:42:ARG:H	1.96	0.78
1:B:10:GLY:O	1:B:11:ASP:HB3	1.84	0.78
1:B:580:ALA:CB	2:D:188:PHE:CZ	2.67	0.78
2:D:34:ASP:OD1	2:D:34:ASP:N	2.15	0.78
1:B:487:LEU:HD12	1:B:488:PRO:HD2	1.64	0.77
1:B:591:VAL:O	1:B:592:VAL:HG12	1.84	0.77
1:B:608:TYR:CD1	1:B:622:GLY:O	2.36	0.77
2:C:27:LYS:HB3	2:C:44:GLN:CD	2.08	0.77
2:C:27:LYS:CB	2:C:44:GLN:CG	2.61	0.77
2:C:161:GLN:O	2:C:165:PHE:HB2	1.82	0.77
2:D:117:SER:O	2:D:122:TYR:CD2	2.38	0.77
1:B:9:PRO:HD2	1:B:352:TYR:OH	1.85	0.77
1:A:15:LYS:HE2	1:A:23:GLN:OE1	1.85	0.77
1:A:286:ARG:HG3	1:A:286:ARG:HH11	1.49	0.77
1:B:151:ASP:OD2	1:B:177:HIS:CE1	2.38	0.77
2:C:53:PHE:CD2	2:C:118:LEU:HB3	2.20	0.77
1:B:450:ALA:HA	1:B:592:VAL:HG21	1.67	0.77
1:B:500:GLU:HG2	1:B:502:LYS:HD3	1.67	0.77
1:B:563:ASN:ND2	1:B:566:LYS:HB2	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:86:ILE:HD13	2:C:104:ILE:CG2	2.15	0.77
1:B:286:ARG:HG3	1:B:286:ARG:NH1	1.97	0.76
1:A:621:PHE:HE1	2:C:136:ILE:HD13	1.50	0.76
1:B:41:LEU:O	1:B:42:LYS:HB2	1.86	0.76
1:A:17:ASP:O	1:A:20:LEU:HD22	1.85	0.76
1:A:409:ILE:HD12	1:A:432:LEU:CD2	1.96	0.76
1:B:143:ASN:ND2	1:B:144:PHE:N	2.32	0.76
1:A:585:PRO:HD2	1:A:588:LEU:HD11	1.68	0.76
1:A:438:GLU:CD	1:A:441:LYS:HD2	2.10	0.76
1:A:512:TRP:NE1	1:A:524:PRO:HG3	2.01	0.76
2:C:5:PRO:HD2	2:C:132:ARG:NH1	2.01	0.76
1:B:17:ASP:OD2	1:B:65:ILE:HD13	1.85	0.76
1:B:80:ASN:C	1:B:80:ASN:ND2	2.43	0.75
1:A:438:GLU:OE1	1:A:441:LYS:HD2	1.86	0.75
1:B:60:LEU:O	1:B:60:LEU:CD1	2.30	0.75
1:B:506:PHE:CE1	1:B:527:LEU:HD11	2.22	0.75
2:C:147:LEU:N	2:C:177:TRP:CH2	2.55	0.75
2:D:140:ILE:HG22	2:D:147:LEU:HB2	1.68	0.75
1:A:621:PHE:HB2	2:C:147:LEU:HD21	1.67	0.75
1:A:37:ASN:HB2	1:A:41:LEU:HD12	1.69	0.74
1:B:592:VAL:O	1:B:592:VAL:CG2	2.35	0.74
2:C:165:PHE:HD2	2:C:177:TRP:HB3	1.51	0.74
2:C:32:GLY:C	2:C:40:ILE:H	1.95	0.74
1:A:552:TYR:CE2	2:C:188:PHE:CE1	2.76	0.74
1:A:29:TYR:OH	1:A:48:MET:HA	1.86	0.74
1:B:147:TRP:CD1	1:B:147:TRP:H	2.03	0.74
1:B:182:GLU:OE1	1:B:182:GLU:HA	1.88	0.74
1:B:542:ALA:O	1:B:543:PHE:HB3	1.88	0.74
1:A:26:ASN:CB	1:A:31:CYS:O	2.36	0.73
1:B:34:GLU:O	1:B:36:CYS:N	2.19	0.73
1:B:57:THR:OG1	1:B:60:LEU:HB2	1.88	0.73
1:A:194:VAL:CG1	1:A:243:GLY:HA3	2.17	0.73
1:A:405:SER:C	1:A:432:LEU:HD13	2.13	0.73
2:C:183:PRO:N	2:C:184:PRO:HD3	2.03	0.73
1:B:39:PHE:O	1:B:40:VAL:HG12	1.89	0.73
1:A:617:LYS:CE	2:C:170:ARG:HG3	2.19	0.73
2:D:17:VAL:CG1	2:D:55:GLY:HA3	2.19	0.73
1:B:48:MET:HE2	1:B:52:PHE:CE2	2.24	0.73
2:D:117:SER:O	2:D:122:TYR:HD2	1.70	0.72
1:A:556:GLY:CA	1:A:587:ASN:OD1	2.37	0.72
2:D:36:TYR:HD1	2:D:36:TYR:C	1.92	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:THR:O	1:B:306:THR:CG2	2.37	0.72
1:A:277:THR:HB	1:A:279:GLU:H	1.55	0.72
1:B:419:SER:HB2	1:B:420:PRO:HD2	1.68	0.72
2:C:47:ILE:CG2	2:C:63:ILE:HG12	2.16	0.72
1:A:18:LYS:O	1:A:19:GLU:C	2.33	0.72
1:A:406:GLN:N	1:A:432:LEU:HD13	2.04	0.72
2:D:147:LEU:H	2:D:177:TRP:HH2	1.38	0.72
1:A:621:PHE:HE1	2:C:152:VAL:HG21	1.55	0.72
2:D:182:ALA:CB	2:D:185:LYS:CE	2.62	0.72
2:D:132:ARG:O	2:D:134:PRO:HD3	1.90	0.72
1:B:196:TYR:CE2	1:B:244:PHE:CD1	2.76	0.72
1:B:239:ASP:O	1:B:241:LYS:HE3	1.89	0.72
1:B:310:THR:CG2	1:B:359:GLY:HA3	2.19	0.72
2:C:69:SER:HA	2:C:73:GLY:N	2.05	0.72
1:A:1:ALA:HB3	1:A:2:PRO:CD	2.14	0.71
1:A:85:PRO:HD2	1:A:168:PRO:O	1.89	0.71
1:B:581:TRP:HA	1:B:616:LEU:HD13	1.72	0.71
1:B:33:LYS:HE3	1:B:33:LYS:HA	1.72	0.71
1:B:80:ASN:C	1:B:80:ASN:HD22	1.98	0.71
2:C:7:HIS:HE1	2:C:161:GLN:O	1.74	0.71
1:B:449:ILE:O	1:B:592:VAL:HG11	1.89	0.71
1:B:462:ARG:C	1:B:463:PHE:CG	2.69	0.71
1:B:497:ALA:HB2	1:B:502:LYS:O	1.90	0.71
2:C:148:TRP:HA	2:C:161:GLN:OE1	1.90	0.71
1:A:10:GLY:CA	1:B:296:ARG:NH1	2.54	0.71
1:B:498:PRO:HD2	1:B:564:GLU:HG3	1.71	0.71
1:B:13:ALA:H	1:B:14:PRO:HD3	1.55	0.71
2:D:159:GLY:O	2:D:163:LYS:HG3	1.91	0.71
1:A:406:GLN:HA	1:A:406:GLN:NE2	2.06	0.71
1:B:430:PRO:HB3	1:B:435:VAL:HG12	1.72	0.71
1:A:133:ILE:HD11	1:A:138:ALA:HB2	1.72	0.70
2:C:29:VAL:CG1	2:C:42:ARG:O	2.38	0.70
2:D:35:ILE:O	2:D:35:ILE:CG2	2.39	0.70
1:B:119:PHE:HB3	1:B:130:PHE:CD2	2.27	0.70
1:B:611:LEU:HD23	1:B:612:GLU:O	1.92	0.70
2:C:147:LEU:O	2:C:177:TRP:CZ2	2.43	0.70
2:D:111:SER:O	2:D:115:LYS:HG2	1.92	0.70
1:B:503:ALA:N	1:B:514:TYR:O	2.24	0.70
2:C:170:ARG:N	2:C:174:SER:O	2.24	0.70
1:A:84:PHE:HE1	1:A:85:PRO:O	1.72	0.70
2:C:46:GLU:HA	2:C:62:PHE:CD1	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:27:LYS:HE3	2:C:62:PHE:CZ	2.26	0.70
1:B:562:TYR:CE2	1:B:564:GLU:OE2	2.40	0.69
2:C:27:LYS:N	2:C:44:GLN:O	2.25	0.69
2:C:29:VAL:HG13	2:C:42:ARG:N	2.07	0.69
1:A:147:TRP:H	1:A:147:TRP:CD1	2.08	0.69
2:C:1:CYS:HB2	2:C:71:VAL:O	1.92	0.69
1:A:413:GLN:O	1:A:416:TYR:O	2.10	0.69
1:B:462:ARG:O	1:B:463:PHE:CD2	2.45	0.69
1:B:591:VAL:C	1:B:592:VAL:CG1	2.64	0.69
2:C:29:VAL:HG22	2:C:43:ILE:HA	0.82	0.69
1:A:143:ASN:ND2	1:A:144:PHE:N	2.39	0.69
2:D:15:ALA:O	2:D:54:LYS:HE3	1.92	0.69
1:A:490:LYS:O	1:A:490:LYS:HG2	1.93	0.69
1:B:37:ASN:O	1:B:41:LEU:HB2	1.93	0.69
1:B:235:ASN:HD21	1:B:237:GLU:HB3	1.57	0.69
1:B:563:ASN:HD21	1:B:566:LYS:HB2	1.56	0.69
2:C:147:LEU:N	2:C:177:TRP:CZ2	2.61	0.69
2:D:7:HIS:HB3	2:D:10:GLN:HB2	1.75	0.69
1:A:159:ASP:OD2	1:A:343:LYS:NZ	2.25	0.69
1:A:563:ASN:O	1:A:566:LYS:O	2.11	0.69
2:D:91:GLU:OE1	2:D:91:GLU:HA	1.93	0.69
1:B:195:LYS:O	1:B:200:ASP:HB2	1.93	0.68
1:B:196:TYR:CZ	1:B:244:PHE:HB3	2.27	0.68
1:A:18:LYS:O	1:A:20:LEU:N	2.26	0.68
1:B:397:THR:HG21	1:B:479:LEU:HD12	1.75	0.68
1:A:49:GLN:HE22	1:A:60:LEU:HB3	1.57	0.68
2:C:29:VAL:HG13	2:C:42:ARG:H	1.58	0.68
1:B:198:ASN:O	1:B:242:TYR:O	2.11	0.68
1:B:473:LYS:CG	1:B:474:PRO:CD	2.69	0.68
1:A:137:GLU:OE2	1:A:141:MET:HE2	1.94	0.67
1:A:561:ARG:NH1	1:A:570:ASP:OD2	2.27	0.67
1:A:266:PHE:O	1:A:266:PHE:CD1	2.48	0.67
1:A:269:GLN:O	3:A:1632:SO4:O1	2.12	0.67
2:D:131:THR:C	2:D:132:ARG:HG3	2.18	0.67
1:B:464:ILE:HG23	1:B:480:VAL:HG12	1.76	0.67
1:B:572:GLY:O	1:B:573:PHE:O	2.13	0.67
1:B:41:LEU:CB	1:B:43:ASP:OD1	2.41	0.67
1:A:25:LEU:O	1:A:29:TYR:CB	2.35	0.67
1:B:198:ASN:O	1:B:199:ALA:HB3	1.95	0.67
1:B:572:GLY:CA	1:B:573:PHE:O	2.43	0.67
1:A:69:ARG:HH12	1:A:341:ASP:HA	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:GLU:HB2	1:A:457:PHE:CE1	2.30	0.67
1:A:25:LEU:HD13	1:A:44:THR:HG22	1.76	0.67
1:A:69:ARG:NH1	1:A:341:ASP:HA	2.10	0.67
1:B:44:THR:HG22	1:B:45:LEU:H	1.59	0.67
1:B:253:MET:HG3	1:B:254:GLY:N	2.09	0.67
2:C:3:CYS:SG	2:C:101:CYS:O	2.53	0.67
2:C:136:ILE:HD11	2:C:152:VAL:HG22	1.72	0.67
2:D:20:ARG:HD2	2:D:107:TRP:CH2	2.30	0.67
1:A:455:GLU:HB2	1:A:457:PHE:HE1	1.60	0.67
1:B:126:THR:HB	1:B:127:PRO:CD	2.25	0.67
1:B:498:PRO:CG	1:B:564:GLU:CG	2.54	0.66
1:B:615:SER:O	1:B:617:LYS:N	2.28	0.66
2:D:170:ARG:N	2:D:174:SER:O	2.26	0.66
1:B:562:TYR:OH	1:B:564:GLU:OE1	2.13	0.66
1:B:573:PHE:HD1	1:B:575:LYS:HE2	1.60	0.66
1:B:80:ASN:ND2	1:B:80:ASN:O	2.28	0.66
1:A:291:THR:HG21	1:A:297:ASP:HB2	1.77	0.66
1:B:6:ILE:O	1:B:7:LYS:HB2	1.96	0.66
1:B:438:GLU:O	1:B:442:GLN:HG2	1.95	0.66
2:C:147:LEU:H	2:C:177:TRP:HH2	1.42	0.66
2:C:152:VAL:CG1	2:C:153:THR:N	2.59	0.66
2:D:146:CYS:HB3	2:D:177:TRP:CE2	2.30	0.66
2:C:29:VAL:CG1	2:C:42:ARG:N	2.59	0.66
1:A:81:TYR:HD2	1:A:86:ARG:NH1	1.93	0.66
1:A:543:PHE:CE1	1:A:552:TYR:HB2	2.31	0.66
1:B:357:LYS:HA	1:B:357:LYS:HZ3	1.58	0.66
1:B:196:TYR:CD2	1:B:244:PHE:HD1	2.11	0.66
1:A:581:TRP:CE2	2:C:188:PHE:HZ	2.14	0.65
2:C:27:LYS:CB	2:C:44:GLN:CD	2.69	0.65
2:D:7:HIS:O	2:D:10:GLN:N	2.27	0.65
1:A:194:VAL:HG13	1:A:243:GLY:HA3	1.78	0.65
1:A:624:ILE:HG23	1:A:625:LYS:N	2.10	0.65
1:B:291:THR:HG21	1:B:297:ASP:OD2	1.96	0.65
1:A:375:ALA:O	1:A:378:HIS:HB2	1.96	0.65
1:A:487:LEU:HD21	1:A:505:PHE:CD2	2.31	0.65
1:A:556:GLY:O	1:A:587:ASN:OD1	2.14	0.65
1:A:588:LEU:HD22	1:A:604:LYS:HB3	1.76	0.65
1:B:403:ARG:HH11	1:B:403:ARG:CG	2.03	0.65
2:C:34:ASP:CG	2:C:35:ILE:H	2.04	0.65
2:C:126:CYS:C	2:C:128:CYS:H	2.04	0.65
2:C:131:THR:O	2:C:148:TRP:HB3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:29:VAL:HG13	2:C:42:ARG:CA	2.27	0.65
2:D:45:TYR:OH	2:D:74:VAL:O	2.14	0.65
1:B:403:ARG:HG2	1:B:403:ARG:NH1	2.02	0.65
2:C:27:LYS:CE	2:C:62:PHE:CE1	2.80	0.65
1:A:447:ASP:O	1:A:492:ASP:O	2.13	0.65
1:B:41:LEU:CD1	1:B:43:ASP:OD2	2.43	0.65
1:B:290:THR:HG22	1:B:299:LYS:HB3	1.78	0.65
1:B:429:THR:CG2	1:B:430:PRO:HD3	1.87	0.65
1:B:480:VAL:O	1:B:482:THR:N	2.30	0.65
2:C:83:GLU:HB2	2:C:107:TRP:HB2	1.79	0.65
2:D:108:ASP:O	2:D:109:THR:OG1	2.09	0.65
1:B:59:ASP:OD1	1:B:59:ASP:O	2.14	0.64
1:B:462:ARG:HB2	1:B:463:PHE:CE1	2.32	0.64
1:B:8:PHE:HZ	1:B:345:TRP:CE2	2.15	0.64
1:B:151:ASP:OD2	1:B:177:HIS:ND1	2.30	0.64
1:A:115:PHE:O	1:A:118:ALA:N	2.30	0.64
1:A:405:SER:C	1:A:432:LEU:CD1	2.70	0.64
1:A:539:VAL:HG12	1:A:540:ASP:N	2.12	0.64
1:A:38:LEU:C	1:A:41:LEU:O	2.41	0.64
1:A:314:ASN:C	1:A:314:ASN:HD22	2.06	0.64
1:A:406:GLN:HE21	1:A:432:LEU:HD12	1.63	0.64
1:A:556:GLY:C	1:A:587:ASN:OD1	2.41	0.64
1:B:591:VAL:C	1:B:592:VAL:HG12	2.23	0.64
1:A:156:ASP:O	1:A:156:ASP:OD1	2.16	0.64
1:B:469:THR:HG21	1:B:471:ARG:HD3	1.79	0.64
1:B:487:LEU:HD12	1:B:488:PRO:CD	2.27	0.64
2:C:43:ILE:HB	2:C:65:THR:CG2	2.26	0.64
2:C:99:THR:O	2:C:100:LEU:C	2.41	0.64
1:B:13:ALA:N	1:B:14:PRO:CD	2.61	0.64
2:D:131:THR:HG22	2:D:132:ARG:N	2.12	0.64
2:D:144:ASP:HB3	2:D:174:SER:HA	1.80	0.64
1:A:621:PHE:CE1	2:C:152:VAL:HG21	2.33	0.64
1:B:531:GLY:HA3	1:B:569:MET:HB2	1.78	0.64
1:A:121:VAL:HG13	1:A:404:LEU:HG	1.79	0.64
2:C:33:ASN:ND2	2:C:37:GLY:O	2.31	0.64
2:D:68:SER:OG	2:D:71:VAL:HG13	1.97	0.64
1:A:232:THR:HG23	1:A:232:THR:O	1.98	0.63
1:B:629:LEU:O	1:B:630:GLY:C	2.40	0.63
2:D:20:ARG:HD2	2:D:107:TRP:CZ3	2.33	0.63
2:D:147:LEU:N	2:D:177:TRP:CH2	2.66	0.63
2:D:17:VAL:HG12	2:D:55:GLY:HA3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:THR:HG22	1:A:432:LEU:H	1.64	0.63
1:B:57:THR:HG23	1:B:60:LEU:HB2	1.78	0.63
2:C:32:GLY:C	2:C:39:PRO:HA	2.23	0.63
2:C:86:ILE:HG12	2:C:104:ILE:HG23	1.80	0.63
1:B:484:TRP:HD1	1:B:514:TYR:CD2	2.16	0.63
2:C:140:ILE:HD13	2:C:145:GLU:HB3	1.81	0.63
1:A:26:ASN:HB2	1:A:31:CYS:N	2.11	0.63
1:B:413:GLN:HG2	1:B:418:ALA:HA	1.80	0.63
2:C:146:CYS:HB3	2:C:177:TRP:CZ2	2.34	0.63
1:A:446:PHE:CZ	1:A:629:LEU:HD22	2.33	0.63
1:A:585:PRO:HD2	1:A:588:LEU:HD21	1.81	0.63
2:C:19:ILE:O	2:C:85:LEU:HA	1.98	0.63
2:C:45:TYR:O	2:C:62:PHE:HA	1.97	0.63
2:C:85:LEU:HD21	2:C:118:LEU:HD21	1.81	0.63
1:B:566:LYS:C	1:B:568:LYS:H	2.06	0.62
1:A:89:LYS:O	1:A:89:LYS:HG2	1.97	0.62
1:B:480:VAL:HG23	1:B:481:ALA:N	2.13	0.62
1:B:548:ASN:ND2	1:B:552:TYR:HE1	1.97	0.62
2:C:146:CYS:HB3	2:C:177:TRP:CE2	2.34	0.62
1:A:137:GLU:CD	1:A:141:MET:HE2	2.24	0.62
1:A:101:GLY:HA3	1:A:143:ASN:ND2	2.15	0.62
1:B:20:LEU:HD22	1:B:69:ARG:NH1	2.15	0.62
1:B:164:HIS:CD2	1:B:177:HIS:HB2	2.33	0.62
1:B:493:ALA:HB3	1:B:506:PHE:CB	2.29	0.62
2:C:63:ILE:HG21	2:C:98:ILE:HD13	1.80	0.62
1:A:29:TYR:CZ	1:A:48:MET:HA	2.34	0.62
1:A:443:ASP:HA	1:A:625:LYS:NZ	2.14	0.62
1:A:26:ASN:HD22	1:A:26:ASN:H	1.45	0.62
2:C:60:ILE:HG13	2:C:96:MET:SD	2.40	0.62
2:C:168:ILE:HG22	2:C:169:LYS:H	1.63	0.62
1:A:533:PRO:HD2	1:A:535:ASP:OD2	2.00	0.62
2:C:74:VAL:HG11	2:C:98:ILE:HD12	1.82	0.62
2:C:130:ILE:HG22	2:C:130:ILE:O	2.00	0.62
1:A:38:LEU:HG	1:A:43:ASP:O	2.00	0.62
1:B:462:ARG:CB	1:B:463:PHE:CE1	2.83	0.62
2:D:56:PRO:C	2:D:58:LYS:H	2.08	0.62
1:A:166:PHE:CD2	1:A:172:VAL:HG13	2.35	0.61
1:B:24:TYR:O	1:B:24:TYR:CD1	2.53	0.61
1:B:100:ILE:HD11	1:B:141:MET:CE	2.30	0.61
1:B:291:THR:HG23	1:B:292:GLU:N	2.15	0.61
1:A:619:VAL:HG12	1:A:620:LYS:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:VAL:CG2	1:B:481:ALA:N	2.63	0.61
1:B:559:PHE:HB3	1:B:577:ILE:HG12	1.82	0.61
2:C:5:PRO:HD2	2:C:132:ARG:HH12	1.65	0.61
1:B:334:CYS:SG	1:B:346:CYS:HB3	2.41	0.61
1:B:431:THR:O	1:B:432:LEU:C	2.41	0.61
2:C:27:LYS:HE2	2:C:62:PHE:CE1	2.35	0.61
2:C:29:VAL:HA	2:C:42:ARG:O	1.99	0.61
2:C:183:PRO:CD	2:C:184:PRO:HD3	2.30	0.61
1:A:539:VAL:CG1	1:A:540:ASP:N	2.63	0.61
1:A:43:ASP:O	1:A:44:THR:CB	2.48	0.61
1:B:100:ILE:HD11	1:B:141:MET:HE3	1.81	0.61
1:B:196:TYR:CE2	1:B:244:PHE:HB2	2.34	0.61
2:D:66:ALA:HB1	2:D:71:VAL:HG23	1.82	0.61
2:D:9:GLN:HG3	2:D:122:TYR:HD1	1.64	0.61
2:C:29:VAL:CG1	2:C:42:ARG:C	2.63	0.61
2:C:191:ILE:O	2:C:191:ILE:HG13	1.99	0.61
1:B:235:ASN:C	1:B:235:ASN:HD22	2.09	0.61
1:B:512:TRP:CE2	1:B:524:PRO:HB3	2.36	0.61
1:A:196:TYR:O	1:A:243:GLY:HA2	2.00	0.60
1:A:511:TYR:CE2	1:A:513:ILE:HD11	2.36	0.60
1:A:315:SER:CB	1:A:348:THR:HG21	2.31	0.60
2:C:83:GLU:OE1	2:C:83:GLU:N	2.33	0.60
2:C:133:CYS:CB	2:C:149:MET:HB3	2.30	0.60
1:A:194:VAL:HG11	1:A:243:GLY:HA3	1.82	0.60
2:C:32:GLY:O	2:C:39:PRO:CA	2.47	0.60
1:B:214:GLU:OE2	1:B:234:TYR:OH	2.11	0.60
1:A:235:ASN:HD22	1:A:238:LYS:H	1.49	0.60
1:A:533:PRO:O	1:A:536:VAL:HG13	2.00	0.60
1:A:612:GLU:HG3	1:A:615:SER:H	1.66	0.60
1:B:38:LEU:HG	1:B:39:PHE:N	2.15	0.60
1:A:252:THR:OG1	1:A:260:GLN:O	2.20	0.60
1:A:286:ARG:HG3	1:A:286:ARG:NH1	2.16	0.60
1:B:522:GLY:O	1:B:525:LYS:HG3	2.02	0.60
2:C:44:GLN:HG3	2:C:64:TYR:CZ	2.37	0.60
2:D:20:ARG:HG3	2:D:51:LYS:HB2	1.83	0.60
1:B:314:ASN:ND2	1:B:358:TRP:H	1.95	0.60
2:D:12:PHE:CD1	2:D:12:PHE:C	2.79	0.60
2:D:49:GLN:NE2	2:D:52:MET:HB2	2.17	0.60
1:A:228:LEU:HB3	1:A:245:CYS:HB2	1.83	0.59
1:A:550:LYS:NZ	2:C:190:ASP:OD2	2.34	0.59
1:B:166:PHE:CD2	1:B:172:VAL:HG13	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:99:THR:C	2:C:101:CYS:N	2.58	0.59
1:B:286:ARG:HH11	1:B:286:ARG:CG	2.02	0.59
2:C:27:LYS:HE3	2:C:62:PHE:CE1	2.36	0.59
1:A:99:ILE:HD11	1:A:115:PHE:HD2	1.66	0.59
1:A:266:PHE:CD1	1:A:266:PHE:C	2.80	0.59
1:A:543:PHE:CD2	1:A:544:ASN:O	2.55	0.59
1:B:13:ALA:N	1:B:14:PRO:HD3	2.16	0.59
1:B:452:ILE:O	1:B:452:ILE:CG2	2.50	0.59
1:B:604:LYS:HE3	1:B:605:GLY:N	2.16	0.59
1:B:610:LYS:O	1:B:619:VAL:HA	2.02	0.59
1:A:405:SER:O	1:A:406:GLN:C	2.44	0.59
1:B:6:ILE:HA	1:B:338:GLY:O	2.02	0.59
2:C:99:THR:O	2:C:102:ASP:N	2.31	0.59
1:A:36:CYS:SG	1:A:44:THR:HG21	2.43	0.59
1:B:495:TYR:HE1	1:B:506:PHE:CD2	2.20	0.59
1:A:36:CYS:CB	1:A:38:LEU:CD1	2.71	0.59
1:A:182:GLU:HA	1:A:182:GLU:OE1	2.02	0.59
1:B:469:THR:OG1	1:B:471:ARG:HD3	2.03	0.59
1:B:612:GLU:CB	1:B:618:SER:HB3	2.21	0.59
2:C:60:ILE:CA	2:C:94:GLY:HA2	2.20	0.59
1:A:60:LEU:HD21	1:A:63:ASN:HB3	1.84	0.59
1:A:440:CYS:O	1:A:441:LYS:C	2.45	0.59
1:B:486:GLU:HG3	1:B:519:LEU:HD22	1.84	0.59
1:B:592:VAL:O	1:B:592:VAL:HG23	2.01	0.59
1:B:622:GLY:HA2	2:D:137:PRO:CB	2.14	0.59
2:D:148:TRP:NE1	2:D:150:ASP:HB3	2.17	0.59
1:A:25:LEU:HD13	1:A:44:THR:CG2	2.33	0.58
1:A:72:ARG:CD	1:A:73:CYS:O	2.49	0.58
1:B:148:GLU:HA	1:B:148:GLU:OE1	2.01	0.58
1:B:41:LEU:HB2	1:B:43:ASP:CG	2.28	0.58
1:B:451:GLN:HG2	1:B:456:ILE:HG12	1.84	0.58
1:A:291:THR:HG23	1:A:293:ASP:H	1.66	0.58
1:A:588:LEU:HD13	1:A:602:PHE:HB3	1.85	0.58
1:B:196:TYR:CD1	1:B:244:PHE:HB2	2.39	0.58
2:C:12:PHE:HE1	2:C:53:PHE:HB3	1.67	0.58
2:C:53:PHE:CE2	2:C:118:LEU:HD13	2.38	0.58
2:C:91:GLU:HB2	2:C:95:LYS:HB2	1.84	0.58
2:C:135:MET:HE2	2:C:137:PRO:HD2	1.85	0.58
1:B:49:GLN:HE22	1:B:60:LEU:HB3	1.69	0.58
2:C:152:VAL:HG13	2:C:153:THR:N	2.18	0.58
2:C:159:GLY:O	2:C:160:HIS:C	2.46	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ILE:CD1	1:A:138:ALA:HB2	2.33	0.58
1:A:437:PRO:HB3	1:A:444:ILE:HD11	1.85	0.58
1:B:207:PRO:HB3	1:B:216:ASN:OD1	2.04	0.58
1:B:250:LEU:O	1:B:261:PRO:HG3	2.02	0.58
1:B:357:LYS:HZ3	1:B:357:LYS:CA	2.17	0.58
2:C:79:GLY:O	2:C:80:GLY:C	2.46	0.58
2:D:126:CYS:O	2:D:127:GLU:C	2.45	0.58
2:C:99:THR:O	2:C:101:CYS:N	2.37	0.58
1:A:535:ASP:O	1:A:537:GLN:N	2.35	0.58
1:A:447:ASP:HB3	1:A:491:ILE:O	2.04	0.58
1:B:487:LEU:HD21	1:B:505:PHE:CD1	2.38	0.58
2:C:168:ILE:HG22	2:C:169:LYS:N	2.18	0.58
1:B:445:VAL:O	1:B:445:VAL:HG13	2.04	0.58
2:D:140:ILE:O	2:D:140:ILE:CG1	2.49	0.58
1:B:532:LEU:C	1:B:532:LEU:HD23	2.28	0.58
1:A:97:TYR:CZ	1:A:132:ARG:HB2	2.39	0.57
1:A:565:VAL:HG23	1:A:566:LYS:HG3	1.85	0.57
1:B:196:TYR:HH	1:B:251:PHE:HE1	1.33	0.57
2:D:164:PHE:HB3	2:D:179:ARG:HG3	1.85	0.57
1:A:313:GLY:HA2	1:A:358:TRP:CZ2	2.38	0.57
1:A:458:PHE:O	1:A:464:ILE:HA	2.04	0.57
1:A:624:ILE:CG2	1:A:625:LYS:N	2.67	0.57
2:D:20:ARG:O	2:D:50:ILE:HG12	2.04	0.57
1:A:57:THR:OG1	1:A:60:LEU:HB2	2.04	0.57
1:B:41:LEU:CB	1:B:43:ASP:CG	2.77	0.57
2:D:149:MET:HB3	2:D:152:VAL:HG11	1.86	0.57
2:C:121:ARG:HG2	2:C:121:ARG:HH11	1.68	0.57
1:A:20:LEU:CD2	1:A:21:ALA:N	2.62	0.57
1:A:511:TYR:HE2	1:A:513:ILE:HD11	1.70	0.57
1:A:548:ASN:ND2	1:A:550:LYS:HB2	2.20	0.57
1:A:617:LYS:NZ	2:C:170:ARG:HG3	2.19	0.57
1:B:146:ARG:O	1:B:147:TRP:C	2.45	0.57
1:B:196:TYR:CD2	1:B:244:PHE:CG	2.75	0.57
2:C:7:HIS:CE1	2:C:161:GLN:O	2.55	0.57
2:C:20:ARG:NH1	2:C:107:TRP:CE2	2.73	0.57
2:C:91:GLU:HB2	2:C:95:LYS:CB	2.34	0.57
2:C:7:HIS:O	2:C:9:GLN:N	2.38	0.57
1:A:34:GLU:OE2	1:A:37:ASN:ND2	2.38	0.57
1:A:474:PRO:HG3	1:A:629:LEU:HD12	1.86	0.57
1:B:532:LEU:HB2	1:B:533:PRO:HD2	1.87	0.57
2:D:21:ALA:HB1	2:D:47:ILE:HB	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:111:SER:C	2:D:115:LYS:HG2	2.29	0.57
2:C:22:LYS:HG2	2:C:23:ALA:N	2.20	0.57
2:D:9:GLN:HG3	2:D:122:TYR:CD1	2.39	0.57
1:A:469:THR:N	1:A:470:PRO:CD	2.68	0.57
1:B:469:THR:O	1:B:472:ASP:OD1	2.23	0.57
2:D:91:GLU:O	2:D:95:LYS:HB2	2.05	0.57
1:A:43:ASP:O	1:A:44:THR:OG1	2.22	0.56
1:A:232:THR:O	1:A:232:THR:CG2	2.53	0.56
1:B:61:ASP:O	1:B:65:ILE:N	2.26	0.56
1:B:452:ILE:O	1:B:452:ILE:HG23	2.04	0.56
2:C:19:ILE:HB	2:C:51:LYS:O	2.05	0.56
2:D:17:VAL:HG13	2:D:55:GLY:HA3	1.86	0.56
1:B:179:ASP:C	1:B:179:ASP:OD1	2.48	0.56
1:B:194:VAL:HG13	1:B:243:GLY:HA3	1.84	0.56
1:A:545:TRP:CD1	1:A:552:TYR:CE1	2.94	0.56
1:A:561:ARG:NH1	1:A:570:ASP:CG	2.64	0.56
1:B:57:THR:HG21	1:B:60:LEU:HB2	1.86	0.56
2:C:32:GLY:HA3	2:C:40:ILE:HB	1.88	0.56
1:B:25:LEU:HD22	1:B:44:THR:CG2	2.36	0.56
1:A:446:PHE:HZ	1:A:629:LEU:HD22	1.71	0.56
1:A:545:TRP:HZ3	1:A:547:LYS:CE	2.09	0.56
1:B:123:SER:O	1:B:124:ASP:C	2.48	0.56
1:A:580:ALA:CB	2:C:188:PHE:CD2	2.88	0.56
1:A:59:ASP:OD1	1:A:59:ASP:N	2.29	0.56
1:A:276:CYS:HB3	1:A:287:TRP:O	2.05	0.56
1:B:147:TRP:CD1	1:B:147:TRP:N	2.72	0.56
1:B:196:TYR:HE1	1:B:251:PHE:HZ	1.46	0.56
2:C:7:HIS:HE1	2:C:162:ALA:HA	1.65	0.56
1:A:311:VAL:O	1:A:360:PHE:HB2	2.06	0.55
1:A:575:LYS:HE3	1:A:579:ASP:HB2	1.88	0.55
2:C:91:GLU:N	2:C:95:LYS:O	2.31	0.55
1:A:527:LEU:O	1:A:530:LEU:HB3	2.07	0.55
1:B:8:PHE:HZ	1:B:345:TRP:CZ2	2.24	0.55
2:C:18:VAL:HG22	2:C:87:ALA:CB	2.37	0.55
1:A:403:ARG:HG2	1:A:403:ARG:NH1	2.09	0.55
1:B:235:ASN:HD22	1:B:238:LYS:H	1.53	0.55
1:A:1:ALA:C	1:A:3:SER:H	2.15	0.55
1:A:481:ALA:HA	1:A:484:TRP:O	2.07	0.55
1:B:617:LYS:HZ2	2:D:174:SER:HB2	1.71	0.55
2:D:78:VAL:HG12	2:D:79:GLY:H	1.72	0.55
1:A:115:PHE:CZ	1:A:142:ILE:HG21	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ARG:O	1:A:147:TRP:C	2.48	0.55
1:A:527:LEU:HB2	1:A:536:VAL:CB	2.36	0.55
1:B:196:TYR:CD1	1:B:196:TYR:N	2.75	0.55
1:B:266:PHE:CE1	1:B:273:TYR:HB2	2.42	0.55
1:B:506:PHE:CD1	1:B:527:LEU:HD11	2.41	0.55
1:A:519:LEU:H	1:A:519:LEU:HD23	1.72	0.55
1:A:621:PHE:CE1	2:C:136:ILE:HD13	2.38	0.55
1:B:439:ILE:HA	1:B:444:ILE:HD12	1.89	0.55
1:A:588:LEU:CD1	1:A:602:PHE:HB3	2.37	0.54
1:B:443:ASP:HA	1:B:625:LYS:HE3	1.89	0.54
1:B:497:ALA:HB1	1:B:500:GLU:O	2.03	0.54
2:D:112:THR:HA	2:D:115:LYS:HG3	1.89	0.54
1:A:18:LYS:O	1:A:21:ALA:N	2.40	0.54
1:A:544:ASN:HA	1:A:550:LYS:O	2.07	0.54
1:A:606:ALA:O	1:A:624:ILE:HG22	2.08	0.54
1:B:387:ASP:OD1	1:B:436:THR:HG21	2.07	0.54
2:C:23:ALA:O	2:C:78:VAL:HG13	2.07	0.54
2:C:25:SER:O	2:C:46:GLU:HB3	2.08	0.54
2:C:140:ILE:HD11	2:C:147:LEU:N	2.23	0.54
1:B:389:GLY:HA2	1:B:479:LEU:HD21	1.90	0.54
2:D:149:MET:HB3	2:D:152:VAL:HG12	1.78	0.54
1:A:439:ILE:CG2	1:A:440:CYS:N	2.66	0.54
2:C:183:PRO:HD2	2:C:184:PRO:HD3	1.88	0.54
2:D:71:VAL:O	2:D:72:CYS:HB2	2.07	0.54
2:D:163:LYS:HB2	2:D:164:PHE:HD1	1.72	0.54
1:A:25:LEU:HD23	1:A:29:TYR:CD2	2.43	0.54
1:A:84:PHE:O	1:A:84:PHE:CG	2.59	0.54
1:A:232:THR:O	1:A:233:THR:CG2	2.56	0.54
1:A:559:PHE:HZ	1:A:575:LYS:HE2	1.72	0.54
1:B:16:THR:HB	1:B:19:GLU:HB3	1.90	0.54
1:B:278:THR:O	1:B:279:GLU:C	2.51	0.54
1:B:286:ARG:NH1	1:B:286:ARG:CG	2.67	0.54
1:B:527:LEU:HD13	1:B:537:GLN:O	2.07	0.54
2:D:154:GLU:O	2:D:155:LYS:CB	2.54	0.54
1:B:495:TYR:CD2	1:B:551:THR:HG21	2.43	0.54
2:C:34:ASP:OD1	2:C:35:ILE:HG13	2.08	0.54
2:D:54:LYS:O	2:D:54:LYS:HG3	2.07	0.54
1:A:458:PHE:CE2	1:A:629:LEU:HB2	2.43	0.54
1:B:123:SER:C	1:B:125:VAL:N	2.65	0.54
1:A:42:LYS:HZ2	1:A:43:ASP:N	2.05	0.53
2:D:187:GLU:O	2:D:187:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:GLN:NE2	1:A:60:LEU:HB3	2.23	0.53
1:B:581:TRP:HA	1:B:616:LEU:CD1	2.37	0.53
1:B:593:ASP:OD2	1:B:601:TYR:CE1	2.62	0.53
2:C:20:ARG:NH1	2:C:107:TRP:CZ2	2.75	0.53
1:B:469:THR:HG23	1:B:471:ARG:HD3	1.89	0.53
1:B:480:VAL:C	1:B:482:THR:N	2.65	0.53
1:A:406:GLN:N	1:A:432:LEU:HD12	2.03	0.53
2:C:140:ILE:CD1	2:C:147:LEU:N	2.72	0.53
1:B:429:THR:HG22	1:B:430:PRO:CD	1.94	0.53
1:B:458:PHE:HB2	1:B:465:TRP:HB2	1.90	0.53
2:D:12:PHE:CD1	2:D:12:PHE:O	2.61	0.53
2:D:63:ILE:HG12	2:D:96:MET:HG2	1.90	0.53
2:D:153:THR:HG22	2:D:154:GLU:N	2.23	0.53
1:A:584:ILE:HD12	1:A:584:ILE:H	1.73	0.53
1:B:61:ASP:O	1:B:62:GLN:C	2.50	0.53
1:B:89:LYS:HD2	1:B:415:LEU:O	2.09	0.53
1:B:558:LYS:HD3	1:B:574:PRO:HB3	1.90	0.53
2:D:164:PHE:HD1	2:D:164:PHE:H	1.57	0.53
1:A:544:ASN:H	1:A:544:ASN:HD22	1.55	0.53
1:B:232:THR:O	1:B:232:THR:CG2	2.57	0.53
1:A:71:PRO:HG2	1:A:71:PRO:O	2.09	0.53
1:B:291:THR:CG2	1:B:292:GLU:N	2.72	0.53
1:A:81:TYR:HD2	1:A:86:ARG:NH2	2.05	0.53
1:A:207:PRO:HA	1:A:215:TYR:O	2.08	0.53
1:A:248:GLU:HB2	1:A:262:CYS:SG	2.49	0.53
1:A:406:GLN:HA	1:A:432:LEU:HD12	0.61	0.53
1:B:28:PHE:CE1	1:B:72:ARG:NE	2.76	0.53
1:B:44:THR:HG22	1:B:45:LEU:N	2.24	0.53
1:B:194:VAL:HG11	1:B:243:GLY:CA	2.34	0.53
1:B:530:LEU:C	1:B:532:LEU:H	1.97	0.53
2:D:7:HIS:NE2	2:D:162:ALA:HA	2.24	0.53
1:A:39:PHE:CD2	1:A:40:VAL:N	2.77	0.53
1:B:550:LYS:NZ	2:D:190:ASP:OD1	2.42	0.53
2:D:37:GLY:O	2:D:39:PRO:HD3	2.09	0.53
2:D:91:GLU:H	2:D:96:MET:HA	1.73	0.52
1:B:3:SER:CB	1:B:4:PRO:HD3	2.27	0.52
1:B:608:TYR:HB3	1:B:624:ILE:HG22	1.91	0.52
1:A:185:THR:O	1:A:367:SER:HA	2.09	0.52
1:B:403:ARG:CG	1:B:403:ARG:NH1	2.67	0.52
2:C:22:LYS:O	2:C:47:ILE:HA	2.09	0.52
1:A:26:ASN:CB	1:A:31:CYS:C	2.83	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:LEU:HD23	1:A:64:THR:HB	1.90	0.52
1:B:325:THR:HA	1:B:329:ASN:O	2.09	0.52
1:A:585:PRO:HD2	1:A:588:LEU:CD1	2.39	0.52
1:B:17:ASP:CG	1:B:65:ILE:HD13	2.35	0.52
1:B:38:LEU:N	1:B:43:ASP:HB2	2.25	0.52
1:B:57:THR:HG1	1:B:60:LEU:HB2	1.74	0.52
1:B:67:THR:O	1:B:70:LYS:HG2	2.09	0.52
2:C:25:SER:O	2:C:46:GLU:CB	2.58	0.52
2:D:47:ILE:HG21	2:D:63:ILE:HD12	1.92	0.52
2:D:77:ASP:OD2	2:D:84:TYR:OH	2.28	0.52
1:A:152:GLY:O	1:A:154:PRO:HD3	2.09	0.52
1:A:548:ASN:HD21	1:A:550:LYS:HB2	1.75	0.52
1:B:512:TRP:HB3	1:B:514:TYR:HE1	1.75	0.52
2:C:85:LEU:HD13	2:C:107:TRP:HZ3	1.74	0.52
1:A:618:SER:OG	1:A:619:VAL:N	2.43	0.52
1:B:57:THR:OG1	1:B:60:LEU:N	2.43	0.52
1:B:468:VAL:HG13	1:B:469:THR:HG22	1.92	0.52
1:B:612:GLU:HB2	1:B:618:SER:CB	2.22	0.52
1:A:405:SER:O	1:A:408:ASP:N	2.43	0.52
1:A:552:TYR:CE2	2:C:188:PHE:CD1	2.97	0.52
1:A:556:GLY:HA2	1:A:587:ASN:OD1	2.09	0.52
2:C:139:TYR:N	2:C:139:TYR:CD1	2.77	0.52
2:D:3:CYS:SG	2:D:101:CYS:N	2.82	0.52
2:D:164:PHE:CD1	2:D:164:PHE:N	2.77	0.52
1:B:506:PHE:HE1	1:B:527:LEU:HD11	1.69	0.52
2:D:113:THR:CG2	2:D:164:PHE:HA	2.40	0.52
1:B:196:TYR:CG	1:B:244:PHE:CD1	2.94	0.52
1:B:613:ASN:O	1:B:614:GLN:C	2.53	0.52
2:C:60:ILE:HG21	2:C:96:MET:SD	2.50	0.52
2:C:74:VAL:CG1	2:C:98:ILE:HD12	2.38	0.52
1:A:29:TYR:CE2	1:A:48:MET:HG2	2.45	0.51
1:A:440:CYS:O	1:A:442:GLN:N	2.43	0.51
1:A:581:TRP:NE1	2:C:188:PHE:HZ	2.07	0.51
1:B:467:THR:HB	1:B:474:PRO:HA	1.92	0.51
1:B:590:ALA:C	1:B:591:VAL:HG12	2.34	0.51
1:A:39:PHE:CG	1:A:40:VAL:N	2.78	0.51
1:A:87:LYS:O	1:A:87:LYS:HD3	2.10	0.51
2:C:51:LYS:HG2	2:C:52:MET:H	1.76	0.51
2:D:110:LEU:HD22	2:D:114:GLN:OE1	2.09	0.51
1:A:190:GLN:HE22	1:A:308:MET:H	1.57	0.51
1:A:461:ASP:O	1:A:489:GLU:O	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:LYS:O	1:B:8:PHE:CD2	2.63	0.51
1:B:579:ASP:O	2:D:185:LYS:HD3	2.11	0.51
2:C:26:GLU:O	2:C:26:GLU:HG3	2.11	0.51
2:C:33:ASN:O	2:C:40:ILE:HG13	2.10	0.51
2:C:73:GLY:O	2:C:100:LEU:HG	2.10	0.51
1:B:149:HIS:NE2	1:B:151:ASP:OD2	2.43	0.51
1:B:196:TYR:HD2	1:B:244:PHE:CD1	2.18	0.51
1:B:566:LYS:O	1:B:568:LYS:N	2.43	0.51
2:C:27:LYS:HB2	2:C:44:GLN:CB	2.40	0.51
1:A:86:ARG:O	1:A:88:PRO:HD3	2.10	0.51
1:A:471:ARG:HG3	1:A:472:ASP:N	2.24	0.51
1:B:194:VAL:HG23	1:B:204:CYS:SG	2.50	0.51
1:B:332:GLU:HG2	1:B:333:SER:OG	2.09	0.51
2:C:17:VAL:HG12	2:C:90:ALA:HB2	1.92	0.51
2:D:18:VAL:HB	2:D:53:PHE:HB2	1.93	0.51
2:D:56:PRO:O	2:D:58:LYS:N	2.44	0.51
1:A:408:ASP:O	1:A:409:ILE:C	2.51	0.51
1:A:629:LEU:O	1:A:630:GLY:C	2.53	0.51
1:A:391:LEU:HD22	1:A:402:PHE:HZ	1.76	0.51
1:B:170:THR:HG22	1:B:171:GLY:H	1.75	0.51
1:B:511:TYR:CE2	1:B:523:TYR:CD2	2.97	0.51
2:D:123:GLN:O	2:D:124:MET:C	2.54	0.51
1:A:84:PHE:CB	1:A:167:ALA:HB3	2.38	0.51
2:C:53:PHE:HD2	2:C:118:LEU:HB3	1.74	0.51
1:A:147:TRP:CD1	1:A:147:TRP:N	2.78	0.51
1:A:314:ASN:HD21	1:A:358:TRP:H	1.58	0.51
1:A:337:ALA:O	1:A:345:TRP:NE1	2.40	0.51
1:A:406:GLN:O	1:A:407:ASP:C	2.54	0.51
1:A:582:ASN:OD1	2:C:170:ARG:NH2	2.43	0.51
1:B:72:ARG:NH2	1:B:77:ASP:OD1	2.35	0.51
1:B:82:ASN:OD1	1:B:83:PHE:N	2.44	0.51
2:C:68:SER:O	2:C:71:VAL:HG23	2.11	0.51
1:A:99:ILE:CD1	1:A:115:PHE:HD2	2.24	0.51
1:B:509:ASN:O	1:B:509:ASN:ND2	2.43	0.51
2:C:20:ARG:HB3	2:C:85:LEU:HD12	1.93	0.51
2:C:85:LEU:HD21	2:C:118:LEU:CD2	2.40	0.51
1:A:472:ASP:O	1:A:630:GLY:HA3	2.11	0.50
1:B:9:PRO:CD	1:B:352:TYR:OH	2.58	0.50
1:B:277:THR:O	1:B:287:TRP:CD1	2.63	0.50
1:B:404:LEU:O	1:B:434:PRO:HD2	2.12	0.50
1:B:592:VAL:O	1:B:592:VAL:HG22	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:GLU:OE1	1:A:202:GLU:N	2.43	0.50
1:A:485:PRO:C	1:A:487:LEU:H	2.19	0.50
2:C:147:LEU:O	2:C:177:TRP:HZ2	1.92	0.50
2:D:123:GLN:O	2:D:126:CYS:N	2.44	0.50
1:A:10:GLY:O	1:B:296:ARG:HD2	2.11	0.50
1:A:42:LYS:C	1:A:46:LYS:HE3	2.36	0.50
1:A:314:ASN:C	1:A:314:ASN:ND2	2.68	0.50
2:C:146:CYS:C	2:C:177:TRP:CZ2	2.90	0.50
1:A:484:TRP:HB3	1:A:514:TYR:CZ	2.47	0.50
1:A:26:ASN:CB	1:A:31:CYS:H	2.18	0.50
1:A:35:SER:O	1:A:36:CYS:C	2.54	0.50
1:A:545:TRP:HE3	1:A:548:ASN:H	1.59	0.50
1:B:495:TYR:N	1:B:495:TYR:CD1	2.80	0.50
1:A:376:PHE:O	1:A:380:MET:HE2	2.11	0.50
1:A:391:LEU:HD22	1:A:402:PHE:CZ	2.47	0.50
1:A:585:PRO:HB2	1:A:588:LEU:HD21	1.94	0.50
1:B:5:ILE:CD1	1:B:327:LEU:CD1	2.81	0.50
2:C:7:HIS:C	2:C:9:GLN:H	2.20	0.50
2:C:12:PHE:CE1	2:C:53:PHE:HB3	2.46	0.50
1:A:431:THR:HG22	1:A:432:LEU:N	2.24	0.50
1:A:584:ILE:HG23	1:A:588:LEU:HD11	1.93	0.50
1:B:100:ILE:CD1	1:B:141:MET:HE3	2.41	0.50
1:B:194:VAL:CG1	1:B:243:GLY:CA	2.83	0.50
1:B:386:GLN:O	1:B:388:PRO:HD3	2.12	0.50
2:D:163:LYS:HB2	2:D:164:PHE:CD1	2.46	0.50
1:A:26:ASN:HB3	1:A:31:CYS:C	2.37	0.50
1:A:534:PRO:C	1:A:536:VAL:H	2.19	0.50
1:B:38:LEU:HD22	1:B:45:LEU:HB2	1.93	0.50
1:B:624:ILE:HA	1:B:628:TRP:HD1	1.76	0.50
2:C:33:ASN:N	2:C:40:ILE:H	2.10	0.50
2:C:41:LYS:O	2:C:67:PRO:CG	2.47	0.50
2:C:165:PHE:CE2	2:C:177:TRP:HB3	2.47	0.50
2:D:78:VAL:HG12	2:D:79:GLY:N	2.26	0.50
1:A:195:LYS:HG3	1:A:251:PHE:HE2	1.76	0.49
1:A:232:THR:C	1:A:233:THR:HG23	2.37	0.49
1:A:305:GLU:HG2	1:A:306:THR:N	2.27	0.49
1:A:539:VAL:CG1	1:A:540:ASP:H	2.25	0.49
1:B:596:GLY:C	1:B:598:GLY:N	2.68	0.49
2:C:1:CYS:HB2	2:C:71:VAL:C	2.36	0.49
1:A:15:LYS:HD3	1:A:24:TYR:HE2	1.76	0.49
1:A:451:GLN:CD	1:A:451:GLN:O	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:585:PRO:CD	1:A:588:LEU:HD21	2.42	0.49
1:B:73:CYS:SG	1:B:374:HIS:NE2	2.85	0.49
1:B:566:LYS:C	1:B:568:LYS:N	2.70	0.49
2:C:121:ARG:O	2:C:122:TYR:C	2.55	0.49
2:D:152:VAL:HG22	2:D:152:VAL:O	2.11	0.49
1:A:617:LYS:HZ3	2:C:174:SER:CB	2.20	0.49
1:B:196:TYR:HE1	1:B:251:PHE:CE1	1.99	0.49
1:B:231:SER:OG	1:B:233:THR:O	2.30	0.49
1:A:47:LYS:NZ	1:A:78:VAL:HG11	2.27	0.49
1:B:548:ASN:ND2	1:B:552:TYR:CE1	2.80	0.49
2:C:80:GLY:O	2:C:81:LYS:CB	2.60	0.49
1:B:464:ILE:HD12	1:B:464:ILE:O	2.11	0.49
2:C:27:LYS:CE	2:C:62:PHE:CZ	2.94	0.49
2:C:44:GLN:HG3	2:C:64:TYR:CE2	2.47	0.49
2:C:88:GLY:HA3	2:C:97:HIS:O	2.13	0.49
1:A:20:LEU:O	1:A:23:GLN:N	2.45	0.49
1:A:552:TYR:HE2	2:C:188:PHE:CD1	2.30	0.49
1:B:41:LEU:O	1:B:42:LYS:CB	2.59	0.49
1:B:64:THR:HG23	1:B:65:ILE:N	2.27	0.49
1:B:194:VAL:O	1:B:200:ASP:O	2.30	0.49
1:B:314:ASN:HD22	1:B:314:ASN:H	1.59	0.49
1:B:579:ASP:C	1:B:579:ASP:OD1	2.55	0.49
2:D:20:ARG:HG2	2:D:53:PHE:HE2	1.78	0.49
1:A:313:GLY:HA2	1:A:358:TRP:CH2	2.48	0.49
1:A:510:GLU:HA	1:A:526:PRO:HA	1.94	0.49
1:A:617:LYS:O	1:A:618:SER:HB2	2.13	0.49
1:B:148:GLU:H	1:B:154:PRO:HA	1.77	0.49
1:B:559:PHE:CE2	2:D:188:PHE:CE2	3.00	0.49
1:A:373:ALA:HB1	1:A:391:LEU:HD21	1.94	0.49
1:B:48:MET:HE2	1:B:52:PHE:HE2	1.73	0.49
1:B:97:TYR:HA	1:B:140:ILE:O	2.13	0.49
2:C:126:CYS:C	2:C:128:CYS:N	2.70	0.49
2:C:183:PRO:N	2:C:184:PRO:CD	2.75	0.49
2:D:9:GLN:OE1	2:D:166:ALA:HA	2.13	0.49
1:A:59:ASP:O	1:A:60:LEU:C	2.56	0.49
1:A:406:GLN:NE2	1:A:432:LEU:HD12	2.28	0.49
1:A:409:ILE:HG12	1:A:432:LEU:CD1	2.01	0.49
1:B:35:SER:O	1:B:36:CYS:SG	2.71	0.49
1:B:530:LEU:O	1:B:532:LEU:HD22	2.12	0.49
1:B:576:LEU:O	1:B:579:ASP:HB3	2.12	0.49
1:A:167:ALA:HB1	1:A:168:PRO:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ASP:HA	1:A:625:LYS:HZ3	1.78	0.49
1:A:512:TRP:CD1	1:A:524:PRO:HG3	2.47	0.49
1:B:531:GLY:HA3	1:B:569:MET:CB	2.43	0.49
2:C:51:LYS:HG2	2:C:52:MET:N	2.28	0.49
2:D:187:GLU:O	2:D:188:PHE:C	2.54	0.49
1:B:25:LEU:HD22	1:B:44:THR:HG22	1.94	0.48
1:B:28:PHE:CZ	1:B:72:ARG:HD3	2.48	0.48
1:B:198:ASN:O	1:B:199:ALA:CB	2.61	0.48
1:B:622:GLY:CA	2:D:137:PRO:CB	2.81	0.48
1:A:576:LEU:C	1:A:578:ALA:H	2.19	0.48
1:B:37:ASN:C	1:B:43:ASP:OD2	2.56	0.48
1:B:168:PRO:HG3	1:B:379:ALA:O	2.13	0.48
2:C:147:LEU:C	2:C:177:TRP:HZ2	2.21	0.48
1:A:545:TRP:CZ3	1:A:547:LYS:CE	2.90	0.48
2:D:78:VAL:O	2:D:81:LYS:HG2	2.13	0.48
1:A:81:TYR:CD2	1:A:86:ARG:NH1	2.77	0.48
1:A:273:TYR:CE2	1:A:277:THR:HG21	2.49	0.48
1:B:8:PHE:CZ	1:B:345:TRP:CE2	2.99	0.48
1:B:336:SER:O	1:B:337:ALA:C	2.54	0.48
2:C:18:VAL:O	2:C:53:PHE:N	2.39	0.48
2:C:135:MET:O	2:C:136:ILE:C	2.56	0.48
1:A:391:LEU:C	1:A:393:ALA:H	2.21	0.48
1:A:403:ARG:NH1	1:A:403:ARG:CG	2.76	0.48
1:B:194:VAL:CG1	1:B:195:LYS:N	2.76	0.48
1:B:235:ASN:ND2	1:B:235:ASN:C	2.72	0.48
1:B:293:ASP:OD1	1:B:293:ASP:C	2.57	0.48
2:C:30:ASP:CG	2:C:31:SER:H	2.21	0.48
2:C:125:GLY:O	2:C:128:CYS:HB2	2.13	0.48
2:C:189:LEU:HG	2:C:190:ASP:N	2.28	0.48
1:B:405:SER:HA	1:B:434:PRO:HD2	1.95	0.48
1:B:462:ARG:HB3	1:B:463:PHE:CE1	2.48	0.48
1:A:532:LEU:HD21	1:A:553:ILE:HD12	1.96	0.48
1:B:106:LEU:HD22	1:B:110:THR:HG21	1.96	0.48
1:B:532:LEU:HD23	1:B:532:LEU:O	2.13	0.48
1:B:580:ALA:HB2	2:D:188:PHE:CE1	2.48	0.48
2:C:140:ILE:HD11	2:C:146:CYS:C	2.39	0.48
1:A:208:PHE:CD1	1:A:231:SER:HB3	2.47	0.48
1:A:579:ASP:CG	2:C:185:LYS:NZ	2.70	0.48
1:B:480:VAL:C	1:B:482:THR:H	2.20	0.48
2:C:136:ILE:CD1	2:C:152:VAL:HG23	2.28	0.48
2:C:158:ASN:OD1	2:C:163:LYS:HE2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:THR:CG2	1:B:65:ILE:N	2.77	0.47
1:B:149:HIS:O	1:B:149:HIS:CD2	2.67	0.47
1:B:195:LYS:HB3	1:B:195:LYS:HE2	1.51	0.47
1:B:253:MET:CE	1:B:254:GLY:H	2.27	0.47
1:B:544:ASN:HA	1:B:550:LYS:O	2.14	0.47
2:D:182:ALA:HB3	2:D:185:LYS:CE	2.34	0.47
1:A:87:LYS:O	1:A:87:LYS:CG	2.61	0.47
1:A:118:ALA:O	1:A:121:VAL:HB	2.14	0.47
1:A:472:ASP:C	1:A:630:GLY:HA3	2.40	0.47
1:B:38:LEU:HD13	1:B:44:THR:O	2.14	0.47
2:C:86:ILE:HG22	2:C:98:ILE:HG22	1.96	0.47
2:C:27:LYS:O	2:C:28:GLU:C	2.56	0.47
2:D:68:SER:H	2:D:71:VAL:CG2	2.27	0.47
1:A:409:ILE:HD11	1:A:432:LEU:HD22	1.84	0.47
1:B:9:PRO:HD2	1:B:352:TYR:HH	1.76	0.47
1:B:37:ASN:HB3	1:B:43:ASP:CG	2.32	0.47
1:B:60:LEU:HD13	1:B:64:THR:H	1.79	0.47
1:B:223:ARG:NH1	1:B:244:PHE:HE2	2.13	0.47
1:A:42:LYS:H	1:A:42:LYS:CE	2.28	0.47
1:A:223:ARG:HE	1:A:223:ARG:HB3	1.48	0.47
1:A:534:PRO:C	1:A:536:VAL:N	2.73	0.47
1:B:469:THR:OG1	1:B:471:ARG:CD	2.62	0.47
1:B:561:ARG:CZ	2:D:188:PHE:HB2	2.45	0.47
2:C:78:VAL:O	2:C:80:GLY:N	2.47	0.47
2:D:113:THR:HG22	2:D:113:THR:O	2.14	0.47
2:D:147:LEU:O	2:D:177:TRP:CZ2	2.67	0.47
1:A:84:PHE:CD1	1:A:84:PHE:O	2.67	0.47
1:A:235:ASN:ND2	1:A:238:LYS:H	2.13	0.47
1:A:439:ILE:HG22	1:A:440:CYS:H	1.77	0.47
1:A:618:SER:CB	2:C:177:TRP:HZ3	2.28	0.47
1:A:621:PHE:CB	2:C:147:LEU:HD21	2.42	0.47
1:B:16:THR:CB	1:B:19:GLU:HB3	2.45	0.47
2:D:7:HIS:CE1	2:D:162:ALA:HA	2.50	0.47
1:A:527:LEU:HB2	1:A:536:VAL:HB	1.96	0.47
1:B:196:TYR:CG	1:B:244:PHE:HD1	2.32	0.47
1:B:458:PHE:CE2	1:B:629:LEU:HD21	2.50	0.47
2:C:86:ILE:HD13	2:C:104:ILE:HG21	1.96	0.47
2:C:114:GLN:O	2:C:117:SER:OG	2.33	0.47
1:A:18:LYS:NZ	1:A:61:ASP:OD1	2.46	0.47
1:A:80:ASN:O	1:A:80:ASN:ND2	2.48	0.47
1:A:624:ILE:CG2	1:A:625:LYS:H	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:19:ILE:HG22	2:C:52:MET:HA	1.97	0.47
2:C:157:ILE:H	2:C:157:ILE:HG13	1.50	0.47
2:D:21:ALA:HB2	2:D:47:ILE:HD13	1.97	0.47
2:D:142:SER:N	2:D:145:GLU:OE2	2.35	0.47
1:A:26:ASN:CB	1:A:31:CYS:N	2.78	0.47
1:A:559:PHE:CZ	2:C:188:PHE:CD2	3.03	0.47
1:B:123:SER:C	1:B:125:VAL:H	2.23	0.47
1:B:539:VAL:HG13	1:B:553:ILE:HG23	1.97	0.47
2:C:86:ILE:CG2	2:C:98:ILE:HG22	2.44	0.47
1:A:545:TRP:HB3	1:A:548:ASN:H	1.80	0.47
2:C:102:ASP:OD1	2:C:103:PHE:N	2.48	0.47
1:A:45:LEU:CD2	1:A:59:ASP:CA	2.75	0.46
1:A:581:TRP:CE2	2:C:188:PHE:CZ	3.00	0.46
1:B:17:ASP:CG	1:B:65:ILE:CD1	2.88	0.46
1:B:495:TYR:CE1	1:B:506:PHE:CD2	3.02	0.46
1:B:570:ASP:OD2	2:D:190:ASP:OD2	2.33	0.46
2:C:5:PRO:O	2:C:6:VAL:HG13	2.16	0.46
2:D:63:ILE:HG12	2:D:96:MET:CG	2.46	0.46
1:A:535:ASP:C	1:A:537:GLN:H	2.22	0.46
1:A:589:ASP:N	1:A:603:PHE:O	2.49	0.46
1:B:486:GLU:CG	1:B:514:TYR:OH	2.63	0.46
2:C:74:VAL:O	2:C:74:VAL:HG12	2.14	0.46
1:A:503:ALA:HB1	1:A:505:PHE:HE1	1.80	0.46
1:B:72:ARG:HH22	1:B:77:ASP:CG	2.20	0.46
2:C:18:VAL:HG22	2:C:87:ALA:HB1	1.96	0.46
2:C:28:GLU:O	2:C:29:VAL:C	2.59	0.46
2:C:78:VAL:HG12	2:C:79:GLY:H	1.81	0.46
2:C:84:TYR:HB3	2:C:86:ILE:HG13	1.96	0.46
2:D:19:ILE:HD12	2:D:21:ALA:HB2	1.98	0.46
1:A:527:LEU:CB	1:A:536:VAL:HG12	2.40	0.46
2:C:53:PHE:CE1	2:C:85:LEU:HD11	2.50	0.46
1:B:437:PRO:HD2	1:B:463:PHE:CD1	2.51	0.46
2:C:80:GLY:O	2:C:81:LYS:HB2	2.16	0.46
1:A:29:TYR:CZ	1:A:48:MET:HG2	2.50	0.46
1:A:117:ARG:NH2	1:A:369:PHE:HB2	2.31	0.46
1:A:446:PHE:CE2	1:A:629:LEU:HD22	2.51	0.46
1:B:57:THR:OG1	1:B:60:LEU:CB	2.62	0.46
1:B:460:LYS:O	1:B:461:ASP:C	2.59	0.46
1:B:495:TYR:CE2	1:B:504:VAL:HG11	2.51	0.46
1:B:561:ARG:O	1:B:569:MET:HG3	2.15	0.46
2:C:69:SER:CA	2:C:73:GLY:HA3	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:TRP:HB3	1:A:514:TYR:CE2	2.49	0.46
1:A:512:TRP:NE1	1:A:524:PRO:CG	2.76	0.46
1:B:206:PHE:HB3	1:B:216:ASN:HA	1.97	0.46
2:C:19:ILE:HG13	2:C:49:GLN:HG3	1.97	0.46
2:C:101:CYS:O	2:C:101:CYS:SG	2.74	0.46
1:A:179:ASP:HB3	1:A:182:GLU:HG2	1.98	0.46
1:B:33:LYS:HE3	1:B:33:LYS:CA	2.44	0.46
1:B:41:LEU:CB	1:B:43:ASP:OD2	2.63	0.46
1:B:396:TYR:CD1	1:B:396:TYR:C	2.94	0.46
2:C:85:LEU:O	2:C:86:ILE:C	2.59	0.46
2:C:135:MET:SD	2:C:135:MET:N	2.88	0.46
1:A:406:GLN:NE2	1:A:432:LEU:HG	2.31	0.46
1:B:80:ASN:O	1:B:80:ASN:CG	2.59	0.46
1:B:404:LEU:HD22	1:B:408:ASP:HB2	1.98	0.46
1:B:574:PRO:C	1:B:575:LYS:HG2	2.41	0.46
2:D:190:ASP:O	2:D:191:ILE:C	2.57	0.46
1:A:109:GLU:OE1	1:A:193:ARG:NH1	2.34	0.46
1:B:29:TYR:N	1:B:29:TYR:CD1	2.84	0.46
1:B:39:PHE:O	1:B:39:PHE:CD1	2.69	0.46
1:B:268:PHE:CD1	1:B:294:TYR:HD2	2.33	0.46
2:C:117:SER:HA	2:C:121:ARG:HB2	1.98	0.46
1:B:253:MET:HE3	1:B:254:GLY:H	1.81	0.45
1:B:290:THR:CG2	1:B:299:LYS:HB3	2.45	0.45
1:B:563:ASN:CG	1:B:566:LYS:HB2	2.41	0.45
1:B:587:ASN:N	1:B:587:ASN:HD22	2.14	0.45
2:C:7:HIS:C	2:C:9:GLN:N	2.74	0.45
2:D:17:VAL:HG12	2:D:52:MET:HE1	1.97	0.45
1:A:309:SER:HB2	1:A:319:PRO:HA	1.98	0.45
1:A:490:LYS:O	1:A:490:LYS:CG	2.63	0.45
1:B:314:ASN:HD22	1:B:314:ASN:C	2.24	0.45
1:A:72:ARG:HH22	1:A:77:ASP:CG	2.23	0.45
1:A:81:TYR:CD2	1:A:86:ARG:NH2	2.83	0.45
1:A:87:LYS:O	1:A:87:LYS:HG2	2.16	0.45
1:A:547:LYS:HE2	1:A:547:LYS:HB3	1.88	0.45
1:A:563:ASN:OD1	1:A:563:ASN:N	2.48	0.45
1:B:130:PHE:CZ	1:B:380:MET:HE3	2.51	0.45
1:B:314:ASN:ND2	1:B:314:ASN:C	2.74	0.45
1:B:499:GLN:OE1	1:B:565:VAL:HG13	2.16	0.45
2:D:25:SER:HB2	2:D:46:GLU:HB3	1.98	0.45
2:D:47:ILE:HD11	2:D:60:ILE:O	2.17	0.45
2:D:191:ILE:H	2:D:191:ILE:HG12	1.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:PHE:O	1:B:116:ALA:C	2.58	0.45
1:B:572:GLY:O	1:B:573:PHE:C	2.51	0.45
2:C:19:ILE:O	2:C:85:LEU:O	2.34	0.45
2:C:86:ILE:HG12	2:C:104:ILE:HA	1.97	0.45
1:B:496:GLU:OE1	1:B:594:LEU:HD22	2.17	0.45
2:C:29:VAL:CA	2:C:42:ARG:O	2.64	0.45
1:A:25:LEU:HD22	1:A:44:THR:HG22	1.97	0.45
1:A:438:GLU:O	1:A:439:ILE:C	2.60	0.45
1:B:133:ILE:O	1:B:133:ILE:CG1	2.51	0.45
2:C:105:VAL:HG21	2:C:110:LEU:HD11	1.99	0.45
1:A:147:TRP:O	1:A:148:GLU:HB3	2.17	0.45
1:A:156:ASP:O	1:A:157:GLY:C	2.59	0.45
1:A:183:LEU:C	1:A:183:LEU:HD12	2.42	0.45
1:A:406:GLN:HE21	1:A:432:LEU:CD1	2.27	0.45
1:A:527:LEU:HB2	1:A:536:VAL:HG11	1.93	0.45
1:B:452:ILE:HD11	1:B:503:ALA:HB1	1.99	0.45
1:A:266:PHE:CZ	1:A:273:TYR:HB2	2.52	0.45
1:A:404:LEU:HD22	1:A:408:ASP:CB	2.46	0.45
1:B:449:ILE:O	1:B:450:ALA:HB2	2.16	0.45
1:A:6:ILE:CG2	1:A:8:PHE:CE1	2.99	0.45
1:A:45:LEU:HD21	1:A:59:ASP:HA	1.90	0.45
1:A:460:LYS:HD2	1:A:460:LYS:HA	1.51	0.45
1:A:559:PHE:CZ	2:C:188:PHE:CE2	3.05	0.45
1:A:584:ILE:HG23	1:A:588:LEU:CD1	2.47	0.45
1:A:621:PHE:HB2	2:C:147:LEU:CD2	2.40	0.45
1:B:461:ASP:O	1:B:462:ARG:HB2	2.17	0.45
1:B:468:VAL:HG13	1:B:469:THR:N	2.32	0.45
2:D:86:ILE:HG22	2:D:87:ALA:N	2.32	0.45
1:A:315:SER:HB3	1:A:318:ALA:HB3	1.98	0.45
1:A:406:GLN:HE21	1:A:432:LEU:CG	2.30	0.45
1:B:543:PHE:CZ	1:B:545:TRP:HD1	2.34	0.45
1:B:593:ASP:OD2	1:B:601:TYR:CD1	2.70	0.45
2:C:19:ILE:HA	2:C:53:PHE:HD1	1.82	0.45
2:C:121:ARG:HH22	2:C:178:TYR:HB3	1.82	0.45
1:A:16:THR:O	1:A:17:ASP:C	2.60	0.44
1:A:20:LEU:C	1:A:22:VAL:N	2.74	0.44
1:B:34:GLU:C	1:B:36:CYS:N	2.76	0.44
1:B:504:VAL:HG13	1:B:513:ILE:HG12	1.98	0.44
1:B:616:LEU:HG	2:D:170:ARG:HH22	1.82	0.44
2:C:57:GLU:H	2:C:57:GLU:HG2	1.50	0.44
1:A:137:GLU:HA	1:A:141:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:TYR:CG	1:B:119:PHE:HE2	2.35	0.44
1:B:405:SER:O	1:B:409:ILE:HG13	2.17	0.44
1:B:548:ASN:O	1:B:550:LYS:HG3	2.17	0.44
2:C:1:CYS:CB	2:C:71:VAL:O	2.63	0.44
2:C:16:ASP:O	2:C:55:GLY:HA2	2.18	0.44
2:C:71:VAL:O	2:C:72:CYS:SG	2.76	0.44
2:D:104:ILE:O	2:D:105:VAL:HG13	2.17	0.44
1:A:125:VAL:O	1:A:125:VAL:HG23	2.17	0.44
1:A:459:PHE:CD2	1:A:464:ILE:HG22	2.52	0.44
1:B:41:LEU:HB2	1:B:43:ASP:OD2	2.17	0.44
1:B:61:ASP:OD1	1:B:61:ASP:N	2.50	0.44
1:B:97:TYR:CG	1:B:119:PHE:CE2	3.05	0.44
2:D:117:SER:C	2:D:122:TYR:HD2	2.26	0.44
1:A:26:ASN:HD22	1:A:26:ASN:N	2.15	0.44
1:A:223:ARG:HH21	1:A:225:ASP:CG	2.23	0.44
1:A:234:TYR:CD2	1:A:521:ARG:HD2	2.52	0.44
1:A:250:LEU:HD23	1:A:250:LEU:HA	1.85	0.44
1:A:368:LEU:O	1:A:369:PHE:C	2.59	0.44
1:B:446:PHE:CZ	1:B:629:LEU:HD11	2.52	0.44
1:B:484:TRP:CD1	1:B:514:TYR:CD2	3.02	0.44
2:D:18:VAL:HG13	2:D:87:ALA:HB2	1.99	0.44
2:D:56:PRO:C	2:D:58:LYS:N	2.73	0.44
1:A:192:VAL:HB	1:A:204:CYS:SG	2.57	0.44
1:A:435:VAL:HG12	1:A:436:THR:H	1.81	0.44
1:B:473:LYS:HG3	1:B:630:GLY:HA2	1.99	0.44
1:B:561:ARG:NH2	2:D:190:ASP:OD1	2.51	0.44
2:C:29:VAL:CG2	2:C:43:ILE:HD13	2.33	0.44
2:D:7:HIS:O	2:D:8:PRO:C	2.60	0.44
1:A:459:PHE:CE2	1:A:464:ILE:HG21	2.53	0.44
1:B:25:LEU:HD22	1:B:44:THR:HG21	1.99	0.44
1:B:452:ILE:HD11	1:B:503:ALA:CB	2.47	0.44
2:C:20:ARG:HD3	2:C:107:TRP:CZ3	2.53	0.44
2:C:20:ARG:HA	2:C:85:LEU:HA	1.98	0.44
1:A:96:THR:O	1:A:139:ASP:HB2	2.17	0.44
1:A:545:TRP:CG	1:A:548:ASN:HB3	2.52	0.44
1:B:70:LYS:HA	1:B:71:PRO:HD2	1.83	0.44
1:B:437:PRO:HB2	1:B:465:TRP:CH2	2.52	0.44
1:B:480:VAL:O	1:B:481:ALA:C	2.61	0.44
1:B:545:TRP:CD1	1:B:548:ASN:HD21	2.35	0.44
1:B:576:LEU:O	1:B:577:ILE:C	2.60	0.44
2:C:23:ALA:C	2:C:78:VAL:HG13	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:THR:O	1:B:367:SER:HA	2.18	0.44
1:B:260:GLN:HA	1:B:261:PRO:HD3	1.82	0.44
1:B:409:ILE:HA	1:B:412:ILE:HG22	2.00	0.44
1:B:497:ALA:HA	1:B:498:PRO:HD3	1.82	0.44
1:A:279:GLU:OE1	1:B:279:GLU:OE1	2.35	0.44
1:B:11:ASP:OD1	1:B:11:ASP:C	2.61	0.44
2:C:136:ILE:H	2:C:136:ILE:HG12	1.38	0.43
2:D:147:LEU:N	2:D:177:TRP:CZ2	2.86	0.43
1:A:252:THR:HG22	1:A:302:PHE:O	2.18	0.43
1:A:335:THR:OG1	1:A:336:SER:N	2.51	0.43
1:A:552:TYR:HE2	2:C:188:PHE:CE1	2.35	0.43
1:B:486:GLU:HG2	1:B:514:TYR:OH	2.18	0.43
2:C:150:ASP:OD1	2:C:161:GLN:HB3	2.18	0.43
1:A:42:LYS:H	1:A:42:LYS:HE3	1.83	0.43
1:A:374:HIS:CD2	1:A:378:HIS:CD2	3.06	0.43
1:B:38:LEU:C	1:B:38:LEU:HD12	2.43	0.43
1:B:140:ILE:HG23	1:B:174:GLY:O	2.17	0.43
1:B:223:ARG:NH2	1:B:225:ASP:OD2	2.50	0.43
1:B:596:GLY:C	1:B:598:GLY:H	2.27	0.43
2:D:102:ASP:O	2:D:104:ILE:N	2.51	0.43
2:D:148:TRP:CE2	2:D:150:ASP:HB3	2.53	0.43
1:A:404:LEU:HD23	1:A:404:LEU:HA	1.75	0.43
1:A:546:SER:OG	1:A:593:ASP:HB3	2.18	0.43
2:C:15:ALA:HB1	2:C:87:ALA:HB1	2.01	0.43
2:C:18:VAL:C	2:C:19:ILE:CG2	2.91	0.43
2:C:74:VAL:HG21	2:C:98:ILE:O	2.18	0.43
2:C:80:GLY:C	2:C:81:LYS:HG3	2.44	0.43
2:C:98:ILE:O	2:C:98:ILE:HG13	2.19	0.43
1:B:64:THR:HG23	1:B:68:MET:HE2	2.01	0.43
1:A:223:ARG:H	1:A:223:ARG:HG2	1.64	0.43
1:A:585:PRO:HD2	1:A:588:LEU:CD2	2.48	0.43
1:B:223:ARG:NH1	1:B:244:PHE:CE2	2.87	0.43
1:B:450:ALA:HA	1:B:592:VAL:CG2	2.44	0.43
2:C:47:ILE:HG21	2:C:63:ILE:HG13	1.95	0.43
2:C:190:ASP:N	2:C:190:ASP:OD1	2.50	0.43
2:D:147:LEU:N	2:D:177:TRP:HH2	2.06	0.43
1:A:18:LYS:NZ	1:A:61:ASP:CG	2.77	0.43
1:A:76:PRO:HG2	1:A:82:ASN:OD1	2.18	0.43
1:A:113:ASP:O	1:A:114:ALA:C	2.61	0.43
1:A:277:THR:HG23	1:B:271:THR:HG21	2.01	0.43
1:A:491:ILE:HD12	1:A:491:ILE:C	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:196:TYR:CD2	1:B:244:PHE:CE1	3.01	0.43
1:B:293:ASP:CG	1:B:296:ARG:HB2	2.43	0.43
1:B:394:PRO:HG2	1:B:395:ILE:N	2.33	0.43
1:B:584:ILE:HA	1:B:585:PRO:HD3	1.78	0.43
2:C:24:VAL:O	2:C:78:VAL:CG1	2.67	0.43
1:B:97:TYR:CD2	1:B:119:PHE:HE2	2.37	0.43
2:C:85:LEU:CD2	2:C:118:LEU:HD21	2.48	0.43
2:D:21:ALA:HA	2:D:48:LYS:O	2.19	0.43
2:D:127:GLU:OE1	2:D:169:LYS:HD3	2.18	0.43
1:A:459:PHE:CD2	1:A:464:ILE:CG2	3.02	0.43
1:A:506:PHE:HE2	1:A:530:LEU:CD2	2.31	0.43
1:A:585:PRO:CB	1:A:588:LEU:HD21	2.48	0.43
1:A:610:LYS:HB3	1:A:620:LYS:HB3	2.00	0.43
1:B:36:CYS:HB3	1:B:38:LEU:HB3	2.01	0.43
1:A:80:ASN:ND2	1:A:84:PHE:CE2	2.87	0.43
1:A:310:THR:HB	1:A:318:ALA:O	2.19	0.43
1:A:511:TYR:HD1	1:A:525:LYS:O	2.01	0.43
1:B:5:ILE:C	1:B:6:ILE:HG13	2.44	0.43
1:B:125:VAL:O	1:B:126:THR:HG23	2.19	0.43
1:B:264:PHE:CZ	1:B:275:SER:HA	2.53	0.43
1:B:430:PRO:HB3	1:B:435:VAL:CG1	2.46	0.43
1:B:491:ILE:HD13	1:B:505:PHE:CE1	2.54	0.43
1:B:582:ASN:O	1:B:583:ALA:HB3	2.18	0.43
2:D:138:CYS:SG	2:D:147:LEU:HD11	2.58	0.43
1:A:629:LEU:O	1:A:629:LEU:HG	2.19	0.42
1:B:543:PHE:CZ	1:B:545:TRP:CD1	3.07	0.42
1:B:559:PHE:HZ	2:D:188:PHE:CE1	2.27	0.42
2:D:52:MET:HG3	2:D:53:PHE:N	2.31	0.42
1:A:295:ASP:HB2	1:B:146:ARG:NH1	2.34	0.42
1:A:473:LYS:HA	1:A:630:GLY:HA3	2.00	0.42
1:B:33:LYS:O	1:B:33:LYS:HG3	2.18	0.42
1:B:103:THR:O	1:B:103:THR:HG23	2.18	0.42
1:B:397:THR:HG21	1:B:479:LEU:CD1	2.47	0.42
1:B:617:LYS:NZ	2:D:174:SER:HB2	2.32	0.42
1:A:490:LYS:HD3	1:A:490:LYS:N	2.34	0.42
1:B:500:GLU:C	1:B:502:LYS:H	2.27	0.42
1:A:54:LEU:H	1:A:54:LEU:CD2	2.20	0.42
1:B:357:LYS:CB	1:B:357:LYS:HZ3	2.18	0.42
1:B:481:ALA:O	1:B:485:PRO:HG3	2.19	0.42
1:B:549:LYS:HA	1:B:549:LYS:HD3	1.80	0.42
1:A:462:ARG:C	1:A:480:VAL:HG13	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:ASP:OD1	1:B:180:ASP:N	2.53	0.42
1:B:480:VAL:CG2	1:B:481:ALA:H	2.30	0.42
2:D:142:SER:HA	2:D:143:PRO:HD3	1.91	0.42
1:A:156:ASP:OD2	1:A:161:LEU:HG	2.19	0.42
1:A:519:LEU:H	1:A:519:LEU:CD2	2.33	0.42
1:A:589:ASP:OD2	1:A:604:LYS:HA	2.19	0.42
1:B:7:LYS:O	1:B:8:PHE:CG	2.72	0.42
1:B:57:THR:CB	1:B:60:LEU:HB2	2.49	0.42
1:B:123:SER:O	1:B:126:THR:N	2.44	0.42
1:B:450:ALA:HA	1:B:592:VAL:HG11	2.00	0.42
1:B:458:PHE:HZ	1:B:628:TRP:HB3	1.83	0.42
1:B:573:PHE:HB3	1:B:574:PRO:HA	2.01	0.42
1:B:608:TYR:CE1	1:B:622:GLY:O	2.71	0.42
2:C:189:LEU:HG	2:C:190:ASP:H	1.84	0.42
2:D:20:ARG:HH21	2:D:83:GLU:CD	2.22	0.42
2:D:151:TRP:CD1	2:D:152:VAL:N	2.88	0.42
1:A:17:ASP:HB3	1:A:18:LYS:H	1.38	0.42
1:B:25:LEU:O	1:B:29:TYR:N	2.50	0.42
2:C:25:SER:H	2:C:46:GLU:HB3	1.83	0.42
2:C:54:LYS:HG2	2:C:55:GLY:H	1.85	0.42
2:D:85:LEU:HB3	2:D:105:VAL:HG23	2.01	0.42
1:A:112:ASP:CG	1:A:132:ARG:HH12	2.27	0.42
1:A:232:THR:C	1:A:233:THR:CG2	2.92	0.42
1:A:264:PHE:HA	1:A:265:PRO:HA	1.76	0.42
1:A:406:GLN:NE2	1:A:432:LEU:CG	2.83	0.42
1:A:446:PHE:HZ	1:A:629:LEU:CD2	2.31	0.42
1:B:70:LYS:HG2	1:B:70:LYS:H	1.66	0.42
1:B:335:THR:OG1	1:B:336:SER:N	2.53	0.42
2:C:74:VAL:HG22	2:C:100:LEU:HA	2.02	0.42
2:C:150:ASP:O	2:C:154:GLU:N	2.52	0.42
1:A:34:GLU:O	1:A:34:GLU:HG2	2.20	0.42
1:A:55:PRO:O	1:A:57:THR:HG23	2.20	0.42
1:B:33:LYS:HA	1:B:33:LYS:CE	2.44	0.42
1:B:59:ASP:OD1	1:B:59:ASP:C	2.63	0.42
1:B:111:VAL:O	1:B:112:ASP:C	2.62	0.42
2:D:113:THR:HG21	2:D:164:PHE:HA	2.00	0.42
1:A:9:PRO:HD3	1:A:352:TYR:OH	2.19	0.42
1:A:235:ASN:ND2	1:A:238:LYS:N	2.68	0.42
1:A:496:GLU:HA	1:A:502:LYS:O	2.20	0.42
1:A:588:LEU:HD12	1:A:602:PHE:CD2	2.55	0.41
2:C:21:ALA:HB1	2:C:47:ILE:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:47:ILE:C	2:C:47:ILE:HD12	2.45	0.41
2:D:30:ASP:OD1	2:D:41:LYS:HE3	2.21	0.41
1:A:87:LYS:HA	1:A:88:PRO:HD3	1.83	0.41
1:A:104:PRO:O	1:A:305:GLU:HG3	2.20	0.41
1:A:368:LEU:HD12	1:A:368:LEU:HA	1.80	0.41
1:A:433:GLY:HA3	1:A:434:PRO:HD3	1.74	0.41
1:A:533:PRO:C	1:A:535:ASP:H	2.27	0.41
1:A:622:GLY:HA2	2:C:136:ILE:HG22	2.02	0.41
1:B:291:THR:CG2	1:B:293:ASP:H	2.32	0.41
2:D:9:GLN:HB2	2:D:122:TYR:HE1	1.83	0.41
1:A:84:PHE:CE1	1:A:85:PRO:C	2.97	0.41
1:A:115:PHE:CE2	1:A:142:ILE:HG21	2.55	0.41
1:A:163:ALA:O	1:A:164:HIS:HB3	2.20	0.41
1:A:576:LEU:C	1:A:578:ALA:N	2.76	0.41
1:A:599:HIS:HA	1:A:611:LEU:O	2.19	0.41
1:B:112:ASP:OD2	1:B:132:ARG:NH2	2.52	0.41
1:B:195:LYS:NZ	1:B:253:MET:SD	2.87	0.41
1:B:406:GLN:CB	1:B:434:PRO:O	2.68	0.41
1:B:484:TRP:HB3	1:B:487:LEU:HB2	2.03	0.41
1:B:591:VAL:C	1:B:592:VAL:HG13	2.46	0.41
2:C:18:VAL:HG22	2:C:87:ALA:HB2	2.01	0.41
2:C:44:GLN:HA	2:C:63:ILE:O	2.20	0.41
1:A:123:SER:O	1:A:125:VAL:N	2.54	0.41
1:A:223:ARG:NH1	1:A:244:PHE:CZ	2.88	0.41
1:A:577:ILE:CG2	1:A:581:TRP:HB2	2.29	0.41
1:B:555:ALA:HB3	1:B:560:TRP:HZ3	1.86	0.41
2:C:9:GLN:HG3	2:C:122:TYR:CD1	2.54	0.41
1:A:10:GLY:HA2	1:B:296:ARG:CZ	2.50	0.41
1:B:404:LEU:HD22	1:B:408:ASP:CB	2.49	0.41
1:B:447:ASP:HB3	1:B:491:ILE:O	2.21	0.41
1:B:581:TRP:HE3	1:B:611:LEU:HD11	1.86	0.41
2:D:140:ILE:HG23	2:D:147:LEU:HB2	2.00	0.41
1:A:18:LYS:HA	1:A:18:LYS:HD2	1.78	0.41
1:A:20:LEU:O	1:A:21:ALA:C	2.62	0.41
1:A:421:ASP:OD1	1:A:421:ASP:N	2.53	0.41
1:A:543:PHE:CE1	1:A:554:PHE:HE2	2.38	0.41
1:B:253:MET:O	1:B:254:GLY:C	2.62	0.41
1:B:273:TYR:CE2	1:B:277:THR:HG21	2.56	0.41
2:C:60:ILE:HD12	2:C:96:MET:HB3	2.02	0.41
2:C:79:GLY:O	2:C:81:LYS:N	2.54	0.41
2:C:97:HIS:CE1	2:C:99:THR:HG22	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:PHE:HE2	1:A:72:ARG:HD2	1.70	0.41
1:B:51:PHE:CD1	1:B:51:PHE:C	2.99	0.41
1:B:291:THR:CG2	1:B:297:ASP:OD2	2.67	0.41
1:B:344:MET:HB3	1:B:344:MET:HE3	1.87	0.41
1:B:409:ILE:O	1:B:410:LYS:C	2.63	0.41
2:C:121:ARG:HH11	2:C:121:ARG:CG	2.33	0.41
2:D:7:HIS:HB3	2:D:10:GLN:CB	2.47	0.41
1:A:60:LEU:HD23	1:A:64:THR:CB	2.51	0.41
1:A:205:LYS:O	1:A:208:PHE:HB3	2.20	0.41
1:B:184:TRP:C	1:B:185:THR:HG23	2.45	0.41
1:B:619:VAL:HG21	2:D:177:TRP:CZ3	2.56	0.41
2:C:121:ARG:NH2	2:C:180:GLY:O	2.45	0.41
1:A:257:ALA:O	1:A:260:GLN:HG2	2.21	0.41
1:A:457:PHE:CD1	1:A:457:PHE:N	2.87	0.41
1:A:503:ALA:HB1	1:A:505:PHE:CE1	2.56	0.41
1:A:536:VAL:O	1:A:537:GLN:C	2.64	0.41
1:A:545:TRP:CD2	1:A:548:ASN:HB3	2.56	0.41
1:B:60:LEU:O	1:B:61:ASP:C	2.64	0.41
1:B:246:PRO:O	1:B:247:HIS:HB2	2.20	0.41
1:B:263:LYS:HB3	1:B:291:THR:O	2.20	0.41
1:B:300:TYR:N	1:B:300:TYR:CD1	2.89	0.41
1:B:376:PHE:HA	1:B:379:ALA:HB3	2.03	0.41
1:B:400:LYS:HD2	1:B:485:PRO:O	2.21	0.41
1:B:420:PRO:O	1:B:421:ASP:HB2	2.19	0.41
1:B:569:MET:HB2	1:B:569:MET:HE3	2.00	0.41
1:B:587:ASN:N	1:B:587:ASN:ND2	2.67	0.41
1:B:596:GLY:O	1:B:599:HIS:ND1	2.53	0.41
1:B:600:SER:O	1:B:611:LEU:HB3	2.20	0.41
2:C:57:GLU:O	2:C:59:ASP:N	2.54	0.41
2:C:86:ILE:HG21	2:C:98:ILE:CG2	2.50	0.41
2:C:190:ASP:OD1	2:C:192:GLU:OE2	2.39	0.41
2:D:75:SER:O	2:D:76:LEU:HD23	2.21	0.41
2:D:123:GLN:O	2:D:125:GLY:N	2.53	0.41
2:D:133:CYS:HB3	2:D:151:TRP:HE1	1.86	0.41
1:A:20:LEU:O	1:A:22:VAL:N	2.54	0.41
1:B:120:GLN:O	1:B:121:VAL:C	2.63	0.41
1:B:256:ASN:O	1:B:258:GLU:HG2	2.21	0.41
2:C:33:ASN:HA	2:C:39:PRO:HA	2.02	0.41
2:C:44:GLN:CG	2:C:64:TYR:CE2	3.04	0.41
1:A:84:PHE:HD1	1:A:85:PRO:O	1.98	0.40
1:A:113:ASP:OD1	1:A:113:ASP:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:THR:C	1:A:128:LEU:H	2.29	0.40
1:B:6:ILE:O	1:B:7:LYS:CB	2.66	0.40
1:B:314:ASN:HD22	1:B:314:ASN:N	2.16	0.40
1:B:337:ALA:O	1:B:345:TRP:NE1	2.42	0.40
1:B:375:ALA:O	1:B:378:HIS:HB2	2.21	0.40
1:B:497:ALA:HB1	1:B:500:GLU:HB3	2.03	0.40
1:B:526:PRO:C	1:B:528:THR:H	2.30	0.40
2:C:43:ILE:H	2:C:43:ILE:HG12	1.68	0.40
2:C:152:VAL:HG12	2:C:153:THR:H	1.86	0.40
2:D:36:TYR:O	2:D:36:TYR:CG	2.58	0.40
1:A:42:LYS:NZ	1:A:43:ASP:OD2	2.49	0.40
1:A:168:PRO:HD2	1:A:381:GLY:HA2	2.04	0.40
1:A:232:THR:O	1:A:233:THR:HG23	2.21	0.40
1:B:110:THR:O	1:B:111:VAL:C	2.62	0.40
1:B:198:ASN:O	1:B:198:ASN:OD1	2.38	0.40
1:B:253:MET:CG	1:B:254:GLY:N	2.83	0.40
1:B:509:ASN:C	1:B:527:LEU:HB2	2.46	0.40
2:C:147:LEU:C	2:C:177:TRP:CZ2	2.98	0.40
2:D:182:ALA:HA	2:D:183:PRO:HD3	1.94	0.40
1:A:42:LYS:NZ	1:A:43:ASP:N	2.68	0.40
1:A:406:GLN:HE21	1:A:432:LEU:HB2	1.86	0.40
1:A:581:TRP:HA	1:A:581:TRP:CE3	2.56	0.40
1:B:539:VAL:O	1:B:539:VAL:HG12	2.20	0.40
1:B:558:LYS:HD3	1:B:574:PRO:CB	2.51	0.40
2:C:2:SER:O	2:C:2:SER:OG	2.37	0.40
1:A:144:PHE:HA	1:A:178:PHE:O	2.22	0.40
1:A:452:ILE:O	1:A:496:GLU:OE1	2.38	0.40
1:A:570:ASP:OD2	2:C:190:ASP:OD2	2.40	0.40
1:B:232:THR:O	1:B:232:THR:HG22	2.21	0.40
1:B:290:THR:O	1:B:290:THR:HG23	2.20	0.40
2:C:60:ILE:HG23	2:C:94:GLY:O	2.20	0.40
2:D:41:LYS:O	2:D:67:PRO:HG3	2.21	0.40
1:A:496:GLU:O	1:A:498:PRO:HD3	2.22	0.40
1:A:550:LYS:HD2	1:A:561:ARG:HE	1.85	0.40
1:B:333:SER:O	1:B:334:CYS:C	2.62	0.40
1:B:484:TRP:HD1	1:B:514:TYR:CE2	2.40	0.40
1:B:489:GLU:O	1:B:490:LYS:HB3	2.21	0.40
1:B:528:THR:HB	1:B:534:PRO:HB3	2.01	0.40
2:C:45:TYR:O	2:C:62:PHE:CA	2.67	0.40

All (3) 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)
2:C:41:LYS:CE	2:D:151:TRP:O[7_645]	1.53	0.67
2:C:135:MET:SD	2:D:42:ARG:NH1[5_545]	1.57	0.63
2:C:41:LYS:NZ	2:D:151:TRP:O[7_645]	1.94	0.26

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	619/631 (98%)	508 (82%)	81 (13%)	30 (5%)	2	11
1	B	618/631 (98%)	513 (83%)	75 (12%)	30 (5%)	1	11
2	C	190/194 (98%)	145 (76%)	27 (14%)	18 (10%)	0	3
2	D	190/194 (98%)	148 (78%)	31 (16%)	11 (6%)	1	8
All	All	1617/1650 (98%)	1314 (81%)	214 (13%)	89 (6%)	1	9

All (89) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	44	THR
1	A	54	LEU
1	A	157	GLY
1	A	439	ILE
1	A	441	LYS
1	A	536	VAL
1	A	619	VAL
1	B	40	VAL
1	B	124	ASP
1	B	419	SER
1	B	531	GLY
1	B	546	SER
1	B	573	PHE
1	B	616	LEU

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Mol	Chain	Res	Type
2	C	29	VAL
2	C	31	SER
2	C	72	CYS
2	C	81	LYS
2	C	86	ILE
2	C	121	ARG
2	D	103	PHE
2	D	153	THR
2	D	191	ILE
1	A	14	PRO
1	A	30	GLY
1	A	33	LYS
1	A	36	CYS
1	A	83	PHE
1	A	171	GLY
1	A	572	GLY
1	A	620	LYS
1	B	7	LYS
1	B	11	ASP
1	B	26	ASN
1	B	32	PRO
1	B	432	LEU
1	B	481	ALA
1	B	567	LYS
1	B	605	GLY
2	C	8	PRO
2	C	58	LYS
2	C	80	GLY
2	C	134	PRO
2	C	160	HIS
2	D	57	GLU
2	D	183	PRO
1	A	15	LYS
1	A	79	ALA
1	A	468	VAL
1	A	486	GLU
1	A	568	LYS
1	A	587	ASN
1	A	616	LEU
1	B	80	ASN
1	B	247	HIS
1	B	501	GLU

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Mol	Chain	Res	Type
1	B	543	PHE
1	B	591	VAL
1	B	613	ASN
2	C	28	GLU
2	D	155	LYS
1	A	32	PRO
1	B	4	PRO
1	B	42	LYS
1	B	437	PRO
1	B	587	ASN
2	C	38	ASN
2	C	100	LEU
2	D	56	PRO
2	D	119	ASN
1	A	21	ALA
1	A	392	MET
1	A	460	LYS
1	A	618	SER
2	C	67	PRO
2	C	79	GLY
2	C	103	PHE
2	D	36	TYR
2	D	124	MET
1	B	498	PRO
1	A	3	SER
1	B	3	SER
1	B	13	ALA
2	D	37	GLY
1	B	592	VAL
1	B	572	GLY
2	C	35	ILE
1	A	485	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	522/527 (99%)	440 (84%)	82 (16%)	2	12
1	B	522/527 (99%)	439 (84%)	83 (16%)	2	12
2	C	166/168 (99%)	139 (84%)	27 (16%)	2	11
2	D	166/168 (99%)	144 (87%)	22 (13%)	4	17
All	All	1376/1390 (99%)	1162 (84%)	214 (16%)	2	12

All (214) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	5	ILE
1	A	6	ILE
1	A	7	LYS
1	A	11	ASP
1	A	12	VAL
1	A	16	THR
1	A	20	LEU
1	A	26	ASN
1	A	28	PHE
1	A	34	GLU
1	A	35	SER
1	A	37	ASN
1	A	42	LYS
1	A	51	PHE
1	A	59	ASP
1	A	61	ASP
1	A	64	THR
1	A	72	ARG
1	A	82	ASN
1	A	87	LYS
1	A	89	LYS
1	A	92	LYS
1	A	100	ILE
1	A	103	THR
1	A	125	VAL
1	A	147	TRP
1	A	158	LYS
1	A	172	VAL
1	A	183	LEU
1	A	188	GLU
1	A	194	VAL
1	A	195	LYS

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Mol	Chain	Res	Type
1	A	200	ASP
1	A	209	LEU
1	A	224	SER
1	A	228	LEU
1	A	231	SER
1	A	232	THR
1	A	235	ASN
1	A	252	THR
1	A	277	THR
1	A	283	ASP
1	A	290	THR
1	A	292	GLU
1	A	310	THR
1	A	314	ASN
1	A	329	ASN
1	A	332	GLU
1	A	333	SER
1	A	340	SER
1	A	343	LYS
1	A	349	THR
1	A	357	LYS
1	A	364	GLN
1	A	395	ILE
1	A	399	THR
1	A	405	SER
1	A	409	ILE
1	A	410	LYS
1	A	421	ASP
1	A	435	VAL
1	A	444	ILE
1	A	445	VAL
1	A	449	ILE
1	A	451	GLN
1	A	460	LYS
1	A	473	LYS
1	A	487	LEU
1	A	494	VAL
1	A	496	GLU
1	A	518	THR
1	A	529	SER
1	A	544	ASN
1	A	545	TRP

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Mol	Chain	Res	Type
1	A	551	THR
1	A	561	ARG
1	A	563	ASN
1	A	570	ASP
1	A	586	ASP
1	A	611	LEU
1	A	616	LEU
1	B	7	LYS
1	B	11	ASP
1	B	15	LYS
1	B	16	THR
1	B	31	CYS
1	B	33	LYS
1	B	34	GLU
1	B	36	CYS
1	B	38	LEU
1	B	40	VAL
1	B	47	LYS
1	B	62	GLN
1	B	65	ILE
1	B	70	LYS
1	B	78	VAL
1	B	80	ASN
1	B	87	LYS
1	B	92	LYS
1	B	103	THR
1	B	131	SER
1	B	133	ILE
1	B	135	ASP
1	B	147	TRP
1	B	148	GLU
1	B	151	ASP
1	B	158	LYS
1	B	170	THR
1	B	172	VAL
1	B	194	VAL
1	B	195	LYS
1	B	196	TYR
1	B	200	ASP
1	B	228	LEU
1	B	231	SER
1	B	232	THR

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Mol	Chain	Res	Type
1	B	235	ASN
1	B	238	LYS
1	B	241	LYS
1	B	272	SER
1	B	282	THR
1	B	286	ARG
1	B	290	THR
1	B	291	THR
1	B	299	LYS
1	B	306	THR
1	B	311	VAL
1	B	314	ASN
1	B	325	THR
1	B	333	SER
1	B	343	LYS
1	B	348	THR
1	B	357	LYS
1	B	395	ILE
1	B	400	LYS
1	B	403	ARG
1	B	429	THR
1	B	435	VAL
1	B	442	GLN
1	B	453	ARG
1	B	460	LYS
1	B	461	ASP
1	B	464	ILE
1	B	466	ARG
1	B	486	GLU
1	B	487	LEU
1	B	491	ILE
1	B	494	VAL
1	B	495	TYR
1	B	527	LEU
1	B	530	LEU
1	B	532	LEU
1	B	536	VAL
1	B	548	ASN
1	B	553	ILE
1	B	563	ASN
1	B	579	ASP
1	B	591	VAL

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Mol	Chain	Res	Type
1	B	592	VAL
1	B	594	LEU
1	B	604	LYS
1	B	614	GLN
1	B	616	LEU
1	B	624	ILE
2	C	19	ILE
2	C	33	ASN
2	C	43	ILE
2	C	57	GLU
2	C	65	THR
2	C	69	SER
2	C	71	VAL
2	C	76	LEU
2	C	100	LEU
2	C	105	VAL
2	C	119	ASN
2	C	120	HIS
2	C	121	ARG
2	C	135	MET
2	C	136	ILE
2	C	139	TYR
2	C	140	ILE
2	C	147	LEU
2	C	149	MET
2	C	152	VAL
2	C	157	ILE
2	C	158	ASN
2	C	168	ILE
2	C	178	TYR
2	C	179	ARG
2	C	188	PHE
2	C	190	ASP
2	D	2	SER
2	D	6	VAL
2	D	12	PHE
2	D	13	CYS
2	D	17	VAL
2	D	20	ARG
2	D	26	GLU
2	D	29	VAL
2	D	34	ASP

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Mol	Chain	Res	Type
2	D	36	TYR
2	D	52	MET
2	D	93	ASP
2	D	101	CYS
2	D	110	LEU
2	D	132	ARG
2	D	136	ILE
2	D	149	MET
2	D	157	ILE
2	D	161	GLN
2	D	164	PHE
2	D	178	TYR
2	D	191	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	37	ASN
1	A	80	ASN
1	A	134	HIS
1	A	143	ASN
1	A	190	GLN
1	A	235	ASN
1	A	260	GLN
1	A	314	ASN
1	A	406	GLN
1	A	544	ASN
1	B	26	ASN
1	B	62	GLN
1	B	80	ASN
1	B	143	ASN
1	B	190	GLN
1	B	235	ASN
1	B	314	ASN
1	B	413	GLN
1	B	442	GLN
1	B	509	ASN
1	B	548	ASN
1	B	563	ASN
1	B	582	ASN
1	B	587	ASN

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Mol	Chain	Res	Type
1	B	595	GLN
1	B	613	ASN
2	C	7	HIS
2	C	9	GLN
2	C	10	GLN
2	C	33	ASN
2	C	38	ASN
2	C	156	ASN
2	D	44	GLN
2	D	49	GLN
2	D	120	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 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	$\# Z > 2$
3	SO4	A	1632	-	4,4,4	0.23	0	6,6,6	0.28	0
3	SO4	B	1632	-	4,4,4	0.22	0	6,6,6	0.13	0

There are no bond length outliers.

There are no bond angle outliers.

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
3	A	1632	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	630:GLY	C	631:CYS	N	2.14
1	A	630:GLY	C	631:CYS	N	2.05

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	624/631 (98%)	0.33	40 (6%)	25	14	27, 36, 45, 74	0
1	B	623/631 (98%)	0.16	29 (4%)	36	19	28, 36, 46, 81	0
2	C	192/194 (98%)	0.69	26 (13%)	7	4	35, 37, 76, 106	0
2	D	192/194 (98%)	0.53	19 (9%)	13	7	36, 37, 75, 107	0
All	All	1631/1650 (98%)	0.33	114 (6%)	22	12	27, 37, 47, 107	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	43	ASP	11.4
1	B	196	TYR	10.1
1	B	36	CYS	6.8
1	B	433	GLY	6.6
1	A	82	ASN	4.9
1	B	37	ASN	4.9
1	B	631	CYS	4.3
1	A	470	PRO	4.2
1	A	58	GLY	4.2
1	A	472	ASP	4.2
1	B	59	ASP	4.1
2	C	180	GLY	3.9
2	C	153	THR	3.9
2	C	34	ASP	3.9
1	B	434	PRO	3.9
1	B	3	SER	3.8
1	B	624	ILE	3.8
1	B	437	PRO	3.8
2	C	77	ASP	3.7
2	C	190	ASP	3.7
1	B	41	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	536	VAL	3.6
2	C	183	PRO	3.6
1	A	31	CYS	3.4
1	A	85	PRO	3.4
1	A	91	ASP	3.3
2	C	1	CYS	3.3
1	A	32	PRO	3.2
2	C	191	ILE	3.2
1	A	24	TYR	3.2
1	A	81	TYR	3.1
1	A	39	PHE	3.1
1	A	84	PHE	3.1
1	A	623	SER	3.1
2	C	40	ILE	3.1
1	A	80	ASN	3.1
1	B	477	PRO	3.0
1	A	40	VAL	3.0
1	B	472	ASP	2.9
2	C	75	SER	2.9
1	B	82	ASN	2.9
2	D	156	ASN	2.9
1	A	43	ASP	2.8
2	D	190	ASP	2.8
2	D	111	SER	2.8
2	D	184	PRO	2.8
2	D	149	MET	2.8
2	D	182	ALA	2.8
1	A	421	ASP	2.8
2	C	188	PHE	2.7
2	D	183	PRO	2.7
2	D	141	SER	2.7
2	D	171	SER	2.7
1	A	403	ARG	2.6
2	C	23	ALA	2.6
2	D	2	SER	2.6
1	B	80	ASN	2.6
2	C	184	PRO	2.6
2	C	187	GLU	2.6
1	A	38	LEU	2.6
1	A	79	ALA	2.6
1	B	440	CYS	2.6
1	A	430	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
2	D	117	SER	2.6
2	C	32	GLY	2.6
1	B	40	VAL	2.6
2	C	113	THR	2.6
1	B	35	SER	2.5
1	A	310	THR	2.5
1	A	545	TRP	2.5
1	B	597	GLY	2.5
2	D	32	GLY	2.5
1	A	16	THR	2.5
2	C	24	VAL	2.5
1	B	418	ALA	2.4
1	A	86	ARG	2.4
1	A	87	LYS	2.4
2	C	175	CYS	2.4
2	D	187	GLU	2.4
1	A	54	LEU	2.4
2	D	112	THR	2.3
2	C	33	ASN	2.3
1	A	320	CYS	2.3
1	B	516	ALA	2.3
2	D	34	ASP	2.3
1	A	83	PHE	2.3
1	B	470	PRO	2.3
2	D	137	PRO	2.3
1	B	60	LEU	2.3
2	C	38	ASN	2.3
1	A	469	THR	2.3
1	B	38	LEU	2.3
1	A	574	PRO	2.3
1	B	32	PRO	2.3
2	C	55	GLY	2.3
1	A	588	LEU	2.3
2	C	92	GLY	2.2
2	D	113	THR	2.2
1	A	211	ASN	2.2
1	B	511	TYR	2.2
1	B	31	CYS	2.2
2	D	101	CYS	2.2
2	C	182	ALA	2.2
2	D	185	LYS	2.2
1	A	35	SER	2.1

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Mol	Chain	Res	Type	RSRZ
2	C	47	ILE	2.1
2	C	181	ALA	2.1
1	A	75	ASN	2.1
1	A	321	VAL	2.1
2	C	70	ALA	2.1
1	B	438	GLU	2.1
1	A	431	THR	2.0
1	A	18	LYS	2.0
1	A	485	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	1632	5/5	0.94	0.07	63,64,65,66	0
3	SO4	B	1632	5/5	0.94	0.06	74,75,75,75	0
4	ZN	A	1633	1/1	0.98	0.03	61,61,61,61	0
5	CA	A	1635	1/1	0.98	0.07	58,58,58,58	0
5	CA	B	1635	1/1	0.98	0.04	40,40,40,40	0
4	ZN	A	1634	1/1	0.99	0.06	72,72,72,72	0
4	ZN	B	1633	1/1	0.99	0.02	50,50,50,50	0
4	ZN	B	1634	1/1	1.00	0.07	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.