



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 20, 2024 – 06:55 AM EST

PDB ID : 4M64
Title : 3D crystal structure of Na⁺/melibiose symporter of Salmonella typhimurium
Authors : Ethayathulla, A.S.; Guan, L.
Deposited on : 2013-08-08
Resolution : 3.35 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

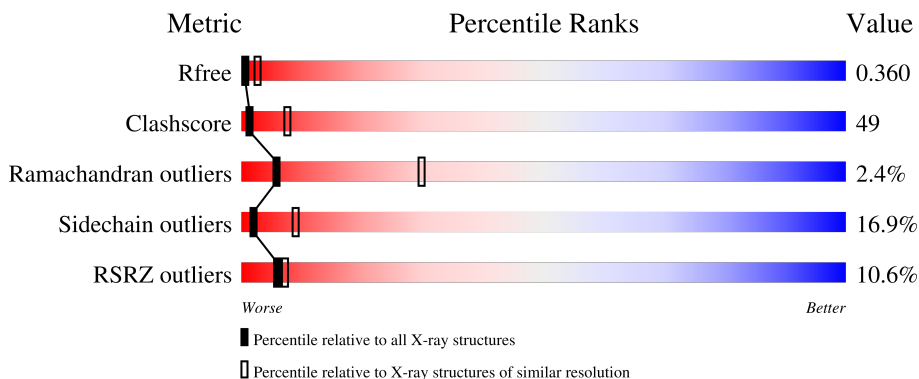
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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}	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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	486	
1	B	486	
1	C	486	
1	D	486	

2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 12982 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 Melibiose carrier protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	448	Total 3442	C 2295	N 540	O 585	S 22	0	0	0
1	B	426	Total 3258	C 2176	N 503	O 558	S 21	0	0	0
1	C	431	Total 3352	C 2242	N 520	O 568	S 22	0	0	0
1	D	382	Total 2930	C 1965	N 449	O 497	S 19	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	LEU	engineered mutation	UNP P30878
A	477	HIS	-	expression tag	UNP P30878
A	478	HIS	-	expression tag	UNP P30878
A	479	HIS	-	expression tag	UNP P30878
A	480	HIS	-	expression tag	UNP P30878
A	481	HIS	-	expression tag	UNP P30878
A	482	HIS	-	expression tag	UNP P30878
A	483	HIS	-	expression tag	UNP P30878
A	484	HIS	-	expression tag	UNP P30878
A	485	HIS	-	expression tag	UNP P30878
A	486	HIS	-	expression tag	UNP P30878
B	5	MET	LEU	engineered mutation	UNP P30878
B	477	HIS	-	expression tag	UNP P30878
B	478	HIS	-	expression tag	UNP P30878
B	479	HIS	-	expression tag	UNP P30878
B	480	HIS	-	expression tag	UNP P30878
B	481	HIS	-	expression tag	UNP P30878
B	482	HIS	-	expression tag	UNP P30878
B	483	HIS	-	expression tag	UNP P30878
B	484	HIS	-	expression tag	UNP P30878
B	485	HIS	-	expression tag	UNP P30878

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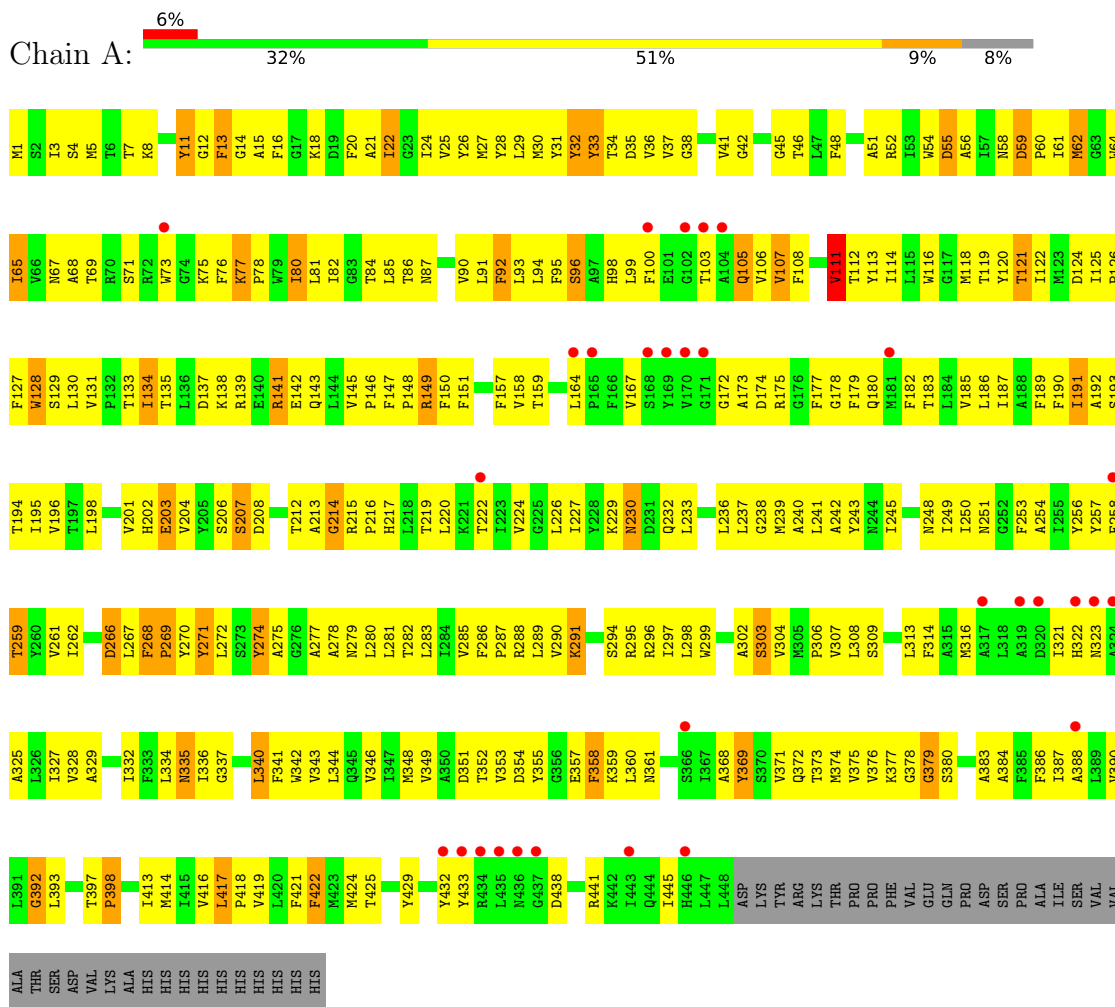
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Chain	Residue	Modelled	Actual	Comment	Reference
B	486	HIS	-	expression tag	UNP P30878
C	5	MET	LEU	engineered mutation	UNP P30878
C	477	HIS	-	expression tag	UNP P30878
C	478	HIS	-	expression tag	UNP P30878
C	479	HIS	-	expression tag	UNP P30878
C	480	HIS	-	expression tag	UNP P30878
C	481	HIS	-	expression tag	UNP P30878
C	482	HIS	-	expression tag	UNP P30878
C	483	HIS	-	expression tag	UNP P30878
C	484	HIS	-	expression tag	UNP P30878
C	485	HIS	-	expression tag	UNP P30878
C	486	HIS	-	expression tag	UNP P30878
D	5	MET	LEU	engineered mutation	UNP P30878
D	477	HIS	-	expression tag	UNP P30878
D	478	HIS	-	expression tag	UNP P30878
D	479	HIS	-	expression tag	UNP P30878
D	480	HIS	-	expression tag	UNP P30878
D	481	HIS	-	expression tag	UNP P30878
D	482	HIS	-	expression tag	UNP P30878
D	483	HIS	-	expression tag	UNP P30878
D	484	HIS	-	expression tag	UNP P30878
D	485	HIS	-	expression tag	UNP P30878
D	486	HIS	-	expression tag	UNP P30878

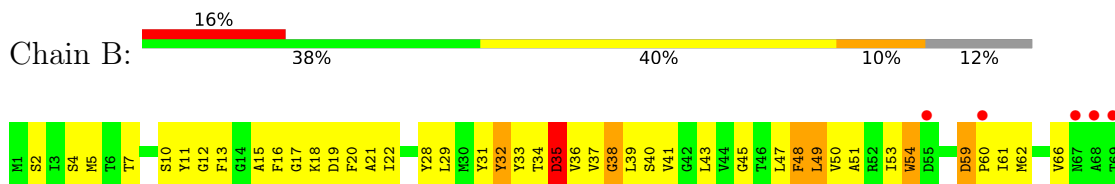
3 Residue-property plots

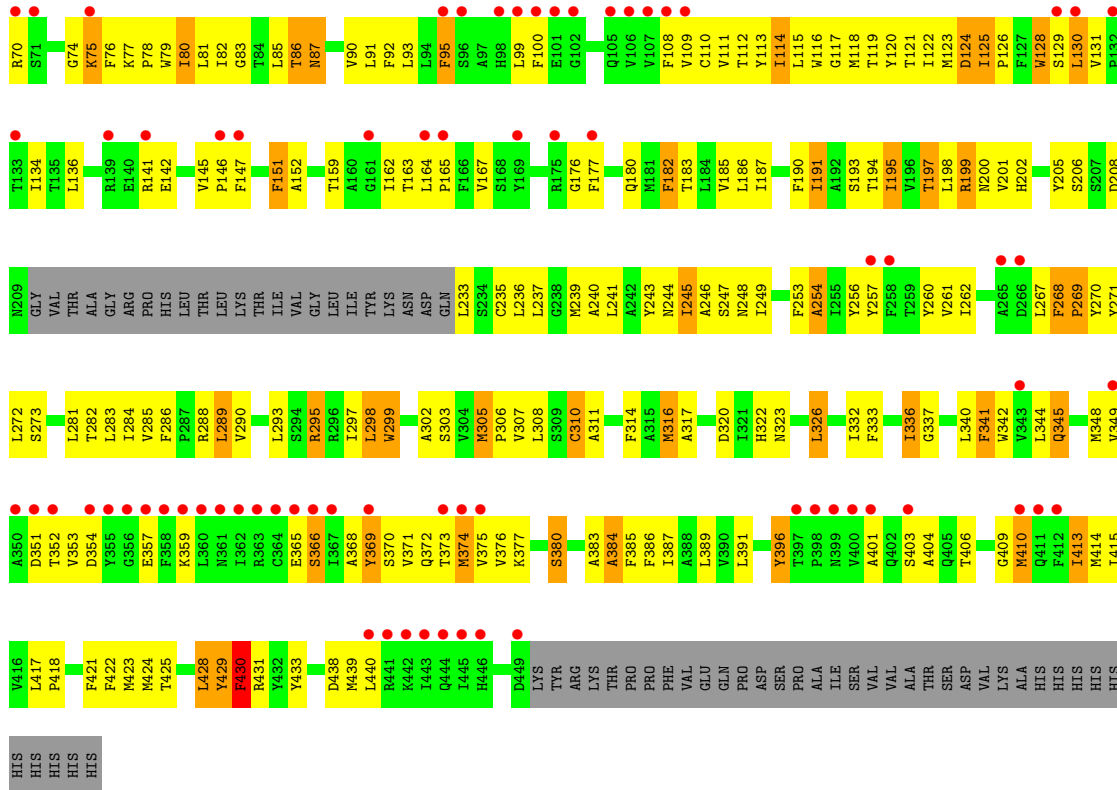
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

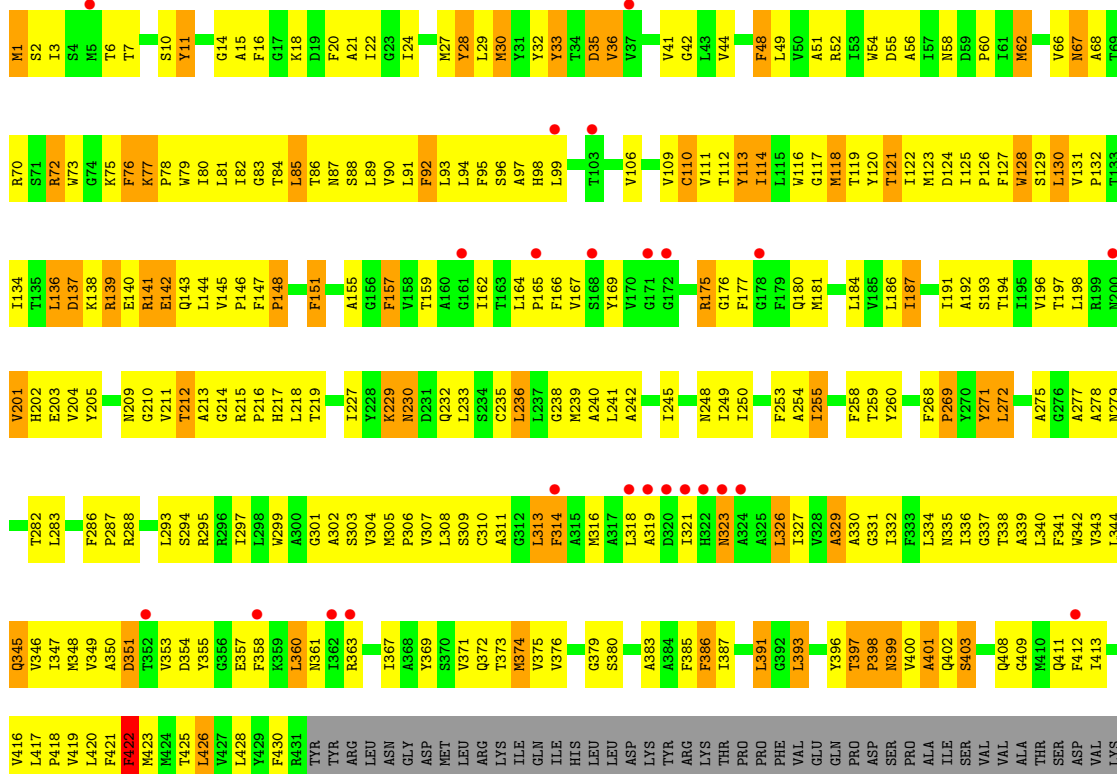


- Molecule 1: Melibiose carrier protein





● Molecule 1: Melibiose carrier protein



ALA
HIS
HIS
HIS
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HIS
HIS

● Molecule 1: Melibiose carrier protein



M1 S2 I3 M5 T6 T7 K8 Y11 G12 F13 G14 A15 F16 G17 K18 D19 F20 A21 I22 G23 I24 V25 Y26 M27 Y28 L29 Y33 G38 L47 F48 A51 R52 I53 W54 D55 D59 P60 I61 M62 G63 W64 I65 V66 M67 A68 T69 R70 S71 R72 W73 G74 K75 F76

K77 F78 W79 R80 L81 I82 G83 T84 L85 L88 T86 S88 L89 W90 I91 F92 F93 L94 L99 S95 SER ALA HIS LEU PHE GLU GLY THR ALA GLN VAL VAL PHE V109 C110 V111 T112 Y113 I114 L115 W116 G117 M118 T119 Y120 I121 I122 M123 D124 I125 I126 F127 M128 S129 L130 W131 V132 T133 I134 T135 L136

D137 K138 R139 E140 R141 E142 Q143 L144 V145 F146 P148 R149 F150 F151 A152 S153 L154 A155 G156 F157 V158 T159 A160 G161 I162 T163 L164 P165 F166 V167 S168 Y169 V170 G171 R175 F182 T183 L184 V185 L186 I187 F190 I191 A192 S193 T194 I195 V196 V197 L198 R199 W200 V201 H202 E203 W204

Y205 D208 N209 GLY THR ALA ARG PRO HIS LEU THR LEU LYS THR ILE VAL GLY LEU ILE TYR LYS ASN ASP GLN L233 S234 C235 L236 L237 G238 M239 A240 N244 I245 A246 N251 Y257 F258 T259 V261 I332 F333 L334 I335 A339 L340 F341 W342 V343 L344 Q345 M348 V349 A350 D351

I284 V285 F286 L289 K291 M292 L293 S294 R295 R296 I297 L298 W299 A300 G301 S303 V304 M305 P306 S309 C310 L313 M316 A317 L318 A319 D320 I321 H322 N323 A324 A325 L326 I327 V328 I332 F333 L334 I335 A339 L340 F341 W342 V343 L344 Q345 M348 V349 A350 D351

T352 V353 D354 Y355 G356 E357 F358 K359 L360 N361 I362 R363 C364 E365 S366 I367 A368 S370 V371 Q372 M374 V375 S380 A383 A384 F385 F386 I387 L388 V389 L391 G395 Y396 T397 P398 ASN VAL ALA GLN SER ALA THR LEU GLN MET LYS ALA HIS I413 M414 I415 V416

L417 P418 V419 L420 F421 F422 L426 F430 ARG TYR ARG LEU ASN GLY MET LEU ARG LYS ILE ILE HIS LEU LEU LYS TYR ARG ARG LYS VAL GLU PRO SER PRO ILE SER VAL VAL THR SER ASP VAL THR ASP VAL LYS ALA HIS HIS HIS

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4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	127.21Å 127.21Å 206.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.64 – 3.35 38.64 – 3.35	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.64-3.35) 99.5 (38.64-3.35)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	47.41 (at 3.32Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.312 , 0.359 0.311 , 0.360	Depositor DCC
R_{free} test set	2712 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	94.7	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.16 , 85.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	0.011 for -h,-k,l 0.039 for h,-h-k,-l 0.012 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	12982	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.36 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3433e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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	0.63	0/3530	0.87	2/4813 (0.0%)
1	B	0.60	0/3342	0.82	3/4561 (0.1%)
1	C	0.66	0/3440	0.91	1/4689 (0.0%)
1	D	0.59	0/3004	0.81	1/4097 (0.0%)
All	All	0.62	0/13316	0.86	7/18160 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	4
1	C	0	4
1	D	0	1
All	All	0	10

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	ARG	NE-CZ-NH1	5.77	123.19	120.30
1	C	55	ASP	CB-CG-OD2	-5.76	113.11	118.30
1	A	55	ASP	CB-CG-OD2	5.43	123.18	118.30
1	B	308	LEU	CA-CB-CG	5.24	127.36	115.30
1	A	340	LEU	CB-CG-CD2	-5.21	102.14	111.00
1	B	298	LEU	CA-CB-CG	5.17	127.20	115.30
1	D	272	LEU	CA-CB-CG	5.16	127.16	115.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	65	ILE	Peptide
1	B	254	ALA	Peptide
1	B	38	GLY	Peptide
1	B	429	TYR	Peptide
1	B	74	GLY	Peptide
1	C	201	VAL	Peptide
1	C	329	ALA	Peptide
1	C	399	ASN	Peptide
1	C	68	ALA	Peptide
1	D	146	PRO	Peptide

5.2 Too-close contacts [\(i\)](#)

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	3442	0	3479	346	0
1	B	3258	0	3249	299	0
1	C	3352	0	3433	352	0
1	D	2930	0	2965	285	0
All	All	12982	0	13126	1273	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 49.

All (1273) 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:D:299:TRP:CB	1:D:344:LEU:HD13	1.63	1.26
1:D:86:THR:CG2	1:D:115:LEU:HG	1.65	1.26
1:C:75:LYS:HG3	1:C:205:TYR:CB	1.77	1.15
1:D:299:TRP:HB2	1:D:344:LEU:CD1	1.77	1.15
1:C:128:TRP:CH2	1:C:373:THR:HG21	1.83	1.13
1:A:3:ILE:HG23	1:A:203:GLU:HG3	1.28	1.11
1:B:93:LEU:HD13	1:B:112:THR:HG21	1.32	1.11
1:D:86:THR:HG21	1:D:115:LEU:HG	1.24	1.09
1:C:250:ILE:O	1:C:254:ALA:HB2	1.52	1.07
1:C:93:LEU:CD2	1:C:112:THR:HB	1.85	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:ILE:HG23	1:A:191:ILE:HG13	1.36	1.06
1:B:352:THR:HA	1:B:433:TYR:OH	1.55	1.06
1:B:306:PRO:HG2	1:B:422:PHE:CD2	1.90	1.05
1:A:24:ILE:HD12	1:A:186:LEU:HD13	1.38	1.05
1:D:75:LYS:HE3	1:D:76:PHE:H	1.18	1.05
1:D:80:ILE:HG22	1:D:126:PRO:HB2	1.32	1.05
1:B:141:ARG:NH1	1:B:354:ASP:HB2	1.72	1.04
1:A:183:THR:HG22	1:A:187:ILE:HD12	1.36	1.04
1:C:175:ARG:HG3	1:C:175:ARG:HH11	1.22	1.03
1:D:353:VAL:HG12	1:D:357:GLU:CB	1.88	1.03
1:D:75:LYS:HG3	1:D:202:HIS:HA	1.38	1.02
1:A:417:LEU:HD23	1:A:418:PRO:HD3	1.37	1.01
1:D:75:LYS:HE3	1:D:76:PHE:N	1.76	1.01
1:D:302:ALA:HA	1:D:305:MET:SD	2.01	1.01
1:D:349:VAL:O	1:D:353:VAL:HG23	1.63	0.99
1:B:352:THR:HA	1:B:433:TYR:CZ	1.97	0.99
1:D:313:LEU:HD12	1:D:313:LEU:O	1.63	0.98
1:C:397:THR:OG1	1:C:398:PRO:HD2	1.61	0.98
1:B:306:PRO:HG2	1:B:422:PHE:CE2	1.99	0.97
1:C:282:THR:HG21	1:C:337:GLY:O	1.63	0.97
1:A:3:ILE:HG23	1:A:203:GLU:CG	1.94	0.97
1:D:79:TRP:CE3	1:D:126:PRO:HB3	1.98	0.97
1:D:137:ASP:O	1:D:138:LYS:HG3	1.61	0.97
1:A:58:ASN:CG	1:A:121:THR:HG21	1.83	0.97
1:D:141:ARG:O	1:D:141:ARG:HG2	1.63	0.97
1:C:142:GLU:O	1:C:146:PRO:HG3	1.65	0.96
1:B:141:ARG:HH12	1:B:354:ASP:HB2	1.27	0.96
1:C:106:VAL:O	1:C:110:CYS:HB2	1.65	0.96
1:B:77:LYS:HA	1:B:201:VAL:HG11	1.45	0.96
1:B:414:MET:O	1:B:418:PRO:HD2	1.67	0.95
1:D:299:TRP:O	1:D:303:SER:HB2	1.67	0.95
1:D:310:CYS:O	1:D:310:CYS:SG	2.25	0.94
1:C:128:TRP:CZ2	1:C:373:THR:HG21	2.02	0.94
1:A:105:GLN:HE21	1:A:105:GLN:N	1.65	0.94
1:D:296:ARG:HA	1:D:344:LEU:HD11	1.45	0.94
1:C:11:TYR:CE2	1:C:130:LEU:HB3	2.03	0.94
1:A:417:LEU:HD23	1:A:418:PRO:CD	1.98	0.93
1:A:283:LEU:O	1:A:287:PRO:HG2	1.69	0.93
1:C:139:ARG:HD2	1:C:139:ARG:N	1.82	0.93
1:C:82:ILE:O	1:C:86:THR:HG23	1.69	0.93
1:A:1:MET:SD	1:A:3:ILE:HB	2.08	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:VAL:HG11	1:B:295:ARG:HG2	1.50	0.93
1:A:3:ILE:CG2	1:A:203:GLU:HG3	1.98	0.92
1:A:7:THR:HG23	1:A:201:VAL:HG13	1.46	0.92
1:D:86:THR:HG22	1:D:90:VAL:CG2	1.99	0.91
1:B:47:LEU:O	1:B:50:VAL:HG12	1.70	0.91
1:C:24:ILE:HD12	1:C:186:LEU:HD13	1.49	0.91
1:C:139:ARG:HH22	1:C:358:PHE:HB2	1.35	0.91
1:B:302:ALA:HA	1:B:305:MET:SD	2.09	0.91
1:A:77:LYS:HG3	1:A:201:VAL:HB	1.53	0.91
1:B:320:ASP:HB2	1:B:323:ASN:CB	2.01	0.91
1:C:78:PRO:HA	1:C:81:LEU:HD23	1.52	0.91
1:C:387:ILE:HG23	1:C:417:LEU:HD11	1.54	0.90
1:C:75:LYS:HG2	1:C:76:PHE:H	1.37	0.90
1:B:112:THR:O	1:B:115:LEU:HB3	1.70	0.89
1:D:236:LEU:HD22	1:D:348:MET:HB3	1.51	0.89
1:C:7:THR:O	1:C:11:TYR:HB2	1.73	0.88
1:D:150:PHE:HD1	1:D:283:LEU:CD2	1.86	0.88
1:B:62:MET:CE	1:B:122:ILE:HD11	2.03	0.88
1:C:93:LEU:HD21	1:C:112:THR:HB	1.54	0.88
1:B:32:TYR:O	1:B:32:TYR:CD1	2.27	0.88
1:D:236:LEU:HD23	1:D:349:VAL:HG23	1.56	0.88
1:B:32:TYR:O	1:B:32:TYR:HD1	1.56	0.87
1:C:21:ALA:HA	1:C:186:LEU:HD11	1.56	0.87
1:A:241:LEU:HD23	1:A:379:GLY:HA3	1.55	0.87
1:D:86:THR:HG21	1:D:115:LEU:CG	2.04	0.87
1:B:352:THR:HA	1:B:433:TYR:CE2	2.10	0.86
1:D:86:THR:HG22	1:D:90:VAL:HG21	1.56	0.86
1:A:261:VAL:HG21	1:A:328:VAL:HG23	1.57	0.86
1:A:397:THR:CG2	1:A:398:PRO:HD2	2.06	0.86
1:C:215:ARG:N	1:C:216:PRO:HD2	1.91	0.86
1:D:414:MET:O	1:D:418:PRO:HD2	1.75	0.86
1:C:75:LYS:CG	1:C:205:TYR:CB	2.53	0.85
1:A:417:LEU:CD2	1:A:418:PRO:HD3	2.05	0.85
1:B:254:ALA:O	1:B:257:TYR:HB3	1.74	0.85
1:D:301:GLY:O	1:D:305:MET:HG3	1.77	0.85
1:C:287:PRO:HG3	1:C:340:LEU:HD22	1.59	0.85
1:A:250:ILE:O	1:A:254:ALA:HB2	1.77	0.85
1:B:32:TYR:CD1	1:B:176:GLY:HA2	2.12	0.85
1:A:87:ASN:HB2	1:A:119:THR:HG21	1.59	0.84
1:B:299:TRP:CE3	1:B:429:TYR:CE2	2.65	0.84
1:B:245:ILE:HG21	1:B:421:PHE:CD2	2.13	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:LYS:HD3	1:B:201:VAL:HB	1.60	0.84
1:A:76:PHE:O	1:A:80:ILE:HG23	1.78	0.84
1:A:344:LEU:O	1:A:348:MET:HG2	1.78	0.84
1:A:3:ILE:HG22	1:A:203:GLU:HB3	1.58	0.84
1:C:3:ILE:HG22	1:C:204:VAL:HG22	1.58	0.84
1:D:296:ARG:HG3	1:D:344:LEU:HD21	1.60	0.83
1:A:202:HIS:O	1:A:203:GLU:OE1	1.97	0.83
1:D:299:TRP:CB	1:D:344:LEU:CD1	2.45	0.83
1:D:244:ASN:CB	1:D:376:VAL:HG11	2.08	0.83
1:C:240:ALA:HB3	1:C:376:VAL:HG21	1.58	0.83
1:C:387:ILE:HG23	1:C:417:LEU:CD1	2.08	0.83
1:A:58:ASN:ND2	1:A:121:THR:HG21	1.93	0.82
1:A:325:ALA:O	1:A:328:VAL:HG12	1.80	0.82
1:C:175:ARG:HD2	1:C:175:ARG:O	1.80	0.82
1:C:239:MET:HG2	1:C:425:THR:HA	1.62	0.82
1:A:86:THR:HG22	1:A:119:THR:OG1	1.80	0.81
1:A:167:VAL:HG23	1:A:182:PHE:CE2	2.14	0.81
1:B:307:VAL:O	1:B:311:ALA:HB2	1.80	0.81
1:A:189:PHE:O	1:A:192:ALA:HB3	1.80	0.81
1:C:15:ALA:HB2	1:C:127:PHE:CE2	2.15	0.81
1:C:140:GLU:HG2	1:C:143:GLN:HB2	1.60	0.81
1:C:212:THR:O	1:C:213:ALA:C	2.18	0.81
1:B:35:ASP:HA	1:B:38:GLY:HA2	1.63	0.80
1:B:39:LEU:HD22	1:B:41:VAL:HG23	1.63	0.80
1:C:387:ILE:CG2	1:C:417:LEU:HD21	2.12	0.80
1:D:125:ILE:HG23	1:D:369:TYR:CD1	2.16	0.80
1:B:87:ASN:HB2	1:B:119:THR:HG21	1.63	0.80
1:D:386:PHE:O	1:D:390:VAL:HG22	1.82	0.80
1:C:387:ILE:O	1:C:391:LEU:HD23	1.81	0.79
1:D:244:ASN:HB3	1:D:376:VAL:HG11	1.64	0.79
1:D:384:ALA:O	1:D:387:ILE:HG13	1.82	0.79
1:C:240:ALA:CB	1:C:376:VAL:HG21	2.12	0.79
1:C:85:LEU:HD11	1:C:194:THR:OG1	1.82	0.79
1:C:144:LEU:O	1:C:148:PRO:HD2	1.82	0.79
1:D:129:SER:HB3	1:D:369:TYR:OH	1.83	0.79
1:A:15:ALA:HB2	1:A:127:PHE:CZ	2.16	0.78
1:C:139:ARG:NH2	1:C:358:PHE:HB2	1.97	0.78
1:C:283:LEU:O	1:C:287:PRO:CD	2.32	0.78
1:D:299:TRP:HB2	1:D:344:LEU:HD13	0.82	0.78
1:C:307:VAL:O	1:C:310:CYS:HB3	1.83	0.78
1:C:77:LYS:HA	1:C:80:ILE:HG12	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:ASP:HB2	1:B:323:ASN:HB2	1.66	0.78
1:A:78:PRO:HA	1:A:81:LEU:HB3	1.66	0.78
1:C:93:LEU:CD2	1:C:112:THR:CB	2.62	0.78
1:D:150:PHE:CD1	1:D:283:LEU:HD23	2.18	0.78
1:C:139:ARG:N	1:C:139:ARG:CD	2.46	0.77
1:C:250:ILE:O	1:C:254:ALA:CB	2.30	0.77
1:A:8:LYS:HA	1:A:11:TYR:HB2	1.65	0.77
1:D:3:ILE:O	1:D:7:THR:HG23	1.84	0.77
1:A:141:ARG:HG3	1:A:142:GLU:N	1.98	0.77
1:D:25:VAL:O	1:D:29:LEU:HG	1.85	0.77
1:A:270:TYR:O	1:A:274:TYR:HB2	1.83	0.77
1:A:15:ALA:HB2	1:A:127:PHE:HZ	1.49	0.76
1:C:236:LEU:HD13	1:C:349:VAL:HA	1.65	0.76
1:A:257:TYR:O	1:A:261:VAL:HG12	1.85	0.76
1:B:320:ASP:HB2	1:B:323:ASN:HB3	1.65	0.76
1:A:183:THR:HG22	1:A:187:ILE:CD1	2.15	0.76
1:C:142:GLU:O	1:C:146:PRO:CG	2.33	0.76
1:A:128:TRP:CD1	1:A:369:TYR:HE1	2.02	0.76
1:B:122:ILE:O	1:B:126:PRO:HD2	1.86	0.76
1:D:150:PHE:HD1	1:D:283:LEU:HD23	1.47	0.76
1:A:90:VAL:HG21	1:A:116:TRP:HB2	1.69	0.75
1:B:75:LYS:O	1:B:78:PRO:HD2	1.87	0.75
1:B:163:THR:HG22	1:B:182:PHE:CZ	2.22	0.75
1:B:299:TRP:CD1	1:B:344:LEU:HB2	2.22	0.75
1:C:387:ILE:HG21	1:C:417:LEU:HD21	1.68	0.75
1:C:387:ILE:HD12	1:C:417:LEU:HD21	1.68	0.74
1:C:78:PRO:HA	1:C:81:LEU:CD2	2.15	0.74
1:C:88:SER:O	1:C:92:PHE:HB2	1.86	0.74
1:C:75:LYS:HD2	1:C:202:HIS:O	1.88	0.74
1:D:129:SER:CB	1:D:369:TYR:OH	2.35	0.74
1:D:245:ILE:HG12	1:D:376:VAL:HG23	1.68	0.74
1:C:58:ASN:CG	1:C:121:THR:HG21	2.08	0.74
1:A:149:ARG:CB	1:A:283:LEU:HD21	2.18	0.74
1:C:374:MET:HE1	1:C:375:VAL:HG12	1.69	0.74
1:C:95:PHE:O	1:C:180:GLN:HG2	1.87	0.73
1:C:397:THR:OG1	1:C:398:PRO:CD	2.35	0.73
1:D:125:ILE:HG23	1:D:369:TYR:CE1	2.22	0.73
1:A:7:THR:O	1:A:11:TYR:HB2	1.88	0.73
1:B:39:LEU:HD23	1:B:39:LEU:O	1.87	0.73
1:C:33:TYR:O	1:C:33:TYR:CD1	2.42	0.73
1:C:282:THR:HG23	1:C:286:PHE:CD1	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:143:GLN:HA	1:C:295:ARG:HH21	1.54	0.73
1:A:92:PHE:CD1	1:A:187:ILE:HD13	2.23	0.73
1:C:283:LEU:O	1:C:287:PRO:HD2	1.88	0.73
1:B:417:LEU:O	1:B:421:PHE:N	2.21	0.72
1:C:44:VAL:O	1:C:48:PHE:N	2.22	0.72
1:C:56:ALA:O	1:C:374:MET:HE3	1.89	0.72
1:D:246:ALA:HB1	1:D:422:PHE:CE1	2.24	0.72
1:A:28:TYR:CZ	1:A:179:PHE:HB2	2.25	0.72
1:A:268:PHE:N	1:A:269:PRO:HD3	2.05	0.72
1:A:80:ILE:HG22	1:A:126:PRO:HB3	1.71	0.72
1:D:75:LYS:O	1:D:78:PRO:HD2	1.90	0.72
1:C:211:VAL:HG12	1:C:212:THR:H	1.53	0.72
1:A:286:PHE:HA	1:A:289:LEU:HD12	1.70	0.72
1:B:299:TRP:CE3	1:B:429:TYR:CD2	2.78	0.72
1:C:3:ILE:HG22	1:C:204:VAL:CG2	2.19	0.72
1:D:244:ASN:HD22	1:D:376:VAL:HG11	1.54	0.72
1:D:86:THR:CG2	1:D:115:LEU:CG	2.57	0.71
1:A:3:ILE:CG2	1:A:203:GLU:CG	2.63	0.71
1:B:244:ASN:ND2	1:B:376:VAL:HG11	2.04	0.71
1:A:215:ARG:N	1:A:216:PRO:HD2	2.04	0.71
1:C:316:MET:O	1:C:319:ALA:HB3	1.89	0.71
1:B:77:LYS:HB2	1:B:201:VAL:HG12	1.71	0.71
1:C:308:LEU:O	1:C:309:SER:C	2.29	0.71
1:D:138:LYS:HD2	1:D:138:LYS:O	1.91	0.71
1:D:380:SER:HA	1:D:383:ALA:HB3	1.72	0.71
1:B:10:SER:O	1:B:13:PHE:HB2	1.91	0.71
1:C:145:VAL:N	1:C:146:PRO:HD2	2.06	0.71
1:D:86:THR:HG22	1:D:90:VAL:HG23	1.71	0.71
1:B:77:LYS:HA	1:B:201:VAL:CG1	2.21	0.71
1:B:298:LEU:HD12	1:B:340:LEU:HD22	1.73	0.71
1:D:353:VAL:CG1	1:D:357:GLU:CB	2.68	0.71
1:A:249:ILE:O	1:A:253:PHE:HB2	1.91	0.70
1:A:282:THR:HG23	1:A:286:PHE:CD1	2.26	0.70
1:A:397:THR:HG23	1:A:398:PRO:HD2	1.72	0.70
1:B:320:ASP:CB	1:B:323:ASN:HB2	2.20	0.70
1:D:271:TYR:CD1	1:D:332:ILE:HD11	2.24	0.70
1:C:391:LEU:HD13	1:C:413:ILE:HD13	1.73	0.70
1:C:30:MET:O	1:C:33:TYR:HB3	1.92	0.70
1:C:128:TRP:CE2	1:C:346:VAL:HG11	2.26	0.70
1:B:142:GLU:HA	1:B:145:VAL:HG23	1.74	0.70
1:D:125:ILE:CG2	1:D:369:TYR:CE1	2.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:ILE:O	1:A:65:ILE:HG12	1.92	0.70
1:C:143:GLN:O	1:C:147:PHE:CD1	2.44	0.70
1:B:77:LYS:HB2	1:B:201:VAL:CG1	2.21	0.69
1:B:131:VAL:O	1:B:134:ILE:HG12	1.92	0.69
1:A:397:THR:HG22	1:A:398:PRO:HD2	1.74	0.69
1:B:141:ARG:NH1	1:B:354:ASP:CB	2.52	0.69
1:C:334:LEU:HD23	1:C:334:LEU:O	1.92	0.69
1:D:153:SER:CB	1:D:283:LEU:HD22	2.22	0.69
1:A:77:LYS:HG3	1:A:201:VAL:CB	2.20	0.69
1:C:301:GLY:O	1:C:305:MET:N	2.25	0.69
1:A:187:ILE:HG23	1:A:191:ILE:CG1	2.19	0.69
1:D:246:ALA:HB1	1:D:422:PHE:CZ	2.27	0.69
1:A:67:ASN:HB3	1:A:217:HIS:CD2	2.28	0.69
1:C:128:TRP:CE3	1:C:346:VAL:HG21	2.27	0.69
1:C:175:ARG:O	1:C:177:PHE:N	2.25	0.69
1:D:391:LEU:HD22	1:D:413:ILE:HD12	1.75	0.69
1:B:51:ALA:HA	1:B:54:TRP:CE3	2.27	0.69
1:A:243:TYR:CE1	1:A:341:PHE:HD2	2.11	0.68
1:C:240:ALA:HB3	1:C:376:VAL:CG2	2.23	0.68
1:C:77:LYS:HB2	1:C:201:VAL:HG21	1.76	0.68
1:C:162:ILE:C	1:C:165:PRO:HD2	2.13	0.68
1:D:77:LYS:O	1:D:81:LEU:CB	2.42	0.68
1:D:380:SER:O	1:D:384:ALA:N	2.26	0.68
1:B:376:VAL:HG23	1:B:377:LYS:HG3	1.75	0.68
1:A:283:LEU:O	1:A:287:PRO:CG	2.41	0.68
1:C:90:VAL:HG11	1:C:116:TRP:N	2.09	0.68
1:C:241:LEU:HD23	1:C:376:VAL:O	1.94	0.68
1:A:346:VAL:HG12	1:A:369:TYR:CE1	2.29	0.68
1:B:122:ILE:HG23	1:B:126:PRO:HG2	1.74	0.68
1:C:27:MET:SD	1:C:159:THR:HG22	2.34	0.68
1:D:147:PHE:HD1	1:D:150:PHE:HD2	1.42	0.68
1:A:95:PHE:O	1:A:180:GLN:CG	2.42	0.68
1:B:62:MET:HE1	1:B:122:ILE:HD11	1.72	0.68
1:B:320:ASP:CB	1:B:323:ASN:CB	2.72	0.68
1:C:93:LEU:HD23	1:C:112:THR:CB	2.23	0.68
1:D:75:LYS:HD2	1:D:201:VAL:HG12	1.75	0.68
1:A:51:ALA:HA	1:A:54:TRP:CG	2.29	0.68
1:A:124:ASP:O	1:A:128:TRP:NE1	2.27	0.68
1:D:83:GLY:HA3	1:D:122:ILE:HD11	1.74	0.68
1:D:147:PHE:CD1	1:D:150:PHE:HD2	2.12	0.68
1:A:21:ALA:HA	1:A:186:LEU:HD11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:THR:HA	1:A:122:ILE:HG22	1.74	0.67
1:B:295:ARG:HB3	1:B:344:LEU:HD11	1.76	0.67
1:B:414:MET:O	1:B:417:LEU:HB2	1.94	0.67
1:D:75:LYS:CE	1:D:76:PHE:H	2.02	0.67
1:D:415:ILE:O	1:D:418:PRO:HG2	1.94	0.67
1:B:77:LYS:CA	1:B:201:VAL:HG11	2.21	0.67
1:B:99:LEU:HD11	1:B:177:PHE:HB2	1.76	0.67
1:C:347:ILE:HA	1:C:369:TYR:OH	1.94	0.67
1:A:32:TYR:O	1:A:36:VAL:HG23	1.93	0.67
1:A:92:PHE:CE1	1:A:187:ILE:HD13	2.29	0.67
1:D:296:ARG:CG	1:D:344:LEU:HD21	2.24	0.67
1:C:347:ILE:HD13	1:C:369:TYR:OH	1.94	0.67
1:A:28:TYR:CE1	1:A:179:PHE:HB2	2.30	0.67
1:C:32:TYR:HA	1:C:35:ASP:HB2	1.75	0.67
1:C:72:ARG:HD3	1:D:109:VAL:HG13	1.74	0.67
1:C:346:VAL:HG12	1:C:369:TYR:CD2	2.30	0.67
1:B:244:ASN:HB3	1:B:376:VAL:HB	1.76	0.67
1:A:192:ALA:HA	1:A:195:ILE:HG22	1.77	0.67
1:B:244:ASN:HD22	1:B:376:VAL:CB	2.07	0.67
1:D:77:LYS:O	1:D:77:LYS:HD3	1.95	0.67
1:A:149:ARG:HB3	1:A:283:LEU:HD21	1.77	0.67
1:B:352:THR:CA	1:B:433:TYR:OH	2.39	0.67
1:C:128:TRP:CZ3	1:C:346:VAL:HG21	2.30	0.67
1:D:77:LYS:O	1:D:81:LEU:HB3	1.95	0.67
1:B:86:THR:HG21	1:B:115:LEU:HD11	1.77	0.67
1:D:122:ILE:O	1:D:126:PRO:HD2	1.95	0.67
1:A:278:ALA:HB1	1:A:336:ILE:HG22	1.77	0.66
1:D:244:ASN:HD22	1:D:376:VAL:CG1	2.07	0.66
1:D:391:LEU:HB2	1:D:413:ILE:HG13	1.78	0.66
1:C:80:ILE:O	1:C:84:THR:HG23	1.95	0.66
1:B:417:LEU:O	1:B:421:PHE:HB2	1.95	0.66
1:D:236:LEU:CD2	1:D:348:MET:HB3	2.22	0.66
1:B:353:VAL:HG21	1:B:366:SER:HB3	1.77	0.66
1:C:211:VAL:HG12	1:C:212:THR:N	2.10	0.66
1:C:215:ARG:N	1:C:216:PRO:CD	2.59	0.66
1:D:86:THR:CG2	1:D:90:VAL:CG2	2.72	0.66
1:B:125:ILE:HD11	1:B:369:TYR:CG	2.31	0.66
1:D:75:LYS:CD	1:D:201:VAL:HG12	2.26	0.66
1:A:321:ILE:H	1:A:321:ILE:HD12	1.60	0.65
1:C:76:PHE:O	1:C:79:TRP:HB3	1.96	0.65
1:C:175:ARG:HH11	1:C:175:ARG:CG	2.05	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:PHE:O	1:A:180:GLN:HB3	1.96	0.65
1:B:4:SER:HB2	1:B:134:ILE:HG21	1.79	0.65
1:D:296:ARG:O	1:D:299:TRP:HB3	1.96	0.65
1:B:77:LYS:O	1:B:81:LEU:HB3	1.97	0.65
1:C:282:THR:HB	1:C:336:ILE:O	1.96	0.65
1:C:342:TRP:O	1:C:346:VAL:HG23	1.97	0.65
1:C:85:LEU:CD1	1:C:194:THR:OG1	2.45	0.65
1:C:176:GLY:O	1:C:180:GLN:N	2.30	0.65
1:D:413:ILE:O	1:D:416:VAL:HG12	1.97	0.65
1:B:85:LEU:HD11	1:B:194:THR:HG21	1.79	0.65
1:A:374:MET:SD	1:A:375:VAL:HG23	2.36	0.64
1:B:125:ILE:HG22	1:B:126:PRO:HD3	1.79	0.64
1:D:292:MET:O	1:D:293:LEU:HG	1.97	0.64
1:B:268:PHE:N	1:B:269:PRO:CD	2.60	0.64
1:B:316:MET:HE3	1:B:316:MET:O	1.96	0.64
1:B:114:ILE:O	1:B:118:MET:N	2.30	0.64
1:B:187:ILE:O	1:B:191:ILE:N	2.30	0.64
1:D:240:ALA:HA	1:D:345:GLN:OE1	1.98	0.64
1:D:244:ASN:HB3	1:D:376:VAL:CG1	2.26	0.64
1:A:93:LEU:HD13	1:A:112:THR:HB	1.79	0.64
1:B:19:ASP:HA	1:B:22:ILE:HG22	1.80	0.64
1:D:306:PRO:HG2	1:D:422:PHE:CD2	2.32	0.64
1:A:127:PHE:CD1	1:A:127:PHE:C	2.70	0.64
1:B:241:LEU:HD22	1:B:375:VAL:HG21	1.79	0.64
1:B:374:MET:HE2	1:B:374:MET:H	1.63	0.64
1:C:75:LYS:HB2	1:C:205:TYR:CB	2.28	0.64
1:C:91:LEU:HD13	1:C:116:TRP:HZ3	1.63	0.64
1:C:116:TRP:O	1:C:117:GLY:C	2.32	0.64
1:D:366:SER:HB2	1:D:369:TYR:CD2	2.33	0.64
1:C:371:VAL:O	1:C:375:VAL:HG22	1.98	0.64
1:D:75:LYS:HE3	1:D:76:PHE:HB2	1.80	0.64
1:D:351:ASP:HA	1:D:354:ASP:HB2	1.80	0.64
1:A:78:PRO:O	1:A:82:ILE:HG12	1.97	0.64
1:C:96:SER:OG	1:D:198:LEU:HD13	1.98	0.64
1:C:229:LYS:HG2	1:C:233:LEU:HB2	1.80	0.64
1:C:299:TRP:O	1:C:302:ALA:HB3	1.97	0.64
1:B:383:ALA:O	1:B:386:PHE:N	2.30	0.64
1:C:82:ILE:O	1:C:86:THR:CG2	2.46	0.64
1:C:304:VAL:O	1:C:307:VAL:HB	1.96	0.64
1:C:387:ILE:HD12	1:C:417:LEU:CD2	2.28	0.64
1:D:7:THR:HG22	1:D:200:ASN:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ALA:HB1	1:B:87:ASN:HD21	1.63	0.63
1:A:98:HIS:CD2	1:A:99:LEU:HB2	2.33	0.63
1:C:242:ALA:HA	1:C:245:ILE:HG12	1.79	0.63
1:A:58:ASN:CG	1:A:121:THR:CG2	2.63	0.63
1:B:391:LEU:HA	1:B:413:ILE:HG21	1.81	0.63
1:C:14:GLY:O	1:C:18:LYS:N	2.24	0.63
1:C:142:GLU:O	1:C:295:ARG:CZ	2.46	0.63
1:D:59:ASP:CG	1:D:60:PRO:HD3	2.19	0.63
1:D:83:GLY:HA3	1:D:122:ILE:CD1	2.27	0.63
1:D:167:VAL:O	1:D:171:GLY:N	2.31	0.63
1:A:91:LEU:HG	1:A:183:THR:HG23	1.79	0.63
1:A:236:LEU:HD11	1:A:348:MET:HB3	1.80	0.63
1:A:245:ILE:CG2	1:A:417:LEU:HD21	2.28	0.63
1:A:438:ASP:O	1:A:441:ARG:N	2.31	0.63
1:B:306:PRO:CG	1:B:422:PHE:CE2	2.77	0.63
1:C:109:VAL:O	1:C:113:TYR:HB2	1.98	0.63
1:D:86:THR:HG23	1:D:115:LEU:HG	1.71	0.63
1:D:366:SER:HB2	1:D:369:TYR:HD2	1.64	0.63
1:B:124:ASP:HB2	1:B:373:THR:HG23	1.81	0.63
1:D:313:LEU:O	1:D:313:LEU:CD1	2.44	0.63
1:C:87:ASN:O	1:C:90:VAL:HG22	1.99	0.63
1:D:282:THR:HA	1:D:285:VAL:HG22	1.80	0.63
1:B:32:TYR:CE1	1:B:176:GLY:HA2	2.34	0.63
1:C:33:TYR:CD1	1:C:33:TYR:C	2.72	0.63
1:C:128:TRP:CD2	1:C:346:VAL:HG11	2.33	0.63
1:D:77:LYS:N	1:D:78:PRO:CD	2.62	0.63
1:D:353:VAL:O	1:D:357:GLU:N	2.29	0.63
1:A:212:THR:HG22	1:A:212:THR:O	1.98	0.63
1:A:250:ILE:O	1:A:254:ALA:CB	2.46	0.63
1:C:128:TRP:CH2	1:C:373:THR:CG2	2.74	0.63
1:D:115:LEU:O	1:D:118:MET:HB3	1.97	0.62
1:B:16:PHE:HB2	1:B:151:PHE:CD2	2.34	0.62
1:C:93:LEU:HD23	1:C:112:THR:OG1	1.99	0.62
1:D:391:LEU:HB2	1:D:413:ILE:CD1	2.29	0.62
1:C:308:LEU:HD23	1:C:334:LEU:HD11	1.82	0.62
1:C:387:ILE:CG2	1:C:417:LEU:CD2	2.77	0.62
1:C:77:LYS:HE2	1:C:197:THR:O	1.99	0.62
1:C:91:LEU:HD13	1:C:116:TRP:CZ3	2.34	0.62
1:C:346:VAL:HG12	1:C:369:TYR:CE2	2.33	0.62
1:A:243:TYR:CZ	1:A:341:PHE:HD2	2.17	0.62
1:D:15:ALA:HB1	1:D:152:ALA:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:305:MET:HB2	1:D:306:PRO:HD3	1.81	0.62
1:D:340:LEU:HG	1:D:340:LEU:O	2.00	0.62
1:A:342:TRP:O	1:A:346:VAL:HG23	1.98	0.62
1:D:59:ASP:OD1	1:D:59:ASP:N	2.33	0.62
1:D:20:PHE:CD2	1:D:186:LEU:HA	2.35	0.62
1:B:268:PHE:N	1:B:269:PRO:HD2	2.15	0.61
1:C:51:ALA:O	1:C:54:TRP:HB2	2.00	0.61
1:C:143:GLN:O	1:C:147:PHE:CE1	2.53	0.61
1:D:20:PHE:HD2	1:D:186:LEU:HA	1.65	0.61
1:A:18:LYS:NZ	1:A:127:PHE:HB2	2.14	0.61
1:B:86:THR:HG21	1:B:115:LEU:CD1	2.30	0.61
1:D:5:MET:SD	1:D:144:LEU:HD22	2.40	0.61
1:A:349:VAL:HG21	1:A:372:GLN:CB	2.30	0.61
1:B:374:MET:H	1:B:374:MET:CE	2.12	0.61
1:C:164:LEU:O	1:C:167:VAL:HG12	1.99	0.61
1:D:47:LEU:HD13	1:D:113:TYR:OH	2.00	0.61
1:D:156:GLY:O	1:D:160:ALA:CB	2.48	0.61
1:D:194:THR:O	1:D:198:LEU:HG	1.99	0.61
1:B:117:GLY:O	1:B:120:TYR:N	2.31	0.61
1:B:142:GLU:HA	1:B:145:VAL:CG2	2.31	0.61
1:D:86:THR:HG21	1:D:115:LEU:CD1	2.30	0.61
1:D:76:PHE:O	1:D:80:ILE:HG23	2.00	0.61
1:A:8:LYS:HD2	1:A:134:ILE:HD13	1.82	0.61
1:A:236:LEU:O	1:A:236:LEU:HD23	2.01	0.61
1:B:112:THR:O	1:B:115:LEU:CB	2.48	0.61
1:C:340:LEU:O	1:C:340:LEU:HG	2.01	0.61
1:B:51:ALA:HA	1:B:54:TRP:CD2	2.35	0.61
1:C:87:ASN:ND2	1:C:119:THR:HG21	2.15	0.61
1:A:58:ASN:ND2	1:A:121:THR:CG2	2.62	0.61
1:B:380:SER:O	1:B:383:ALA:HB3	2.01	0.61
1:C:56:ALA:O	1:C:60:PRO:HD2	2.01	0.61
1:A:240:ALA:HB1	1:A:376:VAL:HG11	1.82	0.61
1:B:417:LEU:O	1:B:421:PHE:CB	2.49	0.61
1:C:14:GLY:O	1:C:18:LYS:HG3	2.01	0.61
1:C:353:VAL:O	1:C:357:GLU:N	2.32	0.61
1:A:73:TRP:CZ2	1:B:109:VAL:HB	2.34	0.60
1:B:21:ALA:HB1	1:B:87:ASN:ND2	2.16	0.60
1:C:216:PRO:HA	1:C:219:THR:HG1	1.66	0.60
1:A:91:LEU:HD13	1:A:116:TRP:HZ3	1.65	0.60
1:D:80:ILE:HG13	1:D:81:LEU:N	2.14	0.60
1:A:5:MET:CG	1:A:135:THR:HG23	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:86:THR:CG2	1:D:90:VAL:HG23	2.32	0.60
1:B:351:ASP:C	1:B:433:TYR:HE2	2.04	0.60
1:B:80:ILE:HG13	1:B:81:LEU:N	2.16	0.60
1:B:115:LEU:HA	1:B:118:MET:HB2	1.82	0.60
1:B:239:MET:HE1	1:B:429:TYR:HB2	1.82	0.60
1:A:105:GLN:HE21	1:A:105:GLN:CA	2.15	0.60
1:A:219:THR:CG2	1:A:360:LEU:HD11	2.32	0.60
1:B:78:PRO:O	1:B:82:ILE:HG12	2.01	0.60
1:D:14:GLY:HA2	1:D:193:SER:OG	2.00	0.60
1:A:24:ILE:CD1	1:A:186:LEU:HD13	2.24	0.60
1:B:373:THR:N	1:B:374:MET:HE2	2.17	0.60
1:C:175:ARG:HG3	1:C:175:ARG:NH1	2.01	0.60
1:C:323:ASN:O	1:C:323:ASN:ND2	2.32	0.60
1:C:380:SER:O	1:C:383:ALA:HB3	2.02	0.60
1:D:156:GLY:O	1:D:160:ALA:HB2	2.02	0.60
1:B:117:GLY:O	1:B:118:MET:C	2.40	0.59
1:B:163:THR:CG2	1:B:182:PHE:CZ	2.85	0.59
1:B:246:ALA:HB1	1:B:422:PHE:CE1	2.37	0.59
1:B:387:ILE:HG21	1:B:414:MET:SD	2.42	0.59
1:B:244:ASN:HD22	1:B:376:VAL:CG1	2.15	0.59
1:C:51:ALA:HA	1:C:54:TRP:CG	2.36	0.59
1:C:321:ILE:HB	1:C:326:LEU:HD13	1.84	0.59
1:D:62:MET:SD	1:D:122:ILE:HG22	2.42	0.59
1:A:77:LYS:CG	1:A:201:VAL:HB	2.31	0.59
1:A:138:LYS:HG3	1:A:139:ARG:HG2	1.84	0.59
1:C:3:ILE:CG2	1:C:204:VAL:HG22	2.32	0.59
1:B:244:ASN:HD22	1:B:376:VAL:HB	1.68	0.59
1:C:143:GLN:HA	1:C:295:ARG:NH2	2.18	0.59
1:B:110:CYS:O	1:B:114:ILE:HG13	2.02	0.59
1:B:285:VAL:O	1:B:288:ARG:HB2	2.02	0.59
1:D:290:VAL:CG1	1:D:298:LEU:HD22	2.32	0.59
1:B:342:TRP:HA	1:B:345:GLN:HG3	1.85	0.59
1:C:343:VAL:O	1:C:347:ILE:HG12	2.03	0.59
1:D:299:TRP:HB3	1:D:344:LEU:CD1	2.31	0.59
1:D:391:LEU:HB2	1:D:413:ILE:CG1	2.33	0.59
1:A:233:LEU:O	1:A:237:LEU:HG	2.02	0.59
1:C:391:LEU:HD13	1:C:413:ILE:HG21	1.83	0.59
1:D:77:LYS:HB3	1:D:78:PRO:HD3	1.85	0.59
1:B:141:ARG:NH1	1:B:351:ASP:HA	2.17	0.59
1:B:340:LEU:HD23	1:B:340:LEU:O	2.03	0.59
1:A:384:ALA:O	1:A:387:ILE:HG13	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:SER:O	1:C:92:PHE:CB	2.50	0.58
1:A:232:GLN:HB2	1:A:352:THR:CG2	2.33	0.58
1:C:91:LEU:HD12	1:C:94:LEU:HD23	1.85	0.58
1:D:75:LYS:HE3	1:D:76:PHE:CB	2.34	0.58
1:A:95:PHE:O	1:A:180:GLN:HG3	2.02	0.58
1:B:195:ILE:HA	1:B:198:LEU:HD12	1.85	0.58
1:C:387:ILE:HG21	1:C:417:LEU:CD2	2.32	0.58
1:D:33:TYR:HD1	1:D:33:TYR:O	1.87	0.58
1:A:195:ILE:HG23	1:A:196:VAL:N	2.19	0.58
1:B:34:THR:CG2	1:B:43:LEU:HG	2.33	0.58
1:C:75:LYS:CB	1:C:205:TYR:CB	2.81	0.58
1:B:77:LYS:CA	1:B:201:VAL:CG1	2.81	0.58
1:D:150:PHE:CD1	1:D:283:LEU:CD2	2.75	0.58
1:A:212:THR:O	1:A:213:ALA:HB3	2.04	0.58
1:D:86:THR:CG2	1:D:90:VAL:HG21	2.31	0.58
1:D:162:ILE:HG13	1:D:165:PRO:HG2	1.85	0.57
1:C:62:MET:HE3	1:C:122:ILE:HD12	1.85	0.57
1:D:236:LEU:HD21	1:D:345:GLN:O	2.04	0.57
1:A:239:MET:HB2	1:A:425:THR:HA	1.87	0.57
1:C:129:SER:C	1:C:132:PRO:HD2	2.25	0.57
1:C:140:GLU:HG2	1:C:143:GLN:CB	2.34	0.57
1:D:244:ASN:ND2	1:D:376:VAL:HG11	2.17	0.57
1:D:290:VAL:HG21	1:D:295:ARG:CZ	2.34	0.57
1:A:118:MET:O	1:A:121:THR:HG23	2.04	0.57
1:B:17:GLY:HA3	1:B:190:PHE:HD1	1.69	0.57
1:B:187:ILE:O	1:B:191:ILE:HB	2.03	0.57
1:C:242:ALA:HB1	1:C:422:PHE:HA	1.85	0.57
1:A:313:LEU:HA	1:A:316:MET:HG2	1.87	0.57
1:B:272:LEU:HA	1:B:332:ILE:HD13	1.86	0.57
1:C:75:LYS:HG2	1:C:76:PHE:N	2.13	0.57
1:D:271:TYR:CD1	1:D:332:ILE:CD1	2.88	0.57
1:A:187:ILE:O	1:A:191:ILE:N	2.32	0.57
1:C:399:ASN:OD1	1:C:399:ASN:N	2.38	0.57
1:A:75:LYS:HG2	1:A:76:PHE:N	2.19	0.57
1:B:49:LEU:O	1:B:53:ILE:HG13	2.05	0.57
1:C:342:TRP:O	1:C:345:GLN:HB2	2.05	0.57
1:C:372:GLN:O	1:C:376:VAL:CG2	2.53	0.57
1:D:290:VAL:HG13	1:D:298:LEU:HD22	1.86	0.57
1:A:73:TRP:HZ2	1:B:109:VAL:HB	1.70	0.57
1:B:180:GLN:HA	1:B:183:THR:HG22	1.87	0.57
1:C:62:MET:CE	1:C:122:ILE:HD12	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:CYS:O	1:C:428:LEU:HD21	2.05	0.57
1:A:332:ILE:O	1:A:335:ASN:N	2.36	0.57
1:B:239:MET:SD	1:B:428:LEU:HB3	2.45	0.57
1:C:275:ALA:HB1	1:C:335:ASN:ND2	2.20	0.57
1:A:30:MET:O	1:A:33:TYR:HB3	2.03	0.57
1:A:282:THR:CB	1:A:337:GLY:HA2	2.35	0.57
1:B:80:ILE:HG21	1:B:130:LEU:HD13	1.87	0.57
1:C:72:ARG:HG2	1:C:73:TRP:O	2.05	0.57
1:C:374:MET:CE	1:C:375:VAL:HG12	2.35	0.57
1:A:232:GLN:HB2	1:A:352:THR:HG21	1.86	0.56
1:A:349:VAL:HG21	1:A:372:GLN:HB2	1.86	0.56
1:D:33:TYR:HE2	1:D:94:LEU:HD21	1.69	0.56
1:D:279:ASN:HA	1:D:282:THR:HG22	1.87	0.56
1:C:87:ASN:CG	1:C:119:THR:HG21	2.26	0.56
1:C:140:GLU:O	1:C:143:GLN:HB2	2.06	0.56
1:A:84:THR:HB	1:A:194:THR:HB	1.87	0.56
1:A:164:LEU:O	1:A:167:VAL:HG12	2.05	0.56
1:A:368:ALA:O	1:A:371:VAL:HG22	2.03	0.56
1:B:401:ALA:HB3	1:B:406:THR:HA	1.87	0.56
1:C:275:ALA:HB1	1:C:335:ASN:HD22	1.70	0.56
1:C:310:CYS:O	1:C:311:ALA:C	2.44	0.56
1:D:79:TRP:CE3	1:D:126:PRO:CB	2.81	0.56
1:A:92:PHE:HD1	1:A:187:ILE:CD1	2.18	0.56
1:B:39:LEU:O	1:B:40:SER:HB3	2.04	0.56
1:C:202:HIS:O	1:C:202:HIS:ND1	2.38	0.56
1:C:302:ALA:O	1:C:306:PRO:HD2	2.05	0.56
1:D:125:ILE:CG2	1:D:369:TYR:CD1	2.87	0.56
1:C:83:GLY:HA2	1:C:122:ILE:HG23	1.87	0.56
1:C:323:ASN:ND2	1:C:323:ASN:C	2.59	0.56
1:A:220:LEU:O	1:A:224:VAL:HG23	2.06	0.56
1:B:93:LEU:HD13	1:B:112:THR:CG2	2.22	0.56
1:B:122:ILE:O	1:B:126:PRO:CD	2.54	0.56
1:B:194:THR:O	1:B:198:LEU:HG	2.06	0.56
1:B:293:LEU:HD21	1:C:321:ILE:HG12	1.88	0.56
1:A:147:PHE:O	1:A:149:ARG:N	2.39	0.56
1:B:18:LYS:HZ3	1:B:123:MET:HA	1.71	0.56
1:D:90:VAL:CG1	1:D:116:TRP:HB2	2.36	0.56
1:A:243:TYR:HE2	1:A:342:TRP:HA	1.70	0.56
1:C:209:ASN:O	1:C:211:VAL:O	2.24	0.56
1:C:416:VAL:O	1:C:419:VAL:HB	2.06	0.56
1:D:124:ASP:HB2	1:D:373:THR:CG2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:PRO:HB3	1:A:343:VAL:HG11	1.87	0.55
1:B:17:GLY:CA	1:B:190:PHE:HD1	2.19	0.55
1:D:29:LEU:HD22	1:D:33:TYR:CZ	2.41	0.55
1:D:124:ASP:HB2	1:D:373:THR:HG21	1.87	0.55
1:D:112:THR:O	1:D:115:LEU:HB3	2.06	0.55
1:A:92:PHE:HD1	1:A:187:ILE:HD13	1.71	0.55
1:A:147:PHE:CZ	1:A:288:ARG:HG2	2.41	0.55
1:C:217:HIS:NE2	1:C:218:LEU:HG	2.22	0.55
1:C:242:ALA:CB	1:C:422:PHE:HA	2.37	0.55
1:A:215:ARG:N	1:A:216:PRO:CD	2.70	0.55
1:A:219:THR:HG21	1:A:360:LEU:HD11	1.89	0.55
1:B:7:THR:O	1:B:11:TYR:N	2.37	0.55
1:B:99:LEU:HD22	1:B:180:GLN:CD	2.27	0.55
1:C:143:GLN:O	1:C:147:PHE:HD1	1.90	0.55
1:C:282:THR:OG1	1:C:337:GLY:HA2	2.07	0.55
1:D:48:PHE:CD1	1:D:51:ALA:HB3	2.41	0.55
1:A:11:TYR:CE2	1:A:130:LEU:HB3	2.42	0.55
1:A:25:VAL:HG11	1:A:116:TRP:HH2	1.71	0.55
1:A:125:ILE:CG2	1:A:126:PRO:HD3	2.37	0.55
1:A:294:SER:O	1:A:297:ILE:HG12	2.06	0.55
1:D:77:LYS:O	1:D:81:LEU:HB2	2.05	0.55
1:D:387:ILE:CG2	1:D:414:MET:SD	2.94	0.55
1:D:391:LEU:HD22	1:D:413:ILE:CD1	2.37	0.55
1:A:250:ILE:O	1:A:254:ALA:N	2.40	0.55
1:B:86:THR:CG2	1:B:115:LEU:HG	2.37	0.55
1:C:241:LEU:HA	1:C:376:VAL:HG13	1.88	0.55
1:D:75:LYS:CE	1:D:76:PHE:HB2	2.36	0.55
1:D:387:ILE:HG22	1:D:417:LEU:HD12	1.87	0.55
1:A:236:LEU:HD13	1:A:349:VAL:HA	1.88	0.55
1:A:299:TRP:O	1:A:303:SER:N	2.39	0.55
1:C:140:GLU:O	1:C:143:GLN:N	2.40	0.55
1:D:415:ILE:HA	1:D:418:PRO:CG	2.37	0.55
1:C:175:ARG:CG	1:C:175:ARG:NH1	2.69	0.55
1:D:391:LEU:HB2	1:D:413:ILE:HD12	1.89	0.55
1:C:77:LYS:N	1:C:78:PRO:HD2	2.21	0.55
1:D:62:MET:O	1:D:79:TRP:HZ2	1.90	0.55
1:C:282:THR:CG2	1:C:282:THR:O	2.55	0.54
1:D:125:ILE:HB	1:D:126:PRO:HD3	1.89	0.54
1:A:51:ALA:O	1:A:54:TRP:HB2	2.07	0.54
1:C:119:THR:HA	1:C:122:ILE:HG22	1.90	0.54
1:B:48:PHE:O	1:B:51:ALA:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:THR:HG22	1:B:182:PHE:HZ	1.72	0.54
1:B:245:ILE:HG21	1:B:421:PHE:CE2	2.43	0.54
1:C:419:VAL:HA	1:C:422:PHE:HB3	1.90	0.54
1:A:13:PHE:CZ	1:A:192:ALA:HB1	2.43	0.54
1:C:386:PHE:CD1	1:C:386:PHE:C	2.81	0.54
1:A:149:ARG:HB2	1:A:283:LEU:HD21	1.90	0.54
1:B:244:ASN:HD22	1:B:376:VAL:HG11	1.68	0.54
1:C:232:GLN:HG2	1:C:232:GLN:O	2.08	0.54
1:C:233:LEU:O	1:C:236:LEU:N	2.31	0.54
1:D:16:PHE:HB2	1:D:151:PHE:CD2	2.42	0.54
1:D:245:ILE:HG12	1:D:376:VAL:CG2	2.36	0.54
1:D:324:ALA:O	1:D:328:VAL:HG23	2.08	0.54
1:C:72:ARG:HG2	1:C:73:TRP:N	2.19	0.54
1:C:139:ARG:HH22	1:C:358:PHE:CB	2.15	0.54
1:C:287:PRO:HG3	1:C:340:LEU:CD2	2.35	0.54
1:D:420:LEU:HD23	1:D:420:LEU:O	2.08	0.54
1:A:8:LYS:HA	1:A:11:TYR:CB	2.34	0.54
1:A:125:ILE:HG23	1:A:126:PRO:HD3	1.89	0.54
1:B:32:TYR:CE1	1:B:176:GLY:CA	2.90	0.54
1:B:285:VAL:HG12	1:B:289:LEU:HD13	1.90	0.54
1:C:387:ILE:HD12	1:C:417:LEU:CG	2.38	0.54
1:A:59:ASP:HB3	1:A:374:MET:HG2	1.89	0.54
1:C:122:ILE:O	1:C:126:PRO:HG2	2.07	0.54
1:D:11:TYR:CD1	1:D:130:LEU:HD22	2.43	0.54
1:C:123:MET:O	1:C:126:PRO:HD2	2.08	0.53
1:D:124:ASP:OD2	1:D:373:THR:CG2	2.56	0.53
1:A:240:ALA:HB1	1:A:376:VAL:CG1	2.38	0.53
1:C:110:CYS:O	1:C:114:ILE:HG12	2.08	0.53
1:C:162:ILE:O	1:C:165:PRO:HD2	2.08	0.53
1:D:125:ILE:HG22	1:D:369:TYR:CE1	2.43	0.53
1:A:236:LEU:CD2	1:A:372:GLN:NE2	2.71	0.53
1:C:310:CYS:SG	1:C:416:VAL:HA	2.49	0.53
1:A:81:LEU:CD1	1:A:85:LEU:HD12	2.39	0.53
1:B:15:ALA:HB1	1:B:152:ALA:HB2	1.89	0.53
1:B:374:MET:HE2	1:B:374:MET:N	2.24	0.53
1:C:177:PHE:O	1:C:180:GLN:HB2	2.08	0.53
1:C:387:ILE:HG23	1:C:417:LEU:HD21	1.90	0.53
1:A:67:ASN:OD1	1:A:220:LEU:HD23	2.08	0.53
1:B:322:HIS:O	1:B:326:LEU:N	2.33	0.53
1:D:285:VAL:O	1:D:289:LEU:HG	2.08	0.53
1:B:286:PHE:O	1:B:290:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:351:ASP:O	1:B:433:TYR:HE2	1.92	0.53
1:C:139:ARG:O	1:C:140:GLU:CB	2.54	0.53
1:C:391:LEU:CD1	1:C:413:ILE:HD13	2.37	0.53
1:A:295:ARG:O	1:A:298:LEU:HB3	2.09	0.53
1:D:135:THR:HB	1:D:141:ARG:HG3	1.89	0.53
1:B:39:LEU:HD22	1:B:41:VAL:CG2	2.38	0.53
1:C:360:LEU:HD22	1:C:361:ASN:OD1	2.07	0.53
1:A:7:THR:HG23	1:A:201:VAL:CG1	2.30	0.53
1:A:18:LYS:O	1:A:22:ILE:HG22	2.09	0.53
1:A:67:ASN:HB3	1:A:217:HIS:HD2	1.71	0.53
1:A:285:VAL:O	1:A:289:LEU:HG	2.08	0.53
1:D:349:VAL:HG11	1:D:366:SER:HB3	1.91	0.53
1:A:62:MET:HE3	1:A:122:ILE:HD12	1.90	0.53
1:B:233:LEU:HG	1:B:368:ALA:HB3	1.90	0.53
1:B:384:ALA:O	1:B:387:ILE:HG13	2.09	0.53
1:B:430:PHE:O	1:B:431:ARG:C	2.47	0.53
1:C:1:MET:SD	1:C:3:ILE:HB	2.49	0.53
1:D:19:ASP:HA	1:D:22:ILE:HG22	1.91	0.53
1:D:111:VAL:HG23	1:D:112:THR:N	2.24	0.53
1:D:268:PHE:N	1:D:269:PRO:CD	2.72	0.52
1:A:352:THR:HA	1:A:355:TYR:CE2	2.44	0.52
1:C:229:LYS:HD2	1:C:229:LYS:O	2.09	0.52
1:D:153:SER:CB	1:D:283:LEU:CD2	2.86	0.52
1:A:59:ASP:CB	1:A:374:MET:HG2	2.39	0.52
1:B:59:ASP:CB	1:B:60:PRO:HD3	2.40	0.52
1:C:78:PRO:O	1:C:81:LEU:HG	2.10	0.52
1:C:79:TRP:CZ2	1:C:125:ILE:HG23	2.44	0.52
1:C:141:ARG:HH21	1:C:351:ASP:CG	2.13	0.52
1:D:128:TRP:HD1	1:D:129:SER:N	2.08	0.52
1:D:153:SER:HB2	1:D:283:LEU:CD2	2.38	0.52
1:B:440:LEU:HD12	1:B:440:LEU:N	2.25	0.52
1:C:124:ASP:OD2	1:C:128:TRP:CZ2	2.63	0.52
1:C:146:PRO:HG3	1:C:295:ARG:NH1	2.24	0.52
1:C:387:ILE:HG23	1:C:417:LEU:CD2	2.38	0.52
1:A:75:LYS:O	1:A:78:PRO:HD2	2.10	0.52
1:B:81:LEU:HD21	1:B:198:LEU:HD23	1.91	0.52
1:B:83:GLY:O	1:B:86:THR:OG1	2.28	0.52
1:C:138:LYS:HA	1:C:139:ARG:HD3	1.90	0.52
1:D:120:TYR:HA	1:D:123:MET:HB2	1.90	0.52
1:A:3:ILE:CG2	1:A:203:GLU:HB3	2.36	0.52
1:A:76:PHE:HB3	1:A:130:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:TYR:HB2	1:B:43:LEU:HD21	1.92	0.52
1:C:235:CYS:O	1:C:428:LEU:CD2	2.58	0.52
1:D:138:LYS:HE3	1:D:139:ARG:HG3	1.90	0.52
1:B:62:MET:HE2	1:B:122:ILE:HD11	1.91	0.52
1:C:144:LEU:O	1:C:148:PRO:CD	2.54	0.52
1:C:192:ALA:O	1:C:196:VAL:HG23	2.09	0.52
1:A:11:TYR:CZ	1:A:130:LEU:HD23	2.44	0.52
1:A:90:VAL:HG21	1:A:116:TRP:CB	2.40	0.52
1:A:183:THR:CG2	1:A:187:ILE:HD12	2.26	0.52
1:D:370:SER:O	1:D:372:GLN:N	2.42	0.52
1:A:125:ILE:O	1:A:129:SER:HB3	2.09	0.52
1:A:346:VAL:CG1	1:A:369:TYR:CE1	2.91	0.52
1:B:243:TYR:O	1:B:247:SER:N	2.38	0.52
1:C:32:TYR:O	1:C:36:VAL:N	2.42	0.52
1:C:138:LYS:C	1:C:139:ARG:CD	2.77	0.52
1:A:87:ASN:CB	1:A:119:THR:HG21	2.36	0.51
1:A:127:PHE:C	1:A:127:PHE:HD1	2.13	0.51
1:C:78:PRO:HD3	1:C:202:HIS:CD2	2.45	0.51
1:A:13:PHE:CD2	1:A:196:VAL:HG21	2.45	0.51
1:A:91:LEU:HD13	1:A:116:TRP:CZ3	2.44	0.51
1:A:241:LEU:O	1:A:245:ILE:HG13	2.11	0.51
1:A:271:TYR:OH	1:A:329:ALA:HA	2.10	0.51
1:B:28:TYR:CE2	1:B:32:TYR:HB2	2.45	0.51
1:B:267:LEU:C	1:B:269:PRO:HD2	2.31	0.51
1:C:91:LEU:CD1	1:C:94:LEU:HD23	2.39	0.51
1:D:396:TYR:O	1:D:398:PRO:HD3	2.10	0.51
1:A:150:PHE:O	1:A:150:PHE:CD1	2.64	0.51
1:B:77:LYS:CD	1:B:201:VAL:HB	2.35	0.51
1:D:384:ALA:O	1:D:387:ILE:CG1	2.55	0.51
1:A:441:ARG:O	1:A:445:ILE:N	2.43	0.51
1:A:441:ARG:O	1:A:445:ILE:CB	2.59	0.51
1:B:81:LEU:CD2	1:B:198:LEU:HD23	2.40	0.51
1:D:79:TRP:CZ3	1:D:126:PRO:HB3	2.42	0.51
1:A:3:ILE:HG22	1:A:203:GLU:CB	2.35	0.51
1:A:25:VAL:HG23	1:A:26:TYR:N	2.25	0.51
1:C:323:ASN:HA	1:C:327:ILE:HG12	1.91	0.51
1:D:8:LYS:HD2	1:D:134:ILE:HG21	1.92	0.51
1:A:236:LEU:HD11	1:A:348:MET:C	2.31	0.51
1:B:342:TRP:O	1:B:345:GLN:HB2	2.10	0.51
1:C:7:THR:HA	1:C:201:VAL:HB	1.93	0.51
1:C:349:VAL:HG11	1:C:369:TYR:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:383:ALA:O	1:C:387:ILE:HB	2.10	0.51
1:D:387:ILE:HG21	1:D:414:MET:SD	2.51	0.51
1:A:73:TRP:HZ2	1:B:109:VAL:CB	2.23	0.51
1:C:110:CYS:O	1:C:111:VAL:C	2.47	0.51
1:B:36:VAL:HG13	1:B:37:VAL:H	1.76	0.51
1:B:77:LYS:HB2	1:B:201:VAL:CB	2.40	0.51
1:A:18:LYS:HZ1	1:A:127:PHE:HB2	1.76	0.51
1:A:353:VAL:O	1:A:357:GLU:N	2.34	0.51
1:C:125:ILE:HG22	1:C:126:PRO:HD3	1.93	0.51
1:D:122:ILE:O	1:D:126:PRO:CD	2.59	0.51
1:A:58:ASN:CB	1:A:121:THR:HG21	2.40	0.50
1:A:230:ASN:OD1	1:A:230:ASN:N	2.41	0.50
1:B:373:THR:O	1:B:376:VAL:HG13	2.11	0.50
1:C:11:TYR:CZ	1:C:130:LEU:HB3	2.45	0.50
1:A:61:ILE:HA	1:A:64:TRP:HB3	1.93	0.50
1:A:272:LEU:HA	1:A:275:ALA:HB3	1.92	0.50
1:A:296:ARG:O	1:A:299:TRP:HB3	2.12	0.50
1:B:17:GLY:CA	1:B:190:PHE:CD1	2.94	0.50
1:B:34:THR:O	1:B:36:VAL:N	2.44	0.50
1:C:99:LEU:HD12	1:C:177:PHE:HB2	1.93	0.50
1:C:399:ASN:O	1:C:401:ALA:N	2.44	0.50
1:D:75:LYS:C	1:D:77:LYS:H	2.12	0.50
1:A:131:VAL:O	1:A:134:ILE:HG12	2.11	0.50
1:A:238:GLY:HA3	1:A:424:MET:SD	2.51	0.50
1:B:413:ILE:HD13	1:B:413:ILE:H	1.77	0.50
1:C:41:VAL:HG13	1:C:42:GLY:H	1.76	0.50
1:A:27:MET:HE2	1:A:159:THR:HB	1.92	0.50
1:A:195:ILE:HG23	1:A:196:VAL:H	1.75	0.50
1:B:77:LYS:CB	1:B:201:VAL:CG1	2.90	0.50
1:B:299:TRP:CD2	1:B:429:TYR:CE2	3.00	0.50
1:C:66:VAL:HG12	1:C:67:ASN:N	2.27	0.50
1:A:282:THR:CG2	1:A:282:THR:O	2.58	0.50
1:A:351:ASP:HA	1:A:354:ASP:CB	2.42	0.50
1:A:355:TYR:HA	1:A:358:PHE:HB2	1.94	0.50
1:B:159:THR:HG22	1:B:159:THR:O	2.10	0.50
1:C:351:ASP:O	1:C:354:ASP:N	2.44	0.50
1:D:153:SER:HB2	1:D:283:LEU:HD21	1.93	0.50
1:A:92:PHE:CD1	1:A:187:ILE:CD1	2.93	0.50
1:A:378:GLY:O	1:A:380:SER:N	2.45	0.50
1:A:380:SER:O	1:A:383:ALA:HB3	2.12	0.50
1:B:182:PHE:O	1:B:185:VAL:HG12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:ARG:HD2	1:C:139:ARG:H	1.71	0.50
1:D:197:THR:O	1:D:201:VAL:HG23	2.12	0.50
1:A:240:ALA:CB	1:A:376:VAL:CG1	2.90	0.50
1:A:322:HIS:O	1:A:323:ASN:HB2	2.12	0.50
1:A:332:ILE:O	1:A:335:ASN:CB	2.60	0.50
1:B:124:ASP:HB2	1:B:373:THR:CG2	2.42	0.50
1:A:290:VAL:HG23	1:A:290:VAL:O	2.12	0.49
1:A:390:VAL:HG12	1:A:413:ILE:HG23	1.94	0.49
1:B:237:LEU:HA	1:B:372:GLN:HE21	1.76	0.49
1:B:391:LEU:HB2	1:B:413:ILE:HD12	1.93	0.49
1:C:349:VAL:CG1	1:C:369:TYR:HA	2.42	0.49
1:B:76:PHE:HA	1:B:79:TRP:CB	2.42	0.49
1:B:241:LEU:O	1:B:245:ILE:HG13	2.12	0.49
1:B:383:ALA:O	1:B:385:PHE:N	2.45	0.49
1:D:77:LYS:CE	1:D:81:LEU:HD22	2.42	0.49
1:C:272:LEU:HA	1:C:275:ALA:HB3	1.94	0.49
1:D:88:SER:HB2	1:D:190:PHE:CD2	2.46	0.49
1:B:130:LEU:O	1:B:134:ILE:HD11	2.13	0.49
1:C:11:TYR:CE2	1:C:127:PHE:HA	2.47	0.49
1:C:16:PHE:O	1:C:20:PHE:HB2	2.11	0.49
1:C:310:CYS:HG	1:C:314:PHE:HD2	1.60	0.49
1:D:17:GLY:HA3	1:D:190:PHE:HD1	1.78	0.49
1:D:85:LEU:HD21	1:D:194:THR:HG21	1.94	0.49
1:D:110:CYS:O	1:D:111:VAL:C	2.50	0.49
1:A:20:PHE:O	1:A:24:ILE:HG13	2.12	0.49
1:A:236:LEU:HD11	1:A:348:MET:CB	2.42	0.49
1:B:17:GLY:HA3	1:B:190:PHE:CD1	2.48	0.49
1:C:236:LEU:HD11	1:C:348:MET:HB3	1.94	0.49
1:D:416:VAL:O	1:D:420:LEU:HB2	2.13	0.49
1:A:242:ALA:HA	1:A:245:ILE:HD12	1.94	0.49
1:B:244:ASN:ND2	1:B:376:VAL:CG1	2.71	0.49
1:B:387:ILE:HG22	1:B:417:LEU:HD22	1.95	0.49
1:C:122:ILE:O	1:C:126:PRO:CG	2.61	0.49
1:D:270:TYR:CD1	1:D:270:TYR:C	2.85	0.49
1:A:11:TYR:CE2	1:A:127:PHE:HA	2.48	0.49
1:A:133:THR:O	1:A:134:ILE:O	2.31	0.49
1:A:397:THR:HG22	1:A:398:PRO:CD	2.42	0.49
1:A:413:ILE:O	1:A:416:VAL:HG12	2.12	0.49
1:B:59:ASP:HB2	1:B:60:PRO:HD3	1.95	0.49
1:B:77:LYS:CB	1:B:78:PRO:HD3	2.42	0.49
1:C:79:TRP:CD1	1:C:122:ILE:HG13	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:SER:O	1:C:132:PRO:HD2	2.13	0.49
1:C:157:PHE:CE1	1:C:277:ALA:HB1	2.48	0.49
1:C:349:VAL:HG13	1:C:350:ALA:N	2.27	0.49
1:A:120:TYR:OH	1:A:377:LYS:NZ	2.46	0.49
1:A:216:PRO:O	1:A:219:THR:HB	2.13	0.49
1:B:34:THR:HG23	1:B:43:LEU:HG	1.94	0.49
1:B:77:LYS:HB2	1:B:201:VAL:HB	1.94	0.49
1:C:33:TYR:HA	1:C:36:VAL:CG1	2.43	0.49
1:D:2:SER:O	1:D:5:MET:N	2.44	0.49
1:A:29:LEU:O	1:A:32:TYR:N	2.43	0.49
1:C:10:SER:HB2	1:C:196:VAL:HG12	1.94	0.49
1:C:125:ILE:HA	1:C:128:TRP:HE1	1.76	0.49
1:D:75:LYS:HG3	1:D:202:HIS:CA	2.27	0.49
1:C:351:ASP:O	1:C:354:ASP:HB2	2.13	0.49
1:D:23:GLY:O	1:D:27:MET:HG2	2.13	0.49
1:A:11:TYR:CE1	1:A:130:LEU:HD23	2.48	0.48
1:A:58:ASN:HD21	1:A:118:MET:HA	1.77	0.48
1:A:243:TYR:OH	1:A:341:PHE:HB3	2.13	0.48
1:A:271:TYR:O	1:A:275:ALA:N	2.44	0.48
1:B:145:VAL:N	1:B:146:PRO:CD	2.76	0.48
1:D:51:ALA:HA	1:D:54:TRP:CD2	2.48	0.48
1:A:222:THR:O	1:A:226:LEU:N	2.38	0.48
1:B:80:ILE:HD13	1:B:130:LEU:HD13	1.95	0.48
1:A:76:PHE:CE2	1:A:126:PRO:HA	2.48	0.48
1:A:321:ILE:HD12	1:A:321:ILE:N	2.25	0.48
1:C:110:CYS:O	1:C:112:THR:N	2.46	0.48
1:C:240:ALA:HB1	1:C:376:VAL:HG21	1.92	0.48
1:A:37:VAL:HG13	1:A:38:GLY:N	2.29	0.48
1:A:203:GLU:O	1:A:206:SER:N	2.46	0.48
1:C:78:PRO:O	1:C:82:ILE:HG12	2.13	0.48
1:C:97:ALA:HA	1:D:199:ARG:HB3	1.95	0.48
1:D:76:PHE:HB3	1:D:80:ILE:HG23	1.95	0.48
1:D:236:LEU:CD2	1:D:349:VAL:HG23	2.37	0.48
1:D:387:ILE:HA	1:D:390:VAL:HG22	1.96	0.48
1:A:4:SER:OG	1:A:134:ILE:HA	2.12	0.48
1:A:227:ILE:O	1:A:227:ILE:HD12	2.14	0.48
1:A:268:PHE:N	1:A:269:PRO:CD	2.74	0.48
1:B:349:VAL:O	1:B:352:THR:HG22	2.13	0.48
1:C:211:VAL:CG1	1:C:212:THR:H	2.23	0.48
1:D:146:PRO:O	1:D:149:ARG:HB2	2.13	0.48
1:D:306:PRO:O	1:D:309:SER:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:MET:HG3	1:A:135:THR:HG23	1.95	0.48
1:A:22:ILE:O	1:A:22:ILE:HG13	2.13	0.48
1:A:187:ILE:CG2	1:A:191:ILE:HG13	2.25	0.48
1:B:121:THR:HG22	1:B:374:MET:HB3	1.95	0.48
1:C:236:LEU:O	1:C:236:LEU:HD23	2.12	0.48
1:C:240:ALA:O	1:C:241:LEU:C	2.50	0.48
1:D:77:LYS:HD3	1:D:77:LYS:C	2.34	0.48
1:D:80:ILE:CG1	1:D:81:LEU:N	2.77	0.48
1:D:417:LEU:O	1:D:421:PHE:N	2.47	0.48
1:A:419:VAL:HA	1:A:422:PHE:HB2	1.94	0.48
1:C:175:ARG:C	1:C:177:PHE:N	2.67	0.48
1:D:3:ILE:HG21	1:D:203:GLU:HG3	1.95	0.48
1:D:415:ILE:HA	1:D:418:PRO:HG2	1.96	0.48
1:A:286:PHE:N	1:A:287:PRO:CD	2.76	0.48
1:B:352:THR:CA	1:B:433:TYR:CE2	2.89	0.48
1:B:354:ASP:O	1:B:359:LYS:N	2.47	0.48
1:C:15:ALA:HB2	1:C:127:PHE:CZ	2.48	0.48
1:C:98:HIS:O	1:C:99:LEU:C	2.52	0.48
1:C:117:GLY:O	1:C:120:TYR:HB3	2.14	0.48
1:C:127:PHE:C	1:C:127:PHE:CD1	2.88	0.48
1:C:191:ILE:HA	1:C:194:THR:HG22	1.95	0.48
1:C:260:TYR:CG	1:C:260:TYR:O	2.66	0.48
1:D:286:PHE:CE2	1:D:339:ALA:CB	2.97	0.48
1:A:182:PHE:O	1:A:185:VAL:HB	2.14	0.48
1:B:36:VAL:HG13	1:B:37:VAL:N	2.28	0.48
1:D:350:ALA:O	1:D:354:ASP:HB2	2.14	0.48
1:A:92:PHE:HE1	1:A:187:ILE:HG21	1.79	0.48
1:C:214:GLY:O	1:C:217:HIS:ND1	2.45	0.48
1:D:75:LYS:HD3	1:D:201:VAL:HG12	1.96	0.48
1:A:122:ILE:O	1:A:126:PRO:HG2	2.14	0.47
1:A:145:VAL:CG1	1:A:146:PRO:HD3	2.43	0.47
1:D:21:ALA:O	1:D:25:VAL:HB	2.14	0.47
1:A:282:THR:HB	1:A:336:ILE:O	2.14	0.47
1:C:84:THR:OG1	1:C:85:LEU:HD13	2.14	0.47
1:D:59:ASP:CG	1:D:60:PRO:CD	2.82	0.47
1:D:125:ILE:H	1:D:126:PRO:HD2	1.79	0.47
1:A:191:ILE:HA	1:A:194:THR:HG22	1.95	0.47
1:A:245:ILE:CG2	1:A:417:LEU:CD2	2.92	0.47
1:A:309:SER:HB3	1:A:334:LEU:HD22	1.96	0.47
1:C:245:ILE:O	1:C:249:ILE:HD13	2.14	0.47
1:A:59:ASP:HA	1:A:62:MET:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:LEU:CB	1:D:368:ALA:HB3	2.44	0.47
1:A:25:VAL:HG11	1:A:116:TRP:CH2	2.49	0.47
1:B:81:LEU:HD21	1:B:198:LEU:CD2	2.44	0.47
1:B:162:ILE:O	1:B:162:ILE:HG22	2.14	0.47
1:B:333:PHE:CE1	1:B:336:ILE:HD12	2.50	0.47
1:C:313:LEU:HB2	1:C:331:GLY:HA3	1.97	0.47
1:C:80:ILE:CD1	1:C:126:PRO:HB3	2.44	0.47
1:D:244:ASN:CB	1:D:376:VAL:HG21	2.45	0.47
1:D:369:TYR:O	1:D:372:GLN:HG2	2.14	0.47
1:A:3:ILE:CG2	1:A:203:GLU:CB	2.93	0.47
1:B:29:LEU:HD23	1:B:33:TYR:CZ	2.50	0.47
1:B:90:VAL:CG1	1:B:116:TRP:HB2	2.45	0.47
1:B:108:PHE:CD1	1:B:108:PHE:N	2.83	0.47
1:B:128:TRP:HD1	1:B:129:SER:N	2.12	0.47
1:B:282:THR:O	1:B:286:PHE:CD2	2.68	0.47
1:C:239:MET:HA	1:C:425:THR:OG1	2.15	0.47
1:C:422:PHE:CG	1:C:422:PHE:O	2.68	0.47
1:D:83:GLY:O	1:D:119:THR:HB	2.14	0.47
1:A:37:VAL:CG1	1:A:38:GLY:N	2.77	0.47
1:A:304:VAL:O	1:A:308:LEU:N	2.47	0.47
1:A:332:ILE:O	1:A:335:ASN:HB2	2.15	0.47
1:B:240:ALA:HA	1:B:345:GLN:HE22	1.80	0.47
1:B:245:ILE:CG2	1:B:421:PHE:CD2	2.94	0.47
1:B:370:SER:O	1:B:374:MET:HE3	2.15	0.47
1:D:320:ASP:OD1	1:D:320:ASP:N	2.48	0.47
1:A:240:ALA:HB2	1:A:372:GLN:HE21	1.80	0.47
1:C:211:VAL:CG1	1:C:212:THR:N	2.78	0.47
1:C:272:LEU:HG	1:C:275:ALA:HB3	1.95	0.47
1:D:124:ASP:CB	1:D:373:THR:HG21	2.45	0.47
1:A:16:PHE:O	1:A:20:PHE:HB2	2.14	0.47
1:B:141:ARG:HH12	1:B:351:ASP:HA	1.80	0.47
1:B:373:THR:HB	1:B:374:MET:HE1	1.96	0.47
1:C:123:MET:C	1:C:126:PRO:HD2	2.35	0.47
1:D:90:VAL:HG12	1:D:90:VAL:O	2.15	0.47
1:A:291:LYS:HD2	1:A:291:LYS:O	2.14	0.46
1:B:236:LEU:HD13	1:B:348:MET:HG2	1.97	0.46
1:C:14:GLY:HA2	1:C:193:SER:OG	2.14	0.46
1:C:216:PRO:HA	1:C:219:THR:OG1	2.14	0.46
1:D:119:THR:HA	1:D:122:ILE:HG13	1.96	0.46
1:A:68:ALA:O	1:A:71:SER:O	2.32	0.46
1:A:128:TRP:CD1	1:A:369:TYR:CE1	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:VAL:HG23	1:A:377:LYS:HG3	1.97	0.46
1:A:388:ALA:O	1:A:392:GLY:HA3	2.15	0.46
1:C:166:PHE:HA	1:C:169:TYR:CD2	2.50	0.46
1:D:184:LEU:O	1:D:187:ILE:HG13	2.14	0.46
1:A:240:ALA:CB	1:A:376:VAL:HG12	2.45	0.46
1:A:257:TYR:OH	1:A:327:ILE:O	2.34	0.46
1:C:268:PHE:N	1:C:269:PRO:HD3	2.30	0.46
1:D:47:LEU:HD13	1:D:113:TYR:CZ	2.51	0.46
1:D:420:LEU:HD22	1:D:421:PHE:CE1	2.51	0.46
1:A:8:LYS:O	1:A:12:GLY:N	2.44	0.46
1:B:81:LEU:HD11	1:B:198:LEU:CD2	2.46	0.46
1:B:136:LEU:HD23	1:B:136:LEU:O	2.15	0.46
1:C:20:PHE:HD1	1:C:155:ALA:HB1	1.79	0.46
1:C:294:SER:O	1:C:297:ILE:HG13	2.16	0.46
1:D:239:MET:SD	1:D:299:TRP:HH2	2.38	0.46
1:A:111:VAL:HG12	1:A:112:THR:N	2.31	0.46
1:A:208:ASP:OD1	1:A:208:ASP:C	2.54	0.46
1:A:239:MET:CB	1:A:425:THR:HA	2.46	0.46
1:A:304:VAL:O	1:A:307:VAL:HB	2.15	0.46
1:B:76:PHE:HA	1:B:79:TRP:HB2	1.98	0.46
1:B:233:LEU:HG	1:B:368:ALA:CB	2.46	0.46
1:B:303:SER:HA	1:B:341:PHE:CZ	2.50	0.46
1:B:341:PHE:CE2	1:B:425:THR:HG21	2.50	0.46
1:C:77:LYS:CB	1:C:201:VAL:CG2	2.94	0.46
1:C:387:ILE:HD12	1:C:417:LEU:HG	1.97	0.46
1:D:380:SER:CA	1:D:383:ALA:HB3	2.45	0.46
1:D:387:ILE:HA	1:D:390:VAL:CG2	2.46	0.46
1:A:282:THR:HB	1:A:337:GLY:HA2	1.97	0.46
1:C:58:ASN:CG	1:C:121:THR:CG2	2.82	0.46
1:C:142:GLU:H	1:C:142:GLU:HG2	1.54	0.46
1:C:426:LEU:O	1:C:430:PHE:N	2.36	0.46
1:D:80:ILE:O	1:D:84:THR:HG23	2.16	0.46
1:A:287:PRO:HA	1:A:340:LEU:HD21	1.98	0.46
1:B:86:THR:HG22	1:B:115:LEU:HG	1.97	0.46
1:D:416:VAL:HG13	1:D:417:LEU:N	2.31	0.46
1:A:14:GLY:O	1:A:18:LYS:N	2.42	0.46
1:B:2:SER:O	1:B:5:MET:N	2.48	0.46
1:B:202:HIS:O	1:B:206:SER:HB2	2.15	0.46
1:C:90:VAL:HG23	1:C:91:LEU:N	2.31	0.46
1:C:98:HIS:HB2	1:D:199:ARG:HE	1.80	0.46
1:C:421:PHE:C	1:C:423:MET:H	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:ILE:HG12	1:D:159:THR:HB	1.98	0.46
1:B:77:LYS:CB	1:B:201:VAL:HG12	2.44	0.46
1:B:373:THR:N	1:B:374:MET:CE	2.78	0.46
1:B:421:PHE:O	1:B:424:MET:HB3	2.15	0.46
1:C:318:LEU:HD21	1:C:409:GLY:HA2	1.98	0.46
1:D:236:LEU:HD11	1:D:345:GLN:HA	1.98	0.46
1:B:167:VAL:HB	1:B:182:PHE:CE2	2.51	0.46
1:C:18:LYS:O	1:C:22:ILE:HG22	2.16	0.46
1:C:80:ILE:CD1	1:C:126:PRO:CB	2.94	0.46
1:A:75:LYS:CG	1:A:76:PHE:N	2.80	0.45
1:B:124:ASP:CB	1:B:373:THR:HG23	2.45	0.45
1:B:295:ARG:HH21	1:B:340:LEU:HD11	1.80	0.45
1:C:340:LEU:O	1:C:340:LEU:CG	2.61	0.45
1:C:393:LEU:HA	1:C:396:TYR:HB3	1.98	0.45
1:D:135:THR:CB	1:D:141:ARG:HG3	2.46	0.45
1:A:216:PRO:HA	1:A:219:THR:OG1	2.16	0.45
1:D:233:LEU:CB	1:D:349:VAL:HG13	2.46	0.45
1:D:239:MET:SD	1:D:299:TRP:CH2	3.09	0.45
1:D:351:ASP:HA	1:D:354:ASP:CB	2.45	0.45
1:A:212:THR:C	1:A:214:GLY:H	2.19	0.45
1:B:28:TYR:CE1	1:B:31:TYR:HB2	2.52	0.45
1:B:83:GLY:HA3	1:B:122:ILE:HG21	1.97	0.45
1:B:370:SER:O	1:B:374:MET:CE	2.64	0.45
1:C:7:THR:HG23	1:C:201:VAL:HB	1.98	0.45
1:C:11:TYR:CZ	1:C:130:LEU:HD23	2.52	0.45
1:C:16:PHE:O	1:C:20:PHE:CB	2.65	0.45
1:C:77:LYS:HB2	1:C:201:VAL:CG2	2.43	0.45
1:D:75:LYS:HE3	1:D:76:PHE:CA	2.43	0.45
1:D:117:GLY:O	1:D:118:MET:C	2.53	0.45
1:D:387:ILE:HB	1:D:414:MET:SD	2.57	0.45
1:A:261:VAL:CG2	1:A:328:VAL:HG23	2.39	0.45
1:B:32:TYR:CD1	1:B:32:TYR:C	2.85	0.45
1:C:241:LEU:HD22	1:C:379:GLY:HA3	1.97	0.45
1:C:279:ASN:HD21	1:C:338:THR:HG23	1.81	0.45
1:D:110:CYS:O	1:D:114:ILE:HB	2.17	0.45
1:D:304:VAL:O	1:D:305:MET:C	2.55	0.45
1:A:172:GLY:O	1:A:173:ALA:HB3	2.17	0.45
1:A:240:ALA:O	1:A:243:TYR:N	2.50	0.45
1:A:372:GLN:O	1:A:376:VAL:HG13	2.15	0.45
1:D:286:PHE:O	1:D:290:VAL:HG22	2.16	0.45
1:D:386:PHE:HA	1:D:389:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:PRO:CA	1:A:340:LEU:HD21	2.46	0.45
1:D:301:GLY:C	1:D:305:MET:HG3	2.35	0.45
1:B:120:TYR:HA	1:B:123:MET:HB2	1.98	0.45
1:B:403:SER:OG	1:B:404:ALA:N	2.50	0.45
1:C:49:LEU:O	1:C:52:ARG:HG2	2.17	0.45
1:C:279:ASN:HA	1:C:336:ILE:HA	1.98	0.45
1:D:375:VAL:HG23	1:D:376:VAL:N	2.32	0.45
1:A:41:VAL:HG11	1:A:105:GLN:HG2	1.98	0.45
1:A:190:PHE:O	1:A:193:SER:N	2.47	0.45
1:B:351:ASP:O	1:B:433:TYR:CE2	2.69	0.45
1:B:428:LEU:HD12	1:B:428:LEU:HA	1.84	0.45
1:D:114:ILE:O	1:D:118:MET:N	2.47	0.45
1:B:261:VAL:HG22	1:B:262:ILE:H	1.82	0.45
1:A:35:ASP:OD2	1:A:175:ARG:NE	2.50	0.45
1:B:13:PHE:O	1:B:193:SER:OG	2.32	0.45
1:B:16:PHE:HB2	1:B:151:PHE:CE2	2.52	0.45
1:B:86:THR:O	1:B:90:VAL:HG23	2.17	0.45
1:C:24:ILE:O	1:C:28:TYR:N	2.37	0.45
1:C:125:ILE:N	1:C:126:PRO:CD	2.80	0.45
1:C:329:ALA:O	1:C:332:ILE:HG12	2.17	0.45
1:D:131:VAL:N	1:D:132:PRO:CD	2.80	0.45
1:A:147:PHE:N	1:A:148:PRO:CD	2.80	0.44
1:A:148:PRO:C	1:A:150:PHE:H	2.21	0.44
1:A:253:PHE:CE2	1:A:414:MET:SD	3.10	0.44
1:B:83:GLY:O	1:B:119:THR:OG1	2.27	0.44
1:B:299:TRP:HD1	1:B:344:LEU:HD13	1.81	0.44
1:D:332:ILE:C	1:D:334:LEU:H	2.19	0.44
1:A:128:TRP:NE1	1:A:346:VAL:HG11	2.31	0.44
1:B:163:THR:CG2	1:B:182:PHE:HZ	2.27	0.44
1:C:131:VAL:HG12	1:C:145:VAL:HG22	1.99	0.44
1:D:258:PHE:HA	1:D:261:VAL:HG22	1.99	0.44
1:D:396:TYR:C	1:D:398:PRO:HD3	2.37	0.44
1:A:127:PHE:CD1	1:A:127:PHE:O	2.71	0.44
1:A:286:PHE:O	1:A:298:LEU:HD21	2.17	0.44
1:A:351:ASP:HA	1:A:354:ASP:HB2	1.98	0.44
1:A:383:ALA:HA	1:A:386:PHE:HB3	2.00	0.44
1:B:76:PHE:O	1:B:80:ILE:HG23	2.18	0.44
1:B:353:VAL:O	1:B:357:GLU:N	2.42	0.44
1:C:235:CYS:SG	1:C:428:LEU:HD11	2.58	0.44
1:C:299:TRP:HA	1:C:302:ALA:HB3	1.99	0.44
1:D:233:LEU:HA	1:D:349:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:333:PHE:O	1:D:336:ILE:HG13	2.18	0.44
1:B:270:TYR:HD2	1:B:271:TYR:CD1	2.36	0.44
1:C:86:THR:HA	1:C:89:LEU:HD12	1.98	0.44
1:A:105:GLN:HE21	1:A:105:GLN:H	1.59	0.44
1:B:59:ASP:HA	1:B:374:MET:SD	2.57	0.44
1:B:77:LYS:HB3	1:B:78:PRO:HD3	1.99	0.44
1:B:145:VAL:N	1:B:146:PRO:HD3	2.32	0.44
1:B:353:VAL:HG11	1:B:365:GLU:O	2.18	0.44
1:B:387:ILE:CG2	1:B:417:LEU:HD22	2.48	0.44
1:B:415:ILE:C	1:B:417:LEU:N	2.70	0.44
1:A:266:ASP:OD1	1:A:266:ASP:N	2.48	0.44
1:B:373:THR:HB	1:B:374:MET:CE	2.48	0.44
1:D:90:VAL:HG11	1:D:116:TRP:HB2	1.99	0.44
1:D:182:PHE:O	1:D:186:LEU:HD13	2.18	0.44
1:D:244:ASN:HB3	1:D:376:VAL:HG21	2.00	0.44
1:A:287:PRO:O	1:A:295:ARG:NH1	2.51	0.44
1:B:35:ASP:HA	1:B:38:GLY:CA	2.42	0.44
1:C:353:VAL:O	1:C:357:GLU:HB2	2.17	0.44
1:D:129:SER:HB2	1:D:369:TYR:OH	2.13	0.44
1:B:439:MET:CB	1:B:440:LEU:HD12	2.47	0.44
1:C:95:PHE:CE1	1:C:184:LEU:HD11	2.52	0.44
1:D:83:GLY:O	1:D:119:THR:CB	2.66	0.44
1:A:32:TYR:CD1	1:A:35:ASP:HB3	2.53	0.44
1:A:75:LYS:HD3	1:A:202:HIS:HA	1.99	0.44
1:A:388:ALA:O	1:A:392:GLY:CA	2.66	0.44
1:C:16:PHE:CE2	1:C:151:PHE:HD2	2.35	0.44
1:C:77:LYS:CE	1:C:201:VAL:HG22	2.47	0.44
1:C:230:ASN:C	1:C:230:ASN:HD22	2.22	0.44
1:D:387:ILE:HG13	1:D:388:ALA:N	2.32	0.44
1:A:148:PRO:O	1:A:150:PHE:N	2.50	0.43
1:A:157:PHE:HB3	1:A:158:VAL:HG23	2.00	0.43
1:A:282:THR:HG21	1:A:337:GLY:HA2	1.99	0.43
1:B:240:ALA:HA	1:B:345:GLN:NE2	2.32	0.43
1:C:142:GLU:HB3	1:C:344:LEU:CD2	2.48	0.43
1:D:75:LYS:HB3	1:D:77:LYS:H	1.83	0.43
1:D:383:ALA:O	1:D:387:ILE:HG23	2.18	0.43
1:A:105:GLN:O	1:A:106:VAL:C	2.56	0.43
1:A:243:TYR:CZ	1:A:341:PHE:CD2	3.02	0.43
1:C:127:PHE:CZ	1:C:131:VAL:HG21	2.52	0.43
1:A:157:PHE:CE1	1:A:277:ALA:HB1	2.54	0.43
1:A:204:VAL:HA	1:A:207:SER:OG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:GLY:O	1:A:393:LEU:HD22	2.18	0.43
1:B:197:THR:O	1:B:201:VAL:HG23	2.19	0.43
1:A:383:ALA:O	1:A:386:PHE:HB3	2.19	0.43
1:C:72:ARG:CG	1:C:73:TRP:N	2.81	0.43
1:D:33:TYR:O	1:D:33:TYR:CD1	2.70	0.43
1:D:75:LYS:C	1:D:77:LYS:N	2.72	0.43
1:D:145:VAL:N	1:D:146:PRO:CD	2.81	0.43
1:D:147:PHE:HD1	1:D:150:PHE:CD2	2.28	0.43
1:B:20:PHE:CD2	1:B:186:LEU:HA	2.53	0.43
1:B:164:LEU:N	1:B:165:PRO:HD2	2.34	0.43
1:B:271:TYR:C	1:B:273:SER:H	2.22	0.43
1:C:2:SER:O	1:C:6:THR:OG1	2.35	0.43
1:C:79:TRP:HZ2	1:C:125:ILE:HG23	1.83	0.43
1:A:195:ILE:HG23	1:A:196:VAL:HG23	2.00	0.43
1:A:429:TYR:CD2	1:A:429:TYR:O	2.71	0.43
1:B:290:VAL:CG1	1:B:295:ARG:HG2	2.35	0.43
1:B:413:ILE:C	1:B:415:ILE:N	2.72	0.43
1:D:125:ILE:O	1:D:128:TRP:CD1	2.72	0.43
1:D:245:ILE:CG1	1:D:376:VAL:HG23	2.43	0.43
1:A:87:ASN:O	1:A:90:VAL:HB	2.18	0.43
1:A:390:VAL:CG1	1:A:413:ILE:HG23	2.49	0.43
1:B:93:LEU:CD1	1:B:112:THR:HG21	2.24	0.43
1:C:139:ARG:HB3	1:C:141:ARG:HH11	1.83	0.43
1:C:255:ILE:O	1:C:258:PHE:HB3	2.19	0.43
1:A:56:ALA:O	1:A:60:PRO:HD2	2.19	0.43
1:B:61:ILE:HD12	1:B:61:ILE:HA	1.87	0.43
1:B:352:THR:N	1:B:433:TYR:HE2	2.16	0.43
1:A:105:GLN:CA	1:A:105:GLN:NE2	2.80	0.43
1:A:302:ALA:O	1:A:306:PRO:HD3	2.19	0.43
1:B:62:MET:SD	1:B:122:ILE:HD11	2.58	0.43
1:B:256:TYR:O	1:B:260:TYR:N	2.52	0.43
1:B:290:VAL:HG12	1:B:290:VAL:O	2.19	0.43
1:B:383:ALA:C	1:B:385:PHE:N	2.71	0.43
1:C:209:ASN:O	1:C:210:GLY:C	2.55	0.43
1:D:117:GLY:O	1:D:120:TYR:N	2.52	0.43
1:A:5:MET:SD	1:A:135:THR:HG23	2.59	0.43
1:A:77:LYS:N	1:A:78:PRO:HD2	2.34	0.43
1:A:145:VAL:HG13	1:A:146:PRO:HD3	2.01	0.43
1:A:240:ALA:O	1:A:241:LEU:C	2.56	0.43
1:B:59:ASP:OD1	1:B:374:MET:HG3	2.19	0.43
1:B:80:ILE:CG1	1:B:81:LEU:N	2.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:PHE:CZ	1:B:425:THR:HG21	2.53	0.43
1:C:58:ASN:CB	1:C:121:THR:HG21	2.48	0.43
1:C:332:ILE:O	1:C:335:ASN:HB2	2.18	0.43
1:D:237:LEU:HD22	1:D:371:VAL:HB	2.01	0.43
1:A:128:TRP:HD1	1:A:369:TYR:HE1	1.62	0.42
1:A:245:ILE:HG21	1:A:417:LEU:HD21	1.99	0.42
1:C:241:LEU:CA	1:C:376:VAL:HG13	2.48	0.42
1:C:313:LEU:HD13	1:C:330:ALA:O	2.18	0.42
1:D:76:PHE:HB3	1:D:80:ILE:CG2	2.49	0.42
1:D:420:LEU:HD22	1:D:421:PHE:CD1	2.54	0.42
1:A:164:LEU:HA	1:A:167:VAL:HG12	2.01	0.42
1:A:377:LYS:O	1:A:378:GLY:C	2.58	0.42
1:B:417:LEU:O	1:B:421:PHE:CG	2.72	0.42
1:C:278:ALA:O	1:C:336:ILE:HG22	2.19	0.42
1:A:81:LEU:HD12	1:A:85:LEU:HD12	2.01	0.42
1:A:351:ASP:HA	1:A:354:ASP:HB3	2.02	0.42
1:B:124:ASP:CG	1:B:373:THR:HG23	2.39	0.42
1:C:249:ILE:O	1:C:253:PHE:HB2	2.18	0.42
1:C:349:VAL:HB	1:C:372:GLN:CB	2.49	0.42
1:D:137:ASP:O	1:D:138:LYS:CG	2.50	0.42
1:D:386:PHE:CD1	1:D:389:LEU:HD12	2.54	0.42
1:A:91:LEU:HD12	1:A:94:LEU:HD13	2.01	0.42
1:A:278:ALA:HB1	1:A:336:ILE:CG2	2.45	0.42
1:C:88:SER:O	1:C:92:PHE:N	2.51	0.42
1:C:279:ASN:OD1	1:C:338:THR:O	2.36	0.42
1:D:55:ASP:OD1	1:D:375:VAL:HB	2.20	0.42
1:D:73:TRP:CB	1:D:209:ASN:HB2	2.50	0.42
1:A:98:HIS:HB2	1:B:199:ARG:HD2	2.02	0.42
1:B:12:GLY:O	1:B:15:ALA:HB3	2.19	0.42
1:B:248:ASN:OD1	1:B:377:LYS:HG2	2.19	0.42
1:C:116:TRP:O	1:C:119:THR:HB	2.20	0.42
1:D:320:ASP:HB2	1:D:323:ASN:HB3	2.01	0.42
1:A:334:LEU:O	1:A:336:ILE:N	2.52	0.42
1:B:236:LEU:HD21	1:B:345:GLN:O	2.19	0.42
1:B:415:ILE:N	1:B:415:ILE:CD1	2.83	0.42
1:C:92:PHE:HD1	1:C:187:ILE:HD13	1.85	0.42
1:A:1:MET:SD	1:A:4:SER:N	2.90	0.42
1:A:31:TYR:O	1:A:34:THR:HB	2.19	0.42
1:A:241:LEU:HD11	1:A:375:VAL:HG12	2.01	0.42
1:A:254:ALA:HB1	1:A:272:LEU:HD21	2.01	0.42
1:A:417:LEU:HD23	1:A:418:PRO:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ILE:HD11	1:B:369:TYR:CD1	2.54	0.42
1:B:167:VAL:HB	1:B:182:PHE:HE2	1.85	0.42
1:B:235:CYS:SG	1:B:236:LEU:N	2.92	0.42
1:B:239:MET:HE3	1:B:239:MET:HB3	1.79	0.42
1:B:281:LEU:HD23	1:B:284:ILE:HD11	2.00	0.42
1:B:383:ALA:O	1:B:384:ALA:C	2.58	0.42
1:D:391:LEU:HD12	1:D:395:GLY:HA3	2.02	0.42
1:A:100:PHE:CE1	1:A:108:PHE:HB2	2.55	0.42
1:A:143:GLN:HA	1:A:295:ARG:HH21	1.84	0.42
1:B:237:LEU:HD13	1:B:371:VAL:HG21	2.01	0.42
1:D:413:ILE:HD13	1:D:413:ILE:H	1.85	0.42
1:A:45:GLY:O	1:A:48:PHE:HB2	2.20	0.42
1:B:81:LEU:CD1	1:B:198:LEU:HD23	2.50	0.42
1:B:86:THR:OG1	1:B:119:THR:OG1	2.33	0.42
1:B:91:LEU:HD13	1:B:186:LEU:HD22	2.02	0.42
1:B:237:LEU:O	1:B:241:LEU:HG	2.19	0.42
1:C:33:TYR:HA	1:C:36:VAL:HG13	2.02	0.42
1:C:413:ILE:HA	1:C:416:VAL:HG12	2.02	0.42
1:A:81:LEU:HD11	1:A:85:LEU:CD1	2.49	0.42
1:A:107:VAL:HB	1:A:108:PHE:H	1.67	0.42
1:A:299:TRP:CZ2	1:A:341:PHE:CZ	3.08	0.42
1:A:342:TRP:CD1	1:A:346:VAL:HG22	2.55	0.42
1:C:118:MET:O	1:C:122:ILE:HG22	2.20	0.42
1:C:233:LEU:HD12	1:C:233:LEU:HA	1.87	0.42
1:D:380:SER:O	1:D:384:ALA:HB2	2.19	0.42
1:A:76:PHE:HE2	1:A:126:PRO:HA	1.84	0.41
1:A:279:ASN:HA	1:A:335:ASN:O	2.19	0.41
1:A:287:PRO:CB	1:A:340:LEU:HD21	2.50	0.41
1:B:32:TYR:CD1	1:B:176:GLY:CA	2.95	0.41
1:B:310:CYS:SG	1:B:311:ALA:N	2.89	0.41
1:A:18:LYS:HZ3	1:A:127:PHE:HB2	1.83	0.41
1:A:282:THR:HG23	1:A:286:PHE:HD1	1.79	0.41
1:B:333:PHE:CZ	1:B:336:ILE:HD12	2.56	0.41
1:C:216:PRO:O	1:C:219:THR:OG1	2.38	0.41
1:D:17:GLY:CA	1:D:190:PHE:HD1	2.33	0.41
1:D:21:ALA:O	1:D:25:VAL:CG2	2.68	0.41
1:D:320:ASP:CB	1:D:323:ASN:HB2	2.50	0.41
1:A:8:LYS:HG3	1:A:131:VAL:HG22	2.01	0.41
1:A:98:HIS:HD2	1:A:99:LEU:HB2	1.80	0.41
1:B:95:PHE:O	1:B:180:GLN:NE2	2.46	0.41
1:C:128:TRP:O	1:C:132:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:417:LEU:HD23	1:C:418:PRO:HD3	2.02	0.41
1:D:77:LYS:HE3	1:D:81:LEU:HD22	2.03	0.41
1:B:162:ILE:O	1:B:162:ILE:CG2	2.68	0.41
1:B:305:MET:HB2	1:B:306:PRO:HD3	2.02	0.41
1:B:396:TYR:O	1:B:396:TYR:HD1	2.03	0.41
1:C:32:TYR:O	1:C:36:VAL:HG12	2.20	0.41
1:C:76:PHE:CE1	1:C:79:TRP:CE3	3.09	0.41
1:A:81:LEU:CD1	1:A:85:LEU:CD1	2.98	0.41
1:A:194:THR:O	1:A:198:LEU:HG	2.21	0.41
1:B:34:THR:HG23	1:B:43:LEU:CD2	2.50	0.41
1:C:372:GLN:O	1:C:376:VAL:HG23	2.19	0.41
1:D:316:MET:O	1:D:317:ALA:HB2	2.19	0.41
1:A:346:VAL:HG12	1:A:369:TYR:CD1	2.56	0.41
1:C:16:PHE:CE2	1:C:151:PHE:CD2	3.09	0.41
1:C:83:GLY:CA	1:C:122:ILE:HG23	2.51	0.41
1:C:299:TRP:CZ2	1:C:341:PHE:CZ	3.08	0.41
1:D:147:PHE:N	1:D:148:PRO:HD2	2.36	0.41
1:A:174:ASP:O	1:A:178:GLY:N	2.53	0.41
1:A:256:TYR:HA	1:A:259:THR:HB	2.02	0.41
1:A:307:VAL:CG2	1:A:422:PHE:CD2	3.04	0.41
1:B:77:LYS:O	1:B:81:LEU:CB	2.65	0.41
1:C:77:LYS:HA	1:C:80:ILE:CG1	2.42	0.41
1:C:242:ALA:HA	1:C:245:ILE:CG1	2.49	0.41
1:C:417:LEU:HA	1:C:420:LEU:HB2	2.02	0.41
1:D:342:TRP:O	1:D:345:GLN:HB2	2.21	0.41
1:D:418:PRO:O	1:D:422:PHE:HD1	2.03	0.41
1:A:214:GLY:C	1:A:216:PRO:HD2	2.40	0.41
1:A:240:ALA:O	1:A:243:TYR:HB3	2.21	0.41
1:A:271:TYR:OH	1:A:329:ALA:CB	2.69	0.41
1:B:99:LEU:CD1	1:B:177:PHE:HB2	2.47	0.41
1:C:240:ALA:HA	1:C:345:GLN:HE22	1.86	0.41
1:C:302:ALA:O	1:C:303:SER:C	2.58	0.41
1:D:91:LEU:HD12	1:D:94:LEU:HB3	2.01	0.41
1:D:426:LEU:O	1:D:426:LEU:HD23	2.20	0.41
1:A:75:LYS:HG2	1:A:77:LYS:H	1.86	0.41
1:B:76:PHE:HA	1:B:79:TRP:HB3	2.02	0.41
1:B:81:LEU:HD11	1:B:198:LEU:HD23	2.03	0.41
1:C:27:MET:O	1:C:27:MET:HG2	2.21	0.41
1:C:58:ASN:ND2	1:C:121:THR:HG21	2.36	0.41
1:C:127:PHE:CE1	1:C:131:VAL:HG21	2.56	0.41
1:C:141:ARG:NH2	1:C:351:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:LEU:N	1:C:376:VAL:HG13	2.36	0.41
1:D:19:ASP:HB3	1:D:155:ALA:HB3	2.03	0.41
1:D:192:ALA:O	1:D:195:ILE:HG22	2.21	0.41
1:D:269:PRO:O	1:D:272:LEU:HB3	2.20	0.41
1:A:28:TYR:O	1:A:29:LEU:C	2.58	0.41
1:A:90:VAL:HG21	1:A:116:TRP:CA	2.51	0.41
1:B:10:SER:O	1:B:13:PHE:N	2.54	0.41
1:B:21:ALA:CB	1:B:87:ASN:ND2	2.83	0.41
1:C:175:ARG:O	1:C:175:ARG:CD	2.62	0.41
1:C:215:ARG:H	1:C:216:PRO:HD2	1.80	0.41
1:B:76:PHE:O	1:B:79:TRP:N	2.54	0.40
1:D:145:VAL:N	1:D:146:PRO:HD3	2.36	0.40
1:A:32:TYR:HA	1:A:35:ASP:HB3	2.02	0.40
1:A:77:LYS:O	1:A:80:ILE:HG13	2.22	0.40
1:A:78:PRO:O	1:A:82:ILE:N	2.55	0.40
1:A:82:ILE:O	1:A:86:THR:CB	2.70	0.40
1:C:136:LEU:O	1:C:138:LYS:N	2.53	0.40
1:C:397:THR:HG1	1:C:398:PRO:HD2	1.78	0.40
1:C:402:GLN:HG3	1:C:403:SER:N	2.35	0.40
1:D:257:TYR:O	1:D:260:TYR:HB3	2.21	0.40
1:B:99:LEU:CD2	1:B:180:GLN:CD	2.90	0.40
1:B:260:TYR:OH	1:B:317:ALA:CB	2.69	0.40
1:B:410:MET:HB3	1:B:413:ILE:HD11	2.04	0.40
1:C:56:ALA:O	1:C:60:PRO:CD	2.68	0.40
1:C:72:ARG:HE	1:C:72:ARG:HB3	1.61	0.40
1:D:150:PHE:HD1	1:D:283:LEU:HD21	1.78	0.40
1:D:236:LEU:HD12	1:D:236:LEU:HA	1.90	0.40
1:B:241:LEU:O	1:B:245:ILE:CG1	2.69	0.40
1:C:238:GLY:HA2	1:C:241:LEU:HD12	2.03	0.40
1:D:322:HIS:O	1:D:326:LEU:HD13	2.22	0.40
1:A:14:GLY:O	1:A:18:LYS:HB2	2.21	0.40
1:C:75:LYS:CD	1:C:202:HIS:O	2.66	0.40
1:D:63:GLY:N	1:D:370:SER:HB3	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	446/486 (92%)	365 (82%)	65 (15%)	16 (4%)	3	22
1	B	422/486 (87%)	360 (85%)	54 (13%)	8 (2%)	8	34
1	C	429/486 (88%)	358 (83%)	63 (15%)	8 (2%)	8	34
1	D	374/486 (77%)	314 (84%)	52 (14%)	8 (2%)	7	32
All	All	1671/1944 (86%)	1397 (84%)	234 (14%)	40 (2%)	6	30

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	ILE
1	A	269	PRO
1	A	271	TYR
1	B	430	PHE
1	C	134	ILE
1	C	269	PRO
1	C	271	TYR
1	D	369	TYR
1	A	96	SER
1	A	107	VAL
1	A	214	GLY
1	A	369	TYR
1	A	392	GLY
1	A	398	PRO
1	B	384	ALA
1	C	137	ASP
1	C	339	ALA
1	C	401	ALA
1	C	422	PHE
1	D	38	GLY
1	D	78	PRO
1	D	371	VAL

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Mol	Chain	Res	Type
1	A	433	TYR
1	D	125	ILE
1	D	317	ALA
1	A	111	VAL
1	A	373	THR
1	A	379	GLY
1	A	432	TYR
1	B	35	ASP
1	A	335	ASN
1	D	268	PHE
1	A	42	GLY
1	B	245	ILE
1	B	337	GLY
1	C	397	THR
1	D	146	PRO
1	B	45	GLY
1	B	249	ILE
1	B	409	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	354/406 (87%)	303 (86%)	51 (14%)	3 14
1	B	331/406 (82%)	272 (82%)	59 (18%)	2 7
1	C	353/406 (87%)	281 (80%)	72 (20%)	1 4
1	D	302/406 (74%)	258 (85%)	44 (15%)	3 13
All	All	1340/1624 (82%)	1114 (83%)	226 (17%)	2 9

All (226) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	TYR
1	A	13	PHE
1	A	22	ILE

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Mol	Chain	Res	Type
1	A	32	TYR
1	A	33	TYR
1	A	46	THR
1	A	52	ARG
1	A	55	ASP
1	A	59	ASP
1	A	62	MET
1	A	69	THR
1	A	77	LYS
1	A	80	ILE
1	A	92	PHE
1	A	96	SER
1	A	103	THR
1	A	105	GLN
1	A	111	VAL
1	A	113	TYR
1	A	114	ILE
1	A	121	THR
1	A	128	TRP
1	A	137	ASP
1	A	141	ARG
1	A	149	ARG
1	A	151	PHE
1	A	191	ILE
1	A	203	GLU
1	A	207	SER
1	A	229	LYS
1	A	230	ASN
1	A	248	ASN
1	A	251	ASN
1	A	258	PHE
1	A	259	THR
1	A	262	ILE
1	A	266	ASP
1	A	267	LEU
1	A	268	PHE
1	A	274	TYR
1	A	280	LEU
1	A	281	LEU
1	A	291	LYS
1	A	303	SER
1	A	314	PHE

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Mol	Chain	Res	Type
1	A	358	PHE
1	A	359	LYS
1	A	361	ASN
1	A	417	LEU
1	A	421	PHE
1	A	422	PHE
1	B	32	TYR
1	B	35	ASP
1	B	48	PHE
1	B	49	LEU
1	B	54	TRP
1	B	59	ASP
1	B	66	VAL
1	B	70	ARG
1	B	75	LYS
1	B	80	ILE
1	B	86	THR
1	B	87	ASN
1	B	92	PHE
1	B	95	PHE
1	B	100	PHE
1	B	111	VAL
1	B	113	TYR
1	B	114	ILE
1	B	124	ASP
1	B	125	ILE
1	B	128	TRP
1	B	130	LEU
1	B	147	PHE
1	B	151	PHE
1	B	182	PHE
1	B	191	ILE
1	B	195	ILE
1	B	197	THR
1	B	200	ASN
1	B	205	TYR
1	B	208	ASP
1	B	253	PHE
1	B	268	PHE
1	B	269	PRO
1	B	283	LEU
1	B	289	LEU

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Mol	Chain	Res	Type
1	B	295	ARG
1	B	297	ILE
1	B	299	TRP
1	B	305	MET
1	B	310	CYS
1	B	314	PHE
1	B	316	MET
1	B	326	LEU
1	B	336	ILE
1	B	341	PHE
1	B	345	GLN
1	B	366	SER
1	B	369	TYR
1	B	374	MET
1	B	380	SER
1	B	389	LEU
1	B	396	TYR
1	B	410	MET
1	B	413	ILE
1	B	423	MET
1	B	428	LEU
1	B	430	PHE
1	B	438	ASP
1	C	1	MET
1	C	11	TYR
1	C	28	TYR
1	C	29	LEU
1	C	30	MET
1	C	33	TYR
1	C	35	ASP
1	C	36	VAL
1	C	48	PHE
1	C	62	MET
1	C	67	ASN
1	C	70	ARG
1	C	72	ARG
1	C	76	PHE
1	C	77	LYS
1	C	85	LEU
1	C	92	PHE
1	C	110	CYS
1	C	113	TYR

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Mol	Chain	Res	Type
1	C	114	ILE
1	C	118	MET
1	C	121	THR
1	C	128	TRP
1	C	130	LEU
1	C	136	LEU
1	C	137	ASP
1	C	139	ARG
1	C	141	ARG
1	C	142	GLU
1	C	148	PRO
1	C	151	PHE
1	C	157	PHE
1	C	175	ARG
1	C	181	MET
1	C	187	ILE
1	C	198	LEU
1	C	203	GLU
1	C	212	THR
1	C	227	ILE
1	C	229	LYS
1	C	230	ASN
1	C	236	LEU
1	C	248	ASN
1	C	255	ILE
1	C	259	THR
1	C	271	TYR
1	C	272	LEU
1	C	288	ARG
1	C	293	LEU
1	C	313	LEU
1	C	314	PHE
1	C	323	ASN
1	C	326	LEU
1	C	345	GLN
1	C	351	ASP
1	C	355	TYR
1	C	360	LEU
1	C	363	ARG
1	C	367	ILE
1	C	374	MET
1	C	385	PHE

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Mol	Chain	Res	Type
1	C	386	PHE
1	C	391	LEU
1	C	393	LEU
1	C	398	PRO
1	C	400	VAL
1	C	403	SER
1	C	408	GLN
1	C	411	GLN
1	C	412	PHE
1	C	422	PHE
1	C	426	LEU
1	D	13	PHE
1	D	19	ASP
1	D	27	MET
1	D	33	TYR
1	D	53	ILE
1	D	59	ASP
1	D	66	VAL
1	D	75	LYS
1	D	80	ILE
1	D	86	THR
1	D	89	LEU
1	D	93	LEU
1	D	110	CYS
1	D	123	MET
1	D	124	ASP
1	D	128	TRP
1	D	134	ILE
1	D	138	LYS
1	D	141	ARG
1	D	143	GLN
1	D	148	PRO
1	D	175	ARG
1	D	191	ILE
1	D	194	THR
1	D	199	ARG
1	D	205	TYR
1	D	208	ASP
1	D	235	CYS
1	D	251	ASN
1	D	257	TYR
1	D	270	TYR

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Mol	Chain	Res	Type
1	D	284	ILE
1	D	299	TRP
1	D	310	CYS
1	D	318	LEU
1	D	322	HIS
1	D	326	LEU
1	D	344	LEU
1	D	369	TYR
1	D	386	PHE
1	D	387	ILE
1	D	396	TYR
1	D	413	ILE
1	D	414	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	ASN
1	A	98	HIS
1	A	105	GLN
1	A	217	HIS
1	A	323	ASN
1	A	335	ASN
1	A	345	GLN
1	A	361	ASN
1	B	67	ASN
1	B	244	ASN
1	B	279	ASN
1	B	335	ASN
1	B	372	GLN
1	C	67	ASN
1	C	105	GLN
1	C	230	ASN
1	C	402	GLN
1	C	411	GLN
1	D	244	ASN

5.3.3 RNA

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	448/486 (92%)	0.03	30 (6%) 17 20	27, 80, 183, 265	25 (5%)
1	B	426/486 (87%)	0.76	78 (18%) 1 1	28, 89, 247, 360	9 (2%)
1	C	431/486 (88%)	0.03	24 (5%) 24 26	24, 76, 168, 340	0
1	D	382/486 (78%)	0.51	46 (12%) 4 5	31, 85, 220, 331	1 (0%)
All	All	1687/1944 (86%)	0.32	178 (10%) 6 7	24, 82, 213, 360	35 (2%)

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	362	ILE	21.4
1	B	350	ALA	19.3
1	C	321	ILE	16.4
1	B	351	ASP	15.7
1	D	412	PHE	15.5
1	D	364	CYS	14.3
1	C	320	ASP	13.9
1	A	436	ASN	13.9
1	D	366	SER	13.3
1	B	411	GLN	13.0
1	B	101	GLU	12.8
1	B	364	CYS	11.6
1	B	352	THR	11.2
1	D	363	ARG	10.3
1	A	320	ASP	10.0
1	B	129	SER	10.0
1	B	108	PHE	9.5
1	B	365	GLU	9.4
1	A	433	TYR	9.4
1	C	319	ALA	9.1
1	C	322	HIS	9.0

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Mol	Chain	Res	Type	RSRZ
1	B	363	ARG	8.9
1	D	351	ASP	8.8
1	A	323	ASN	8.6
1	B	354	ASP	8.3
1	D	361	ASN	8.3
1	D	169	TYR	8.1
1	D	267	LEU	7.8
1	D	350	ALA	7.5
1	B	349	VAL	7.5
1	B	265	ALA	7.3
1	D	411	GLN	7.1
1	B	366	SER	7.1
1	A	434	ARG	6.8
1	B	374	MET	6.7
1	C	318	LEU	6.5
1	D	354	ASP	6.5
1	B	165	PRO	6.4
1	C	323	ASN	6.3
1	B	362	ILE	6.0
1	B	355	TYR	6.0
1	B	399	ASN	6.0
1	D	70	ARG	5.9
1	A	324	ALA	5.9
1	D	266	ASP	5.7
1	D	157	PHE	5.6
1	D	355	TYR	5.6
1	D	349	VAL	5.4
1	D	357	GLU	5.3
1	B	100	PHE	5.2
1	B	106	VAL	5.2
1	B	105	GLN	5.1
1	B	102	GLY	5.1
1	B	69	THR	5.0
1	B	164	LEU	5.0
1	B	99	LEU	4.7
1	B	359	LYS	4.7
1	A	181	MET	4.6
1	D	69	THR	4.6
1	B	410	MET	4.6
1	A	171	GLY	4.6
1	A	435	LEU	4.5
1	B	401	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	100	PHE	4.4
1	C	358	PHE	4.4
1	B	70	ARG	4.3
1	D	365	GLU	4.3
1	C	200	ASN	4.2
1	B	445	ILE	4.2
1	C	171	GLY	4.1
1	C	412	PHE	4.1
1	D	141	ARG	4.1
1	D	360	LEU	4.1
1	A	73	TRP	4.1
1	D	67	ASN	4.0
1	B	397	THR	3.9
1	C	5	MET	3.9
1	B	442	LYS	3.8
1	D	164	LEU	3.8
1	B	141	ARG	3.8
1	D	16	PHE	3.7
1	D	352	THR	3.7
1	D	370	SER	3.7
1	B	107	VAL	3.7
1	A	165	PRO	3.6
1	B	357	GLU	3.6
1	B	96	SER	3.5
1	D	158	VAL	3.5
1	B	266	ASP	3.4
1	C	103	THR	3.4
1	C	324	ALA	3.4
1	D	142	GLU	3.4
1	C	178	GLY	3.4
1	A	446	HIS	3.4
1	A	437	GLY	3.3
1	D	367	ILE	3.3
1	D	369	TYR	3.2
1	B	67	ASN	3.2
1	A	319	ALA	3.2
1	B	446	HIS	3.2
1	B	360	LEU	3.2
1	B	369	TYR	3.1
1	B	177	PHE	3.1
1	A	388	ALA	3.1
1	B	449	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	322	HIS	3.0
1	B	95	PHE	3.0
1	B	444	GLN	2.9
1	B	367	ILE	2.9
1	B	412	PHE	2.9
1	D	150	PHE	2.9
1	B	443	ILE	2.9
1	B	133	THR	2.8
1	C	37	VAL	2.8
1	A	103	THR	2.8
1	B	161	GLY	2.8
1	B	361	ASN	2.8
1	B	398	PRO	2.8
1	A	164	LEU	2.7
1	B	440	LEU	2.7
1	B	400	VAL	2.6
1	A	443	ILE	2.6
1	B	146	PRO	2.6
1	C	161	GLY	2.6
1	B	175	ARG	2.6
1	B	132	PRO	2.6
1	B	147	PHE	2.6
1	B	109	VAL	2.6
1	C	314	PHE	2.5
1	B	373	THR	2.5
1	C	99	LEU	2.5
1	B	71	SER	2.5
1	A	317	ALA	2.5
1	C	172	GLY	2.5
1	A	258	PHE	2.5
1	B	343	VAL	2.5
1	B	55	ASP	2.4
1	A	366	SER	2.4
1	C	363	ARG	2.4
1	A	432	TYR	2.4
1	B	257	TYR	2.4
1	D	65	ILE	2.4
1	A	102	GLY	2.4
1	B	403	SER	2.4
1	D	396	TYR	2.4
1	B	375	VAL	2.4
1	D	356	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	441	ARG	2.4
1	A	169	TYR	2.4
1	C	362	ILE	2.4
1	D	358	PHE	2.4
1	B	130	LEU	2.3
1	B	356	GLY	2.3
1	D	353	VAL	2.3
1	D	163	THR	2.3
1	D	71	SER	2.3
1	C	352	THR	2.3
1	D	373	THR	2.3
1	D	375	VAL	2.2
1	D	124	ASP	2.2
1	D	348	MET	2.2
1	B	75	LYS	2.2
1	A	222	THR	2.2
1	B	139	ARG	2.2
1	C	168	SER	2.1
1	B	98	HIS	2.1
1	A	168	SER	2.1
1	A	104	ALA	2.1
1	B	169	TYR	2.1
1	D	340	LEU	2.1
1	B	258	PHE	2.1
1	B	68	ALA	2.0
1	B	358	PHE	2.0
1	C	165	PRO	2.0
1	D	130	LEU	2.0
1	A	170	VAL	2.0
1	D	200	ASN	2.0
1	B	60	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 monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.