



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 08:00 pm BST

PDB ID : 3NOC
Title : Designed ankyrin repeat protein (DARPin) binders to AcrB: Plasticity of the Interface
Authors : Monroe, N.; Briand, C.; Gruetter, M.G.
Deposited on : 2010-06-25
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

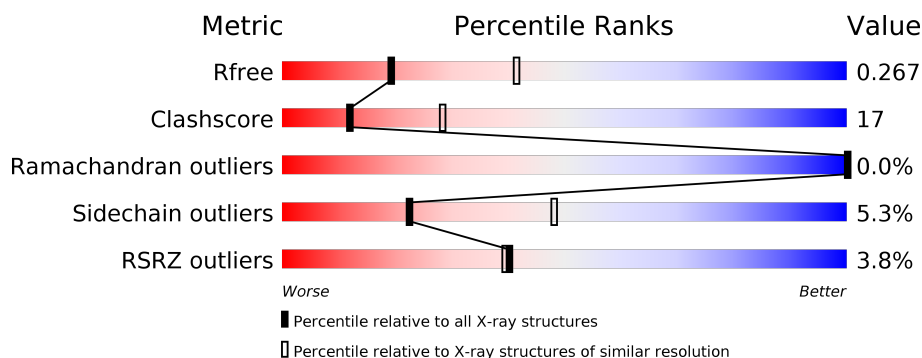
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	1049	<div> <div>3%</div> <div>67%</div> <div>28%</div> <div>• •</div> </div>
1	B	1049	<div> <div>%</div> <div>70%</div> <div>26%</div> <div>• •</div> </div>
1	C	1049	<div> <div>2%</div> <div>71%</div> <div>25%</div> <div>• •</div> </div>
2	D	169	<div> <div>8%</div> <div>60%</div> <div>26%</div> <div>5%</div> <div>9%</div> </div>
2	E	169	<div> <div>28%</div> <div>41%</div> <div>40%</div> <div>8%</div> <div>•</div> <div>10%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25558 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1028	Total	C	N	O	S	5	0	0
			7569	4878	1234	1417	40			
1	B	1026	Total	C	N	O	S	2	0	0
			7632	4916	1248	1426	42			
1	C	1034	Total	C	N	O	S	0	0	0
			7690	4957	1264	1426	43			

- Molecule 2 is a protein called Designed ankyrin repeat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	154	Total	C	N	O	S	0	0	0
			1128	708	208	211	1			
2	E	152	Total	C	N	O		11	0	0
			1101	691	205	205				

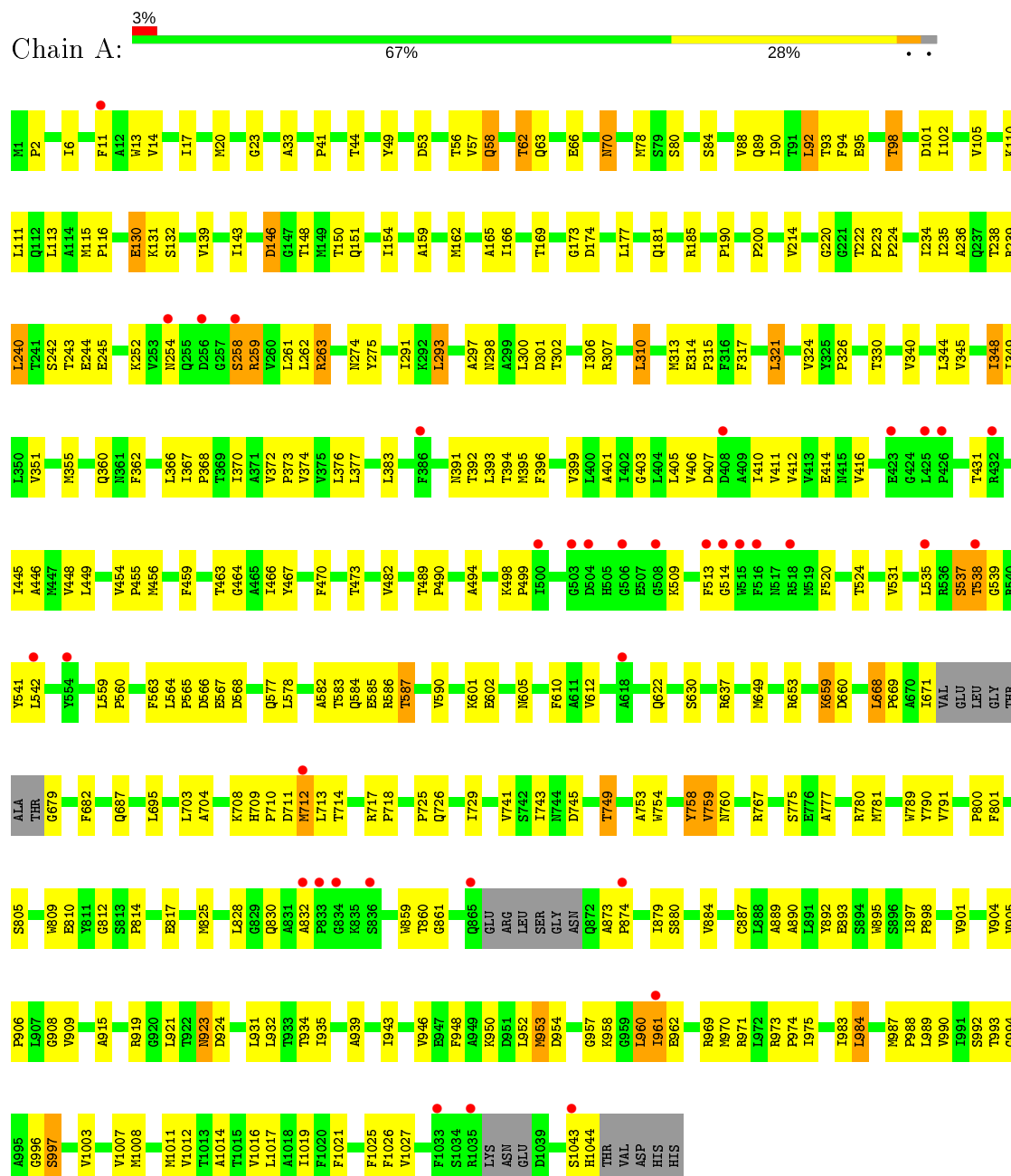
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		
3	B	132	Total	O	0	0
			132	132		
3	C	151	Total	O	0	0
			151	151		
3	D	17	Total	O	0	0
			17	17		
3	E	5	Total	O	0	0
			5	5		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Acriflavine resistance protein B

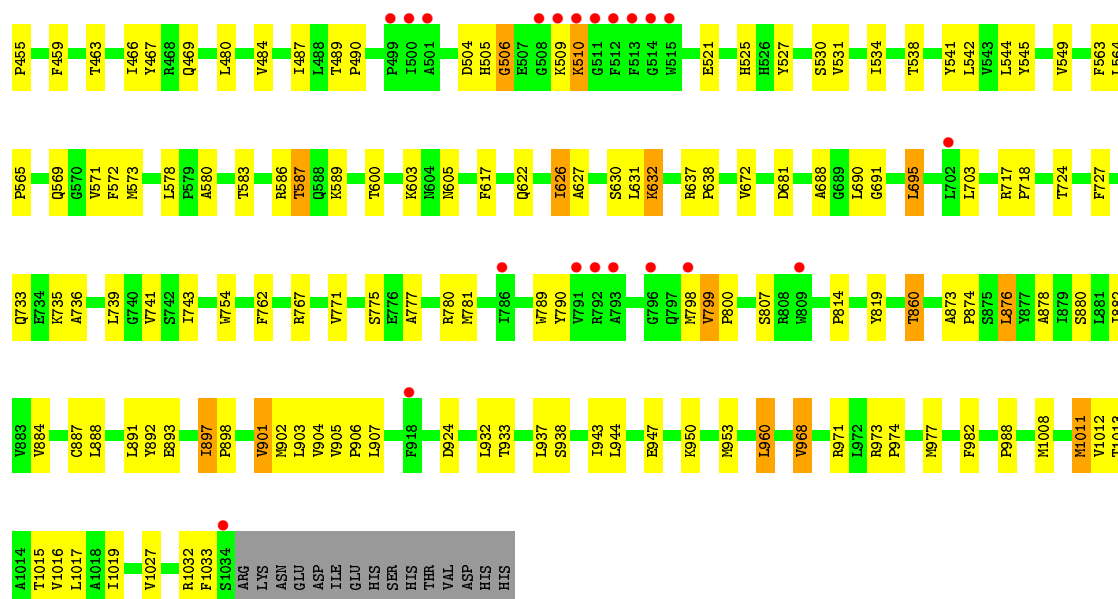


[illegible]

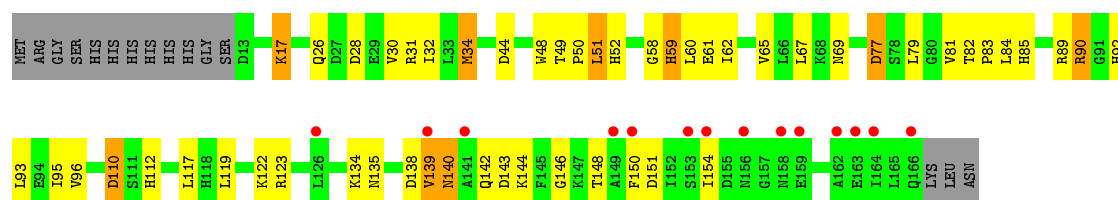
Chain C:

71% 2% 25%

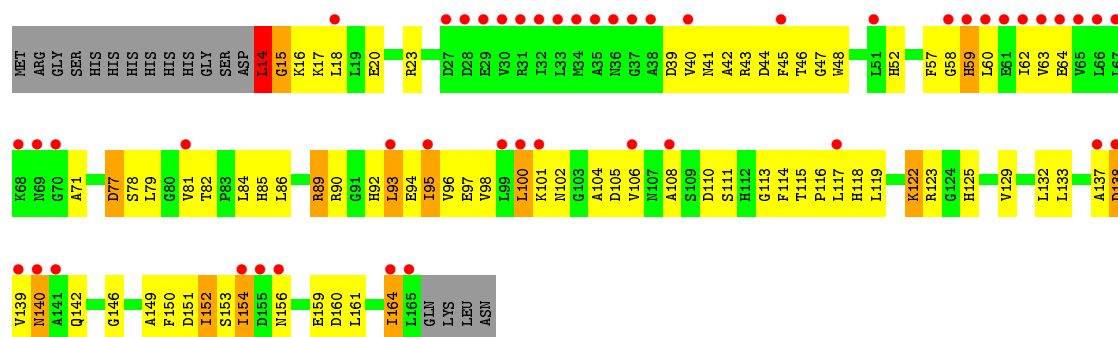
M1 M2 M3 M4 M5 M6 M7 M8 M9 M10 M11 M12 M13 M14 M15 M16 M17 M18 M19 M20 M21 M22 M23 M24 M25 M26 M27 M28 M29 M30 M31 M32 M33 M34 M35 M36 M37 M38 M39 M40 M41 M42 M43 M44 M45 M46 M47 M48 M49 M50 M51 M52 M53 M54 M55 M56 M57 M58 M59 M60 M61 M62 M63 M64 M65 M66 M67 M68 M69 M70 M71 M72 M73 M74 M75 M76 M77 M78 M79 M80 M81 M82 M83 M84 M85 M86 M87 M88 M89 M90 M91 M92 M93 M94 M95 M96 M97 M98 M99 M100 M101 M102 M103 M104 M105 M106 M107 M108 M109 M110 M111 M112 M113 M114 M115 M116 M117 M118 M119 M120 M121 M122 M123 M124 M125 M126 M127 M128 M129 M130 M131 M132 M133 M134 M135 M136 M137 M138 M139 M140 M141 M142 M143 M144 M145 M146 M147 M148 M149 M150 M151 M152 M153 M154 M155 M156 M157 M158 M159 M160 M161 M162 M163 M164 M165 M166 M167 M168 M169 M170 M171 M172 M173 M174 M175 M176 M177 M178 M179 M180 M181 M182 M183 M184 M185 M186 M187 M188 M189 M190 M191 M192 M193 M194 M195 M196 M197 M198 M199 M200 M201 M202 M203 M204 M205 M206 M207 M208 M209 M210 M211 M212 M213 M214 M215 M216 M217 M218 M219 M220 M221 M222 M223 M224 M225 M226 M227 M228 M229 M230 M231 M232 M233 M234 M235 M236 M237 M238 M239 M240 M241 M242 M243 M244 M245 M246 M247 M248 M249 M250 M251 M252 M253 M254 M255 M256 M257 M258 M259 M260 M261 M262 M263 M264 M265 M266 M267 M268 M269 M270 M271 M272 M273 M274 M275 M276 M277 M278 M279 M280 M281 M282 M283 M284 M285 M286 M287 M288 M289 M290 M291 M292 M293 M294 M295 M296 M297 M298 M299 M300 M301 M302 M303 M304 M305 M306 M307 M308 M309 M310 M311 M312 M313 M



• Molecule 2: Designed ankyrin repeat protein



• Molecule 2: Designed ankyrin repeat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.85Å 158.92Å 245.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 2.70 49.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.21-2.70) 99.0 (49.21-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.6.2_432	Depositor
R, R_{free}	0.242 , 0.268 0.239 , 0.267	Depositor DCC
R_{free} test set	1548 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	25558	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.42	0/7702	0.44	1/10496 (0.0%)
1	B	0.43	0/7768	0.43	1/10581 (0.0%)
1	C	0.38	0/7828	0.42	1/10661 (0.0%)
2	D	0.89	0/1145	0.70	2/1554 (0.1%)
2	E	0.78	0/1117	0.78	2/1519 (0.1%)
All	All	0.47	0/25560	0.47	7/34811 (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	C	0	1
All	All	0	2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	15	GLY	N-CA-C	-8.78	91.16	113.10
2	E	14	LEU	N-CA-C	-7.29	91.32	111.00
1	C	506	GLY	N-CA-C	-6.26	97.44	113.10
2	D	58	GLY	N-CA-C	5.75	127.47	113.10
1	B	864	TYR	N-CA-C	-5.21	96.94	111.00
1	A	235	ILE	C-N-CA	5.14	134.54	121.70
2	D	90	ARG	N-CA-C	-5.07	97.30	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	759	VAL	Peptide
1	C	235	ILE	Peptide

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	7569	0	7466	266	0
1	B	7632	0	7566	219	0
1	C	7690	0	7693	240	0
2	D	1128	0	1096	56	0
2	E	1101	0	1067	127	0
3	A	133	0	0	18	0
3	B	132	0	0	14	0
3	C	151	0	0	13	0
3	D	17	0	0	2	0
3	E	5	0	0	1	0
All	All	25558	0	24888	861	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (861) 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:A:960:LEU:HD12	1:A:961:ILE:N	1.40	1.32
2:E:18:LEU:HD13	2:E:18:LEU:O	1.35	1.24
1:A:960:LEU:HD12	1:A:960:LEU:C	1.53	1.24
1:C:509:LYS:O	1:C:510:LYS:HE3	1.37	1.18
1:A:259:ARG:N	1:A:259:ARG:HD3	1.44	1.15
2:E:92:HIS:O	2:E:96:VAL:HG23	1.46	1.14
1:C:509:LYS:HG3	1:C:510:LYS:HG3	1.27	1.13
1:C:125:GLN:NE2	1:C:125:GLN:HA	1.64	1.10
2:D:138:ASP:HB3	2:D:140:ASN:ND2	1.68	1.09
2:E:82:THR:OG1	2:E:85:HIS:HD2	1.35	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:GLN:HA	1:A:62:THR:HG23	1.37	1.06
1:C:510:LYS:N	1:C:510:LYS:HD2	1.66	1.05
2:E:57:PHE:HB3	2:E:59:HIS:HE1	1.21	1.04
2:E:93:LEU:H	2:E:93:LEU:HD23	1.18	1.01
1:A:649:MET:HG3	3:A:1169:HOH:O	1.62	0.98
2:E:18:LEU:HD13	2:E:18:LEU:C	1.81	0.97
1:B:456:MET:HE3	1:B:471:SER:HB2	1.47	0.96
2:D:138:ASP:CB	2:D:140:ASN:ND2	2.29	0.96
1:A:960:LEU:CD1	1:A:960:LEU:C	2.30	0.96
1:B:146:ASP:HB2	1:B:320:GLY:HA3	1.47	0.96
2:E:93:LEU:HD23	2:E:93:LEU:N	1.75	0.95
2:E:82:THR:OG1	2:E:85:HIS:CD2	2.20	0.95
1:A:259:ARG:N	1:A:259:ARG:CD	2.30	0.94
1:A:960:LEU:CD1	1:A:961:ILE:N	2.30	0.94
1:A:259:ARG:H	1:A:259:ARG:HD3	1.21	0.94
1:A:960:LEU:HD12	1:A:961:ILE:CA	1.98	0.93
1:C:510:LYS:H	1:C:510:LYS:HD2	1.28	0.93
2:E:57:PHE:HB3	2:E:59:HIS:CE1	2.03	0.91
1:C:125:GLN:HE21	1:C:125:GLN:CA	1.81	0.90
2:E:93:LEU:H	2:E:93:LEU:CD2	1.83	0.90
1:A:242:SER:OG	1:A:245:GLU:HG3	1.71	0.90
1:C:125:GLN:NE2	1:C:125:GLN:CA	2.30	0.90
2:E:93:LEU:HA	2:E:96:VAL:CG2	2.00	0.90
1:B:717:ARG:HG2	1:B:717:ARG:HH11	1.37	0.89
1:C:509:LYS:CG	1:C:510:LYS:HG3	2.02	0.89
2:D:17:LYS:HZ3	2:D:17:LYS:HB2	1.39	0.88
2:D:140:ASN:ND2	2:D:140:ASN:H	1.61	0.88
2:E:152:ILE:HG22	2:E:153:SER:N	1.90	0.87
2:E:152:ILE:CG2	2:E:153:SER:N	2.38	0.86
2:D:138:ASP:HB3	2:D:140:ASN:HD22	1.33	0.86
2:E:161:LEU:HA	2:E:164:ILE:HG13	1.58	0.86
2:E:84:LEU:HD23	2:E:116:PRO:HG2	1.58	0.86
2:D:138:ASP:CB	2:D:140:ASN:HD21	1.88	0.85
2:D:60:LEU:HD12	2:D:95:ILE:HD13	1.58	0.85
2:E:57:PHE:O	2:E:59:HIS:CE1	2.29	0.84
1:C:510:LYS:N	1:C:510:LYS:CD	2.30	0.82
2:E:48:TRP:CD1	2:E:77:ASP:OD1	2.34	0.81
2:E:93:LEU:HA	2:E:96:VAL:HG23	1.61	0.81
1:A:712:MET:HA	1:A:832:ALA:HB2	1.62	0.81
1:A:749:THR:HG21	1:A:791:VAL:HG12	1.63	0.81
1:B:420:MET:HB3	3:B:1156:HOH:O	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:150:PHE:CE1	2:D:154:ILE:HD11	2.15	0.80
1:B:126:GLY:HA3	1:C:116:PRO:HB3	1.64	0.80
2:E:18:LEU:C	2:E:18:LEU:CD1	2.50	0.79
1:B:977:MET:HB3	3:B:1109:HOH:O	1.83	0.79
1:C:162:MET:HA	1:C:313:MET:HE1	1.63	0.78
1:B:108:GLN:HG3	1:C:112:GLN:HG3	1.65	0.78
2:D:140:ASN:ND2	2:D:140:ASN:N	2.29	0.77
1:A:44:THR:HG23	3:A:1116:HOH:O	1.84	0.77
2:E:122:LYS:HG3	2:E:152:ILE:HD11	1.65	0.77
1:A:890:ALA:HB2	1:C:14:VAL:HG21	1.65	0.77
1:C:139:VAL:O	1:C:326:PRO:HD2	1.83	0.77
1:C:937:LEU:HD13	1:C:1011:MET:HG2	1.67	0.77
2:E:92:HIS:O	2:E:96:VAL:CG2	2.30	0.77
1:C:587:THR:HG21	1:C:622:GLN:O	1.85	0.76
2:E:122:LYS:HA	2:E:152:ILE:HD11	1.68	0.76
2:D:17:LYS:NZ	2:D:17:LYS:HB2	2.01	0.75
1:C:248:LYS:HE2	2:E:156:ASN:HA	1.69	0.74
2:E:92:HIS:C	2:E:96:VAL:HG23	2.08	0.74
2:E:79:LEU:O	2:E:111:SER:CB	2.35	0.74
1:A:181:GLN:HE22	1:A:767:ARG:HH11	1.32	0.74
1:B:966:ASP:HB2	3:B:1170:HOH:O	1.86	0.74
1:A:407:ASP:O	1:A:411:VAL:HG23	1.88	0.74
2:E:59:HIS:ND1	2:E:59:HIS:N	2.32	0.74
1:C:372:VAL:HG22	1:C:373:PRO:HD3	1.71	0.73
1:A:258:SER:C	1:A:259:ARG:HD3	2.09	0.73
1:B:977:MET:SD	3:B:1109:HOH:O	2.46	0.73
1:A:132:SER:HB3	1:A:173:GLY:HA3	1.71	0.73
2:E:40:VAL:CG1	2:E:71:ALA:HB2	2.19	0.73
1:A:401:ALA:O	1:A:405:LEU:HG	1.87	0.73
1:B:150:THR:O	1:B:154:ILE:HD12	1.89	0.73
1:A:399:VAL:HG11	1:A:989:LEU:HD11	1.72	0.71
1:A:975:ILE:HG21	1:A:1019:ILE:HD11	1.71	0.71
1:A:957:GLY:O	1:A:958:LYS:HG2	1.90	0.71
1:B:445:ILE:HD13	1:B:940:LYS:HG3	1.70	0.71
1:A:537:SER:OG	1:A:538:THR:C	2.29	0.71
1:A:953:MET:HG3	1:A:958:LYS:O	1.92	0.70
1:A:300:LEU:HD23	1:A:330:THR:HG23	1.74	0.70
1:A:214:VAL:HG23	1:A:236:ALA:HB3	1.73	0.70
2:E:138:ASP:C	2:E:138:ASP:OD1	2.30	0.70
2:E:93:LEU:CA	2:E:96:VAL:HG23	2.20	0.70
1:C:573:MET:HE1	1:C:617:PHE:HE2	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:876:LEU:HD11	1:C:932:LEU:HD11	1.72	0.70
2:E:161:LEU:HD23	2:E:161:LEU:H	1.55	0.70
1:A:113:LEU:HD11	1:C:128:SER:HB3	1.74	0.69
1:C:447:MET:SD	1:C:887:CYS:HB3	2.33	0.69
2:E:14:LEU:O	2:E:15:GLY:C	2.29	0.69
1:C:509:LYS:O	1:C:510:LYS:CE	2.30	0.69
1:C:509:LYS:C	1:C:510:LYS:HE3	2.12	0.69
1:B:355:MET:HG2	1:B:365:THR:HA	1.75	0.68
2:D:143:ASP:OD1	2:D:143:ASP:C	2.30	0.68
1:A:983:ILE:HG23	1:A:1008:MET:HG3	1.74	0.68
1:B:310:LEU:HD13	1:B:323:ILE:HD12	1.75	0.68
1:A:767:ARG:HA	1:B:63:GLN:NE2	2.08	0.68
2:E:79:LEU:O	2:E:111:SER:HB2	1.93	0.68
1:A:411:VAL:HA	3:A:1171:HOH:O	1.92	0.68
1:A:414:GLU:HG2	1:A:974:PRO:HB3	1.76	0.68
1:A:539:GLY:HA2	1:A:542:LEU:HD23	1.74	0.68
1:B:668:LEU:H	1:B:668:LEU:HD23	1.58	0.68
1:B:873:ALA:HB3	1:B:874:PRO:HD3	1.76	0.68
1:A:275:TYR:CD1	1:C:223:PRO:HG3	2.29	0.68
1:B:220:GLY:HA2	1:C:781:MET:SD	2.34	0.68
1:B:403:GLY:HA3	1:B:982:PHE:CE2	2.30	0.67
1:C:459:PHE:CE1	1:C:876:LEU:HD23	2.29	0.67
1:C:982:PHE:CD2	1:C:1011:MET:HG3	2.29	0.67
2:D:49:THR:H	2:D:52:HIS:CD2	2.13	0.67
1:B:877:TYR:HA	1:B:880:SER:HB3	1.76	0.67
1:C:703:LEU:HD11	1:C:718:PRO:HG3	1.76	0.67
1:C:343:THR:HG23	1:C:988:PRO:HB2	1.77	0.67
1:A:909:VAL:HG22	1:A:931:LEU:HD21	1.77	0.67
2:E:40:VAL:HG12	2:E:71:ALA:HB2	1.76	0.66
2:E:150:PHE:O	2:E:154:ILE:CG1	2.42	0.66
1:C:415:ASN:HD21	1:C:437:GLN:HE21	1.41	0.66
1:C:901:VAL:O	1:C:904:VAL:HG12	1.95	0.66
1:B:354:VAL:HG21	1:B:981:ALA:HB2	1.78	0.66
1:B:717:ARG:NH1	1:B:717:ARG:HG2	2.11	0.66
2:E:45:PHE:CE1	2:E:46:THR:HG23	2.31	0.66
1:B:184:MET:CE	1:B:268:ILE:HG22	2.27	0.65
1:A:754:TRP:HZ3	1:C:219:LEU:HD23	1.61	0.65
2:E:151:ASP:HA	2:E:154:ILE:CD1	2.26	0.65
1:B:454:VAL:HG12	1:B:455:PRO:HD3	1.79	0.65
1:C:505:HIS:ND1	1:C:505:HIS:O	2.30	0.65
2:E:150:PHE:O	2:E:154:ILE:HG12	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:138:ASP:CA	2:D:140:ASN:HD21	2.09	0.65
2:E:43:ARG:HG2	2:E:47:GLY:O	1.96	0.65
1:A:367:ILE:HB	1:A:368:PRO:HD3	1.79	0.65
1:A:535:LEU:O	1:A:538:THR:HB	1.95	0.65
2:E:110:ASP:OD2	2:E:113:GLY:N	2.30	0.65
1:B:375:VAL:O	1:B:379:THR:HG23	1.97	0.65
1:A:960:LEU:HD12	1:A:961:ILE:HA	1.78	0.64
2:E:39:ASP:OD2	2:E:40:VAL:N	2.30	0.64
1:A:166:ILE:HD11	1:A:310:LEU:HD13	1.77	0.64
1:C:248:LYS:O	1:C:261:LEU:HD22	1.97	0.64
2:E:57:PHE:CB	2:E:59:HIS:HE1	2.05	0.64
1:A:994:GLY:N	1:A:997:SER:OG	2.29	0.64
1:A:957:GLY:O	1:A:958:LYS:CG	2.45	0.64
1:C:904:VAL:HG13	1:C:938:SER:HB3	1.78	0.64
1:A:223:PRO:HG3	1:B:275:TYR:CG	2.33	0.64
2:E:20:GLU:OE1	2:E:23:ARG:NE	2.30	0.64
1:B:151:GLN:HE22	1:B:278:ILE:HA	1.63	0.64
1:A:531:VAL:O	1:A:535:LEU:HG	1.98	0.64
1:A:578:LEU:HD22	1:A:587:THR:HG23	1.80	0.64
2:E:79:LEU:O	2:E:111:SER:HB3	1.98	0.63
1:B:676:THR:HG22	1:B:676:THR:O	1.98	0.63
1:C:626:ILE:HD13	1:C:627:ALA:N	2.12	0.63
2:E:48:TRP:HD1	2:E:77:ASP:OD1	1.79	0.63
1:C:505:HIS:CG	1:C:505:HIS:O	2.52	0.63
1:A:711:ASP:OD1	1:A:712:MET:N	2.30	0.63
1:C:527:TYR:CE2	1:C:968:VAL:HG13	2.33	0.63
2:E:63:VAL:HG21	2:E:95:ILE:HD13	1.81	0.63
1:A:711:ASP:N	1:A:711:ASP:OD1	2.30	0.63
1:A:448:VAL:HG23	1:A:449:LEU:HD12	1.79	0.63
1:B:966:ASP:N	3:B:1170:HOH:O	2.32	0.62
2:D:140:ASN:HD22	2:D:140:ASN:N	1.96	0.62
1:C:370:ILE:O	1:C:373:PRO:HD2	1.99	0.62
1:B:1022:VAL:HG22	1:B:1023:PRO:HD3	1.80	0.62
1:B:340:VAL:HG21	1:B:395:MET:HB3	1.81	0.62
1:C:34:GLN:HB2	1:C:333:VAL:HG13	1.81	0.62
1:B:676:THR:O	1:B:677:ALA:HB2	1.99	0.62
1:C:580:ALA:HB1	1:C:724:THR:HG22	1.82	0.62
1:A:372:VAL:HB	1:A:373:PRO:HD3	1.80	0.62
1:B:204:ILE:O	1:B:208:LYS:HG3	1.99	0.62
1:C:193:LEU:HD12	1:C:265:VAL:HB	1.81	0.62
1:A:445:ILE:HG23	1:A:449:LEU:HD13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:PHE:O	1:A:952:LEU:HG	2.00	0.62
2:E:44:ASP:OD2	2:E:47:GLY:N	2.31	0.62
2:D:150:PHE:CZ	2:D:154:ILE:HD11	2.35	0.62
2:D:112:HIS:O	2:D:144:LYS:HB2	2.00	0.62
2:D:17:LYS:NZ	2:D:17:LYS:CB	2.61	0.61
1:A:566:ASP:CA	3:A:1096:HOH:O	2.47	0.61
2:E:84:LEU:HD23	2:E:116:PRO:CG	2.30	0.61
2:E:39:ASP:OD2	2:E:41:ASN:N	2.29	0.61
1:C:125:GLN:HE21	1:C:125:GLN:N	1.99	0.61
1:C:68:ASN:HD22	1:C:114:ALA:HB2	1.65	0.61
1:A:659:LYS:HD3	1:A:659:LYS:H	1.66	0.61
2:D:77:ASP:HB3	2:D:79:LEU:H	1.64	0.61
1:A:431:THR:HG21	1:A:494:ALA:HB2	1.83	0.61
2:E:152:ILE:HG22	2:E:153:SER:H	1.65	0.61
1:A:214:VAL:CG2	1:A:236:ALA:CB	2.79	0.61
1:A:745:ASP:O	1:A:749:THR:HG22	2.01	0.61
2:E:60:LEU:HD13	2:E:95:ILE:HG12	1.83	0.61
1:A:214:VAL:HG23	1:A:236:ALA:CB	2.31	0.61
1:A:566:ASP:HA	3:A:1096:HOH:O	1.99	0.61
1:C:897:ILE:N	1:C:898:PRO:HD2	2.16	0.60
2:D:81:VAL:HG23	2:D:110:ASP:OD2	2.01	0.60
1:B:242:SER:OG	1:B:245:GLU:HG3	2.01	0.60
1:A:261:LEU:HD12	1:A:263:ARG:NH1	2.15	0.60
1:C:367:ILE:HB	1:C:368:PRO:HD3	1.83	0.60
1:A:326:PRO:O	1:A:630:SER:HB2	2.01	0.60
2:E:89:ARG:HB3	2:E:119:LEU:HB3	1.82	0.60
2:E:110:ASP:C	2:E:110:ASP:OD2	2.38	0.60
1:A:94:PHE:HB3	1:A:98:THR:HG21	1.83	0.60
2:E:15:GLY:HA3	2:E:42:ALA:HB1	1.82	0.60
1:B:414:GLU:OE2	1:B:974:PRO:HG3	2.02	0.60
1:B:471:SER:O	1:B:475:VAL:HG23	2.00	0.60
1:B:367:ILE:HB	1:B:368:PRO:HD3	1.84	0.59
2:E:115:THR:O	2:E:118:HIS:N	2.35	0.59
1:C:688:ALA:HB3	1:C:690:LEU:HD13	1.84	0.59
1:A:960:LEU:HD13	1:A:1027:VAL:HG12	1.82	0.59
1:C:790:TYR:CE1	1:C:800:PRO:HG3	2.38	0.59
1:B:362:PHE:O	1:B:365:THR:HG22	2.02	0.59
1:B:974:PRO:O	1:B:978:THR:HG22	2.02	0.59
1:C:57:VAL:HG13	1:C:82:SER:HB3	1.85	0.59
1:A:78:MET:HG3	1:A:92:LEU:HD22	1.85	0.59
1:C:248:LYS:O	1:C:249:ILE:C	2.41	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:82:THR:OG1	2:D:85:HIS:ND1	2.35	0.59
1:A:58:GLN:HA	1:A:62:THR:CG2	2.24	0.58
1:B:274:ASN:H	1:B:274:ASN:HD22	1.51	0.58
1:B:574:THR:HG21	1:B:598:TYR:OH	2.03	0.58
1:B:790:TYR:CE1	1:B:800:PRO:HG3	2.38	0.58
2:D:44:ASP:C	2:D:44:ASP:OD1	2.39	0.58
1:B:26:ALA:O	1:B:30:LEU:HB2	2.02	0.58
1:A:139:VAL:O	1:A:326:PRO:HD2	2.03	0.58
1:A:567:GLU:N	3:A:1096:HOH:O	2.36	0.58
1:A:190:PRO:HG3	1:A:789:TRP:CZ2	2.39	0.58
1:B:712:MET:HG2	1:B:843:LEU:HD22	1.86	0.58
2:D:110:ASP:HB3	2:D:112:HIS:H	1.69	0.58
1:B:703:LEU:HD11	1:B:718:PRO:HG3	1.85	0.58
1:C:521:GLU:O	1:C:525:HIS:HD2	1.87	0.58
1:B:223:PRO:HG3	1:C:275:TYR:CG	2.39	0.58
1:B:347:ALA:O	1:B:351:VAL:HG23	2.04	0.57
1:C:393:LEU:HD13	1:C:466:ILE:HG23	1.86	0.57
1:A:326:PRO:HB3	1:A:610:PHE:HB2	1.86	0.57
1:A:790:TYR:CE1	1:A:800:PRO:HG3	2.39	0.57
1:B:278:ILE:HD11	1:B:588:GLN:OE1	2.05	0.57
1:B:864:TYR:O	1:B:865:GLN:C	2.40	0.57
1:A:559:LEU:HD12	1:A:560:PRO:HD2	1.85	0.57
1:B:559:LEU:HD12	1:B:560:PRO:CD	2.34	0.57
2:D:150:PHE:CZ	2:D:154:ILE:CD1	2.87	0.57
1:A:362:PHE:O	1:A:366:LEU:HD13	2.05	0.57
1:C:75:LEU:HD21	1:C:92:LEU:HB3	1.86	0.57
1:A:102:ILE:HD13	1:C:101:ASP:HB3	1.86	0.57
1:A:537:SER:CB	1:A:538:THR:HA	2.35	0.57
1:B:423:GLU:HA	1:B:502:LYS:HE2	1.85	0.57
2:E:122:LYS:CA	2:E:152:ILE:HD11	2.33	0.57
2:E:151:ASP:HA	2:E:154:ILE:HG13	1.87	0.56
2:E:18:LEU:CD1	2:E:18:LEU:O	2.30	0.56
1:A:90:ILE:HG22	1:A:92:LEU:HD21	1.87	0.56
1:C:115:MET:N	1:C:116:PRO:HD2	2.20	0.56
1:A:687:GLN:HG3	1:C:316:PHE:CZ	2.40	0.56
1:B:274:ASN:N	1:B:274:ASN:HD22	2.02	0.56
1:A:725:PRO:HA	1:A:810:GLU:O	2.06	0.56
1:B:745:ASP:O	1:B:749:THR:HG23	2.04	0.56
2:D:28:ASP:O	2:D:32:ILE:HG13	2.05	0.56
1:B:372:VAL:HB	1:B:373:PRO:HD3	1.86	0.56
1:A:412:VAL:O	1:A:416:VAL:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:57:PHE:CB	2:E:59:HIS:CE1	2.84	0.56
1:B:910:ILE:HG23	1:B:1013:THR:HG21	1.88	0.56
2:D:48:TRP:CD1	2:D:77:ASP:OD1	2.59	0.56
1:C:873:ALA:HB3	1:C:874:PRO:HD3	1.87	0.56
1:A:223:PRO:HD2	1:B:780:ARG:HH22	1.71	0.56
1:C:222:THR:HA	1:C:224:PRO:HD3	1.88	0.56
2:D:150:PHE:CE1	2:D:154:ILE:CD1	2.87	0.55
1:A:317:PHE:HB3	1:A:321:LEU:HB3	1.88	0.55
1:A:905:VAL:HB	1:A:906:PRO:HD3	1.87	0.55
1:C:569:GLN:NE2	3:C:1116:HOH:O	2.38	0.55
1:A:563:PHE:O	1:A:924:ASP:HB2	2.07	0.55
1:C:361:ASN:OD1	1:C:362:PHE:N	2.39	0.55
1:C:681:ASP:HB2	3:C:1143:HOH:O	2.07	0.55
2:E:84:LEU:CD2	2:E:116:PRO:HG2	2.35	0.55
1:B:403:GLY:HA3	1:B:982:PHE:HE2	1.70	0.55
1:B:679:GLY:HA3	1:B:829:GLY:O	2.07	0.55
1:B:656:SER:N	3:B:1112:HOH:O	2.40	0.55
1:B:679:GLY:HA2	1:B:830:GLN:HA	1.89	0.55
2:E:85:HIS:HE1	2:E:114:PHE:O	1.89	0.55
1:A:582:ALA:HA	1:A:586:ARG:NH2	2.22	0.54
1:B:184:MET:HE2	1:B:268:ILE:HG22	1.88	0.54
1:B:302:THR:O	1:B:306:ILE:HG23	2.07	0.54
1:B:36:PRO:HG3	1:B:391:ASN:ND2	2.22	0.54
2:E:39:ASP:OD2	2:E:39:ASP:C	2.43	0.54
1:B:521:GLU:O	1:B:524:THR:HG22	2.07	0.54
2:E:44:ASP:CG	2:E:46:THR:OG1	2.46	0.54
1:B:351:VAL:O	1:B:355:MET:HB2	2.08	0.54
1:C:605:ASN:O	1:C:632:LYS:HG2	2.07	0.54
1:C:361:ASN:O	1:C:365:THR:HG22	2.08	0.54
1:A:275:TYR:CG	1:C:223:PRO:HG3	2.43	0.54
1:A:1016:VAL:HG23	1:A:1017:LEU:HD13	1.89	0.54
2:E:161:LEU:HD23	2:E:161:LEU:N	2.23	0.54
1:B:713:LEU:HD13	1:B:843:LEU:HD23	1.88	0.54
2:E:149:ALA:O	2:E:152:ILE:HG22	2.08	0.54
2:E:151:ASP:HA	2:E:154:ILE:HD11	1.90	0.54
1:A:873:ALA:HB3	1:A:874:PRO:HD3	1.88	0.54
1:A:403:GLY:O	1:A:406:VAL:HG12	2.08	0.54
1:B:908:GLY:HA2	1:B:1014:ALA:HB2	1.88	0.54
1:B:647:ILE:HG23	3:B:1164:HOH:O	2.08	0.53
1:C:36:PRO:HG3	1:C:391:ASN:ND2	2.23	0.53
2:E:14:LEU:N	2:E:17:LYS:H	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:679:GLY:N	3:A:1084:HOH:O	2.39	0.53
1:A:653:ARG:NH2	3:A:1169:HOH:O	2.37	0.53
1:A:668:LEU:HD23	1:A:668:LEU:H	1.74	0.53
1:B:717:ARG:HH11	1:B:717:ARG:CG	2.16	0.53
1:C:509:LYS:C	1:C:510:LYS:CD	2.77	0.53
1:C:15:ILE:O	1:C:19:ILE:HG12	2.07	0.53
1:A:214:VAL:CG2	1:A:236:ALA:HB1	2.39	0.53
1:A:777:ALA:O	1:A:781:MET:HG2	2.08	0.53
1:C:4:PHE:O	1:C:8:ARG:HG2	2.09	0.53
1:A:973:ARG:N	1:A:974:PRO:HD2	2.23	0.53
1:C:509:LYS:HB2	1:C:510:LYS:HA	1.91	0.53
1:C:943:ILE:O	1:C:947:GLU:HB3	2.08	0.53
1:A:537:SER:CB	1:A:538:THR:CA	2.87	0.53
1:A:709:HIS:N	1:A:710:PRO:HD3	2.23	0.53
2:D:59:HIS:N	2:D:59:HIS:CD2	2.77	0.53
2:E:115:THR:O	2:E:117:LEU:N	2.42	0.53
1:B:966:ASP:CA	3:B:1170:HOH:O	2.57	0.52
1:A:889:ALA:O	1:C:10:ILE:HD11	2.09	0.52
1:C:336:SER:O	1:C:340:VAL:HG23	2.08	0.52
2:E:150:PHE:O	2:E:154:ILE:HG13	2.09	0.52
1:B:571:VAL:HG12	1:B:630:SER:HA	1.92	0.52
1:C:509:LYS:HB2	1:C:510:LYS:CA	2.39	0.52
1:B:223:PRO:HD2	1:C:780:ARG:HH22	1.73	0.52
1:C:897:ILE:O	1:C:901:VAL:HG12	2.08	0.52
1:A:584:GLN:HG3	3:A:1055:HOH:O	2.10	0.52
1:B:924:ASP:O	1:B:928:GLN:HG3	2.10	0.52
2:E:41:ASN:HD22	2:E:41:ASN:N	2.06	0.52
1:A:934:THR:HG23	1:A:1011:MET:HE3	1.92	0.52
2:D:49:THR:H	2:D:52:HIS:HD2	1.56	0.52
2:E:123:ARG:HB3	2:E:125:HIS:NE2	2.24	0.52
1:A:383:LEU:HD21	1:A:473:THR:HG22	1.92	0.52
1:A:961:ILE:CG2	1:A:962:GLU:N	2.72	0.52
1:B:47:ALA:HB3	1:B:88:VAL:CG1	2.38	0.52
2:D:142:GLN:HB3	2:D:146:GLY:HA2	1.92	0.52
1:B:585:GLU:HB2	3:B:1071:HOH:O	2.08	0.52
1:C:164:ASP:HB2	3:C:1117:HOH:O	2.09	0.52
2:D:148:THR:H	2:D:151:ASP:HB2	1.74	0.52
1:A:586:ARG:NH1	3:A:1131:HOH:O	2.43	0.52
1:C:509:LYS:CB	1:C:510:LYS:HG3	2.38	0.52
1:C:1015:THR:O	1:C:1019:ILE:HB	2.10	0.52
1:A:58:GLN:NE2	3:A:1127:HOH:O	2.31	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:GLY:HA3	1:C:116:PRO:CB	2.39	0.52
1:B:379:THR:HG21	1:B:477:ALA:HA	1.92	0.52
1:C:48:SER:O	1:C:50:PRO:HD3	2.10	0.52
1:C:973:ARG:HB3	1:C:974:PRO:HD3	1.92	0.52
1:A:407:ASP:OD1	1:A:411:VAL:HG23	2.10	0.51
1:B:375:VAL:HG11	1:B:405:LEU:HD22	1.91	0.51
1:C:332:PHE:HA	1:C:335:ILE:HG22	1.92	0.51
1:A:780:ARG:HH22	1:C:223:PRO:HD2	1.74	0.51
1:B:805:SER:O	2:D:144:LYS:NZ	2.43	0.51
1:C:302:THR:O	1:C:306:ILE:HG13	2.10	0.51
2:D:138:ASP:CG	2:D:140:ASN:ND2	2.63	0.51
2:E:57:PHE:O	2:E:59:HIS:ND1	2.43	0.51
1:A:780:ARG:NH2	1:C:223:PRO:HD2	2.25	0.51
1:B:973:ARG:HB3	1:B:974:PRO:HD3	1.92	0.51
1:C:150:THR:O	1:C:154:ILE:HG13	2.11	0.51
1:C:361:ASN:C	1:C:361:ASN:OD1	2.46	0.51
1:B:655:PHE:C	3:B:1112:HOH:O	2.48	0.51
1:B:719:ASN:HB2	1:B:828:LEU:HG	1.93	0.51
1:C:84:SER:OG	1:C:814:PRO:HA	2.10	0.51
2:E:140:ASN:OD1	2:E:140:ASN:N	2.43	0.51
2:E:52:HIS:HD2	2:E:86:LEU:HD11	1.76	0.51
1:B:215:ALA:HB1	1:C:51:GLY:HA3	1.92	0.51
1:A:781:MET:HB3	1:C:228:GLN:OE1	2.11	0.51
1:B:864:TYR:O	1:B:865:GLN:CB	2.55	0.51
1:B:944:LEU:HD13	1:B:971:ARG:NH1	2.25	0.51
2:E:101:LYS:HG2	2:E:102:ASN:HD22	1.75	0.51
1:B:435:MET:O	1:B:439:GLN:HG3	2.11	0.51
1:B:679:GLY:CA	1:B:829:GLY:O	2.59	0.51
2:D:150:PHE:HB2	3:D:181:HOH:O	2.11	0.51
2:E:122:LYS:HA	2:E:152:ILE:CD1	2.37	0.51
1:C:185:ARG:HG3	1:C:271:GLY:HA3	1.93	0.51
1:A:393:LEU:HD22	1:A:470:PHE:HE1	1.76	0.50
1:B:47:ALA:HB3	1:B:88:VAL:HG13	1.94	0.50
1:A:150:THR:O	1:A:154:ILE:HG13	2.11	0.50
1:A:754:TRP:CZ3	1:C:219:LEU:HD23	2.45	0.50
1:C:489:THR:HB	1:C:490:PRO:HD3	1.92	0.50
1:C:819:TYR:OH	1:C:860:THR:HG23	2.11	0.50
1:A:360:GLN:HG2	1:A:513:PHE:CD2	2.47	0.50
1:A:393:LEU:HD11	1:A:466:ILE:HG13	1.94	0.50
1:A:11:PHE:CD2	1:B:890:ALA:HB1	2.47	0.50
1:A:463:THR:O	1:A:467:TYR:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:THR:HG22	1:C:213:GLN:NE2	2.26	0.50
1:A:923:ASN:HD22	1:A:923:ASN:C	2.14	0.50
2:E:105:ASP:HB3	2:E:108:ALA:HB2	1.93	0.50
1:A:351:VAL:O	1:A:355:MET:HG2	2.11	0.50
1:C:242:SER:OG	1:C:244:GLU:HG2	2.11	0.50
2:E:15:GLY:HA2	2:E:42:ALA:CB	2.42	0.50
1:A:407:ASP:OD1	1:A:407:ASP:O	2.30	0.50
1:B:559:LEU:HD12	1:B:560:PRO:HD2	1.93	0.50
1:C:372:VAL:CG2	1:C:373:PRO:HD3	2.40	0.50
2:D:92:HIS:O	2:D:96:VAL:HG23	2.12	0.50
1:B:184:MET:HE1	1:B:243:THR:HB	1.93	0.50
1:C:356:TYR:O	1:C:360:GLN:HA	2.11	0.50
1:C:572:PHE:HE2	1:C:631:LEU:HD21	1.75	0.50
1:C:904:VAL:HG23	1:C:907:LEU:HD12	1.92	0.50
2:E:44:ASP:OD2	2:E:46:THR:OG1	2.30	0.50
2:E:93:LEU:O	2:E:96:VAL:N	2.44	0.50
1:B:871:ASN:HD22	1:B:872:GLN:HG3	1.77	0.50
1:C:362:PHE:HA	1:C:365:THR:HG22	1.94	0.50
2:E:44:ASP:OD2	2:E:48:TRP:N	2.44	0.50
1:A:743:ILE:HD12	1:A:743:ILE:H	1.77	0.49
1:B:224:PRO:HA	1:C:781:MET:CE	2.41	0.49
1:A:537:SER:OG	1:A:539:GLY:N	2.45	0.49
1:C:167:SER:HB3	3:C:1079:HOH:O	2.11	0.49
1:C:888:LEU:HD13	1:C:901:VAL:HG11	1.94	0.49
2:D:77:ASP:HB2	2:D:81:VAL:N	2.27	0.49
1:A:220:GLY:HA2	1:B:781:MET:SD	2.52	0.49
1:A:412:VAL:HG11	1:A:489:THR:HG22	1.93	0.49
2:D:138:ASP:CG	2:D:140:ASN:HD21	2.16	0.49
2:D:77:ASP:HB2	2:D:81:VAL:H	1.76	0.49
1:B:709:HIS:N	1:B:710:PRO:HD3	2.27	0.49
1:B:793:ALA:HA	3:B:1095:HOH:O	2.11	0.49
1:B:126:GLY:CA	1:C:116:PRO:HB3	2.39	0.49
1:A:809:TRP:CE2	2:E:46:THR:HG22	2.47	0.49
1:C:454:VAL:HB	1:C:455:PRO:HD3	1.94	0.49
1:A:489:THR:HB	1:A:490:PRO:HD3	1.94	0.49
1:C:691:GLY:O	1:C:695:LEU:HB2	2.13	0.49
1:A:893:GLU:OE2	1:C:8:ARG:HB3	2.12	0.49
2:E:151:ASP:HA	2:E:154:ILE:CG1	2.43	0.49
1:B:414:GLU:CD	1:B:974:PRO:HG3	2.33	0.49
2:E:77:ASP:HB2	2:E:81:VAL:H	1.78	0.49
1:A:291:ILE:HD13	1:A:306:ILE:HD13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:15:GLY:CA	2:E:42:ALA:HB1	2.42	0.49
1:A:391:ASN:H	1:A:394:THR:HB	1.78	0.49
2:E:133:LEU:HD23	2:E:137:ALA:HB3	1.93	0.49
2:E:90:ARG:HB3	2:E:92:HIS:CD2	2.48	0.49
1:A:660:ASP:CB	3:A:1173:HOH:O	2.61	0.48
1:A:860:THR:HG22	1:A:861:GLY:H	1.77	0.48
1:B:250:LEU:HD21	1:B:259:ARG:HB3	1.94	0.48
1:B:2:PRO:O	1:B:6:ILE:HG13	2.12	0.48
1:C:531:VAL:O	1:C:534:ILE:HG12	2.12	0.48
1:A:130:GLU:HG2	1:A:174:ASP:HB2	1.96	0.48
1:A:78:MET:HG3	1:A:92:LEU:CD2	2.42	0.48
1:B:987:MET:HB2	1:B:988:PRO:HD3	1.95	0.48
1:C:950:LYS:HA	1:C:953:MET:HE2	1.96	0.48
2:E:57:PHE:C	2:E:59:HIS:CE1	2.86	0.48
1:A:946:VAL:HG13	1:A:1026:PHE:CE1	2.48	0.48
1:A:370:ILE:O	1:A:374:VAL:HG23	2.14	0.48
1:B:463:THR:HG22	1:B:467:TYR:HE1	1.79	0.48
1:C:586:ARG:NH2	3:C:1091:HOH:O	2.46	0.48
1:C:65:ILE:O	1:C:69:MET:HG2	2.13	0.48
1:C:905:VAL:HB	1:C:906:PRO:HD3	1.95	0.48
2:D:51:LEU:HD11	2:D:67:LEU:HD21	1.95	0.48
1:A:13:TRP:O	1:A:17:ILE:HG13	2.14	0.48
1:A:445:ILE:HA	1:A:448:VAL:HG22	1.96	0.48
1:B:456:MET:HG2	1:B:467:TYR:HB3	1.95	0.48
1:C:1008:MET:O	1:C:1012:VAL:HG23	2.13	0.48
1:C:281:PHE:CE2	1:C:324:VAL:HG21	2.49	0.48
2:E:44:ASP:OD1	2:E:46:THR:OG1	2.30	0.48
1:A:162:MET:HG2	1:A:313:MET:HE3	1.95	0.48
1:A:578:LEU:HD13	1:A:587:THR:HG22	1.96	0.48
1:A:63:GLN:HE22	1:C:767:ARG:HA	1.79	0.48
1:A:758:TYR:HE1	1:A:760:ASN:O	1.96	0.48
1:A:66:GLU:HG2	1:A:78:MET:HE2	1.94	0.48
1:C:1:FME:HB2	1:C:2:PRO:HD3	1.95	0.48
1:C:351:VAL:HG21	1:C:402:ILE:HG22	1.95	0.48
1:C:76:MET:CG	1:C:95:GLU:HG3	2.44	0.48
2:D:52:HIS:CE1	2:D:83:PRO:HD3	2.49	0.48
2:E:60:LEU:HD11	2:E:98:VAL:HG21	1.94	0.48
1:B:455:PRO:HG2	1:B:880:SER:HB2	1.96	0.48
2:E:41:ASN:ND2	2:E:41:ASN:N	2.62	0.48
1:A:214:VAL:CG2	1:A:236:ALA:HB3	2.39	0.48
1:A:537:SER:HB3	1:A:538:THR:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:960:LEU:CD1	1:A:961:ILE:CA	2.81	0.48
1:B:681:ASP:HB3	1:B:860:THR:O	2.12	0.48
1:B:241:THR:HA	1:B:763:ILE:O	2.14	0.48
1:C:167:SER:CB	3:C:1079:HOH:O	2.62	0.48
1:C:350:LEU:O	1:C:354:VAL:HG23	2.13	0.48
1:B:463:THR:HG22	1:B:467:TYR:CE1	2.48	0.48
1:B:729:ILE:HD11	1:B:786:ILE:HD13	1.95	0.48
1:C:971:ARG:C	1:C:974:PRO:HD2	2.34	0.48
1:A:146:ASP:N	1:A:146:ASP:OD1	2.43	0.47
1:A:340:VAL:HG11	1:A:395:MET:HB3	1.96	0.47
1:A:960:LEU:CD1	1:A:961:ILE:HA	2.42	0.47
1:A:993:THR:HA	1:A:997:SER:HB3	1.94	0.47
1:B:944:LEU:HD13	1:B:971:ARG:HH11	1.79	0.47
1:A:781:MET:SD	1:C:220:GLY:HA2	2.54	0.47
1:B:420:MET:CE	1:B:499:PRO:HA	2.44	0.47
1:B:893:GLU:O	1:B:893:GLU:HG3	2.14	0.47
1:B:223:PRO:HD2	1:C:780:ARG:NH2	2.29	0.47
2:D:17:LYS:HZ3	2:D:17:LYS:CB	2.15	0.47
1:A:105:VAL:HG13	3:A:1057:HOH:O	2.13	0.47
1:C:637:ARG:N	1:C:638:PRO:HD3	2.30	0.47
1:C:733:GLN:HG2	3:C:1178:HOH:O	2.13	0.47
1:A:2:PRO:O	1:A:6:ILE:HG13	2.14	0.47
1:A:355:MET:HE2	1:A:368:PRO:HG2	1.96	0.47
1:A:703:LEU:HD11	1:A:718:PRO:HG3	1.97	0.47
1:C:33:ALA:O	1:C:391:ASN:HA	2.15	0.47
2:E:110:ASP:OD2	2:E:114:PHE:N	2.41	0.47
1:A:1043:SER:HA	1:A:1044:HIS:HA	1.50	0.47
1:A:601:LYS:NZ	3:A:1106:HOH:O	2.39	0.47
1:A:915:ALA:O	1:A:919:ARG:HB2	2.15	0.47
1:B:362:PHE:HA	1:B:365:THR:HG22	1.96	0.47
1:B:901:VAL:O	1:B:904:VAL:HG22	2.15	0.47
1:C:578:LEU:HD13	1:C:587:THR:HB	1.95	0.47
1:B:527:TYR:OH	1:B:1019:ILE:HB	2.15	0.47
1:A:33:ALA:O	1:A:391:ASN:HA	2.15	0.47
1:B:595:THR:HG23	1:B:609:VAL:HB	1.96	0.47
1:B:777:ALA:O	1:B:781:MET:HG2	2.15	0.47
1:C:166:ILE:HD11	1:C:310:LEU:HD13	1.96	0.47
2:E:161:LEU:H	2:E:161:LEU:CD2	2.27	0.47
1:A:669:PRO:O	1:A:671:ILE:HA	2.14	0.47
1:B:121:GLU:CD	1:B:121:GLU:H	2.17	0.47
1:B:379:THR:CG2	1:B:477:ALA:HA	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:600:THR:O	1:C:603:LYS:HE3	2.15	0.47
2:E:40:VAL:HG11	2:E:71:ALA:HB2	1.95	0.47
2:E:40:VAL:C	2:E:41:ASN:HD22	2.18	0.47
1:B:363:ARG:HB3	1:B:496:MET:O	2.15	0.47
1:C:326:PRO:O	1:C:630:SER:HB2	2.14	0.47
2:E:123:ARG:NH2	3:E:170:HOH:O	2.48	0.47
1:A:101:ASP:OD1	1:A:131:LYS:HE2	2.15	0.46
1:A:222:THR:HA	1:A:224:PRO:HD3	1.97	0.46
1:A:243:THR:HG23	3:A:1135:HOH:O	2.14	0.46
1:A:520:PHE:O	1:A:524:THR:HG23	2.14	0.46
1:B:844:MET:HE3	1:B:844:MET:HA	1.96	0.46
1:C:741:VAL:HG11	1:C:799:VAL:HG11	1.96	0.46
1:C:880:SER:O	1:C:884:VAL:HG23	2.15	0.46
1:A:259:ARG:H	1:A:259:ARG:CD	2.08	0.46
1:C:452:VAL:HG23	1:C:453:PHE:CD1	2.50	0.46
1:C:743:ILE:HG12	1:C:743:ILE:O	2.15	0.46
1:A:396:PHE:CD2	1:A:1003:VAL:HG21	2.50	0.46
1:B:149:MET:HB2	1:B:153:ASP:CB	2.45	0.46
1:B:880:SER:O	1:B:884:VAL:HG23	2.15	0.46
1:C:463:THR:HG22	1:C:467:TYR:CZ	2.51	0.46
1:C:799:VAL:HA	1:C:800:PRO:HD3	1.78	0.46
1:A:252:LYS:HE3	1:A:254:ASN:OD1	2.15	0.46
1:A:704:ALA:O	1:A:708:LYS:HG3	2.14	0.46
1:B:1022:VAL:N	1:B:1023:PRO:CD	2.79	0.46
1:B:330:THR:HB	1:B:331:PRO:HD3	1.95	0.46
1:A:880:SER:O	1:A:884:VAL:HG23	2.16	0.46
1:B:775:SER:HB2	1:B:789:TRP:CZ2	2.51	0.46
1:B:714:THR:HG23	1:B:830:GLN:HG3	1.97	0.46
1:C:184:MET:HB3	1:C:771:VAL:HG22	1.98	0.46
2:D:65:VAL:O	2:D:69:ASN:ND2	2.47	0.46
2:E:122:LYS:CG	2:E:152:ILE:HD11	2.40	0.46
2:E:93:LEU:O	2:E:97:GLU:N	2.32	0.46
1:A:817:GLU:OE1	1:A:825:MET:HA	2.15	0.46
1:B:621:GLY:O	1:B:624:THR:HG22	2.16	0.46
1:A:20:MET:CE	1:A:374:VAL:HG22	2.46	0.46
1:B:676:THR:O	1:B:677:ALA:CB	2.64	0.46
1:A:53:ASP:OD1	1:A:56:THR:HG23	2.16	0.46
1:C:40:PRO:HB3	1:C:94:PHE:O	2.15	0.46
2:D:143:ASP:O	2:D:146:GLY:N	2.39	0.46
1:A:446:ALA:HB2	1:A:482:VAL:HG21	1.96	0.46
1:A:987:MET:HB3	1:A:988:PRO:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:MET:HE3	1:B:268:ILE:HG22	1.98	0.46
1:B:620:ARG:HA	1:B:624:THR:HG21	1.98	0.46
1:A:622:GLN:NE2	1:C:222:THR:HG23	2.31	0.46
1:C:5:PHE:CG	1:C:487:ILE:HG23	2.51	0.46
2:E:100:LEU:HD11	2:E:106:VAL:HG22	1.97	0.46
1:A:541:TYR:O	1:A:542:LEU:C	2.52	0.46
1:B:146:ASP:HB3	1:B:148:THR:HG22	1.97	0.46
1:B:342:LYS:O	1:B:346:GLU:HG2	2.16	0.46
1:B:400:LEU:HD21	1:B:1003:VAL:HB	1.98	0.46
1:C:7:ASP:C	1:C:9:PRO:HD3	2.36	0.46
1:B:115:MET:N	1:B:116:PRO:CD	2.79	0.45
1:B:314:GLU:N	1:B:315:PRO:CD	2.79	0.45
1:C:530:SER:O	1:C:534:ILE:HG23	2.16	0.45
1:C:54:ALA:HA	1:C:57:VAL:HG12	1.98	0.45
1:A:115:MET:HB2	1:A:116:PRO:HD3	1.98	0.45
2:E:161:LEU:O	2:E:164:ILE:HB	2.16	0.45
1:A:895:TRP:CZ2	1:C:10:ILE:HB	2.52	0.45
1:B:192:GLU:HG2	1:B:264:ASP:O	2.16	0.45
1:B:565:PRO:HG3	1:B:924:ASP:OD1	2.15	0.45
1:C:314:GLU:HA	1:C:317:PHE:CE2	2.52	0.45
1:C:404:LEU:HD13	1:C:982:PHE:HD1	1.82	0.45
1:C:431:THR:O	1:C:435:MET:HG2	2.15	0.45
1:B:293:LEU:CD2	1:B:297:ALA:HB3	2.46	0.45
1:C:1033:PHE:CD1	1:C:1033:PHE:N	2.84	0.45
1:C:563:PHE:O	1:C:924:ASP:HB2	2.15	0.45
2:E:94:GLU:O	2:E:98:VAL:HG23	2.17	0.45
1:A:240:LEU:N	1:A:240:LEU:CD1	2.79	0.45
1:A:679:GLY:HA2	1:A:830:GLN:HA	1.98	0.45
1:A:790:TYR:HE1	1:A:800:PRO:HG3	1.79	0.45
1:A:860:THR:HG22	1:A:861:GLY:N	2.31	0.45
1:B:139:VAL:HG22	1:B:327:TYR:HB3	1.98	0.45
1:C:181:GLN:OE1	1:C:767:ARG:HD3	2.16	0.45
2:D:138:ASP:CA	2:D:140:ASN:ND2	2.75	0.45
1:A:392:THR:O	1:A:396:PHE:HD1	2.00	0.45
1:A:537:SER:N	1:A:538:THR:HA	2.32	0.45
1:A:93:THR:HG23	3:A:1058:HOH:O	2.17	0.45
1:B:166:ILE:O	1:B:172:VAL:HG11	2.17	0.45
1:B:879:ILE:O	1:B:883:VAL:HG23	2.16	0.45
1:C:152:GLU:HG2	1:C:182:TYR:HE1	1.82	0.45
1:C:2:PRO:O	1:C:6:ILE:HG13	2.16	0.45
2:E:15:GLY:CA	2:E:42:ALA:CB	2.95	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:743:ILE:HD12	1:A:743:ILE:N	2.32	0.45
1:C:57:VAL:CG1	1:C:82:SER:HB3	2.46	0.45
2:E:81:VAL:HG11	2:E:86:LEU:HD21	1.99	0.45
1:A:84:SER:OG	1:A:814:PRO:HA	2.17	0.45
1:B:484:VAL:HG13	1:B:488:LEU:HB3	1.98	0.45
1:B:733:GLN:HE22	1:B:743:ILE:HG13	1.82	0.45
2:D:89:ARG:C	2:D:90:ARG:O	2.55	0.45
2:E:40:VAL:HG12	2:E:71:ALA:CB	2.46	0.45
1:A:302:THR:O	1:A:306:ILE:HG13	2.17	0.45
1:A:345:VAL:O	1:A:349:ILE:HG13	2.16	0.45
1:A:200:PRO:HD2	1:A:749:THR:HB	1.99	0.45
1:A:879:ILE:HD12	1:A:880:SER:N	2.32	0.45
1:B:278:ILE:HG12	1:B:613:ASN:HB3	1.99	0.45
1:C:509:LYS:C	1:C:510:LYS:CE	2.79	0.45
2:D:122:LYS:HB2	2:D:122:LYS:NZ	2.32	0.45
1:B:1022:VAL:CG2	1:B:1023:PRO:HD3	2.46	0.44
1:B:278:ILE:HG13	1:B:278:ILE:O	2.17	0.44
1:C:777:ALA:O	1:C:781:MET:HG2	2.17	0.44
1:C:898:PRO:O	1:C:902:MET:HG2	2.17	0.44
1:B:441:ALA:O	1:B:445:ILE:HG13	2.17	0.44
1:B:914:LEU:HA	1:B:914:LEU:HD13	1.88	0.44
1:B:973:ARG:O	1:B:977:MET:HG3	2.16	0.44
1:C:504:ASP:O	1:C:506:GLY:O	2.34	0.44
1:A:969:ARG:HG3	1:A:970:MET:N	2.31	0.44
1:B:75:LEU:HD21	1:B:92:LEU:HB3	1.99	0.44
1:B:956:GLU:HG3	1:B:958:LYS:HE2	1.98	0.44
1:C:36:PRO:HG2	1:C:469:GLN:HG3	1.98	0.44
1:C:527:TYR:HE2	1:C:968:VAL:HG13	1.80	0.44
2:E:90:ARG:CB	2:E:92:HIS:CD2	3.00	0.44
1:B:717:ARG:NH1	1:B:717:ARG:CG	2.75	0.44
1:C:11:PHE:O	1:C:14:VAL:HG22	2.16	0.44
1:C:239:ARG:CG	1:C:762:PHE:HA	2.47	0.44
1:C:944:LEU:O	1:C:971:ARG:HG3	2.17	0.44
2:E:132:LEU:O	2:E:137:ALA:HB2	2.17	0.44
2:E:57:PHE:O	2:E:59:HIS:HE1	1.94	0.44
1:B:189:ASN:HA	1:B:190:PRO:HD2	1.81	0.44
1:B:255:GLN:H	1:B:255:GLN:CD	2.21	0.44
1:C:131:LYS:NZ	3:C:1170:HOH:O	2.47	0.44
2:D:61:GLU:O	2:D:65:VAL:HG23	2.17	0.44
2:E:60:LEU:HD12	2:E:63:VAL:HB	1.99	0.44
1:A:370:ILE:O	1:A:373:PRO:HD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:ARG:O	1:A:590:VAL:HG23	2.16	0.44
1:A:961:ILE:HG23	1:A:962:GLU:N	2.33	0.44
1:B:990:VAL:HG13	1:B:1005:THR:HG22	1.99	0.44
1:C:193:LEU:CD1	1:C:265:VAL:HB	2.46	0.44
1:C:404:LEU:HD13	1:C:982:PHE:CD1	2.52	0.44
2:E:159:GLU:O	2:E:160:ASP:C	2.56	0.44
1:A:908:GLY:HA2	1:A:1014:ALA:HB2	2.00	0.44
1:A:159:ALA:HB2	1:A:177:LEU:HD22	1.99	0.44
1:A:344:LEU:O	1:A:348:ILE:HG22	2.18	0.44
1:A:412:VAL:HG11	1:A:489:THR:CG2	2.47	0.44
1:B:240:LEU:CD1	1:B:240:LEU:N	2.80	0.44
1:B:188:MET:HA	1:B:266:ALA:HB2	2.00	0.44
1:B:919:ARG:HB3	1:B:921:LEU:HD13	1.99	0.44
1:B:967:ALA:HA	1:B:970:MET:HE3	1.99	0.44
1:C:166:ILE:HD11	1:C:310:LEU:CD1	2.47	0.44
1:C:69:MET:HE1	1:C:107:VAL:HG13	1.99	0.44
1:A:223:PRO:HA	1:A:224:PRO:HD3	1.78	0.44
1:A:307:ARG:HH22	1:A:330:THR:HG21	1.83	0.44
1:A:950:LYS:O	1:A:954:ASP:CB	2.65	0.44
1:B:968:VAL:HG21	1:B:1023:PRO:HG3	1.99	0.44
1:B:725:PRO:HA	1:B:810:GLU:O	2.17	0.44
1:C:1033:PHE:HD1	1:C:1033:PHE:N	2.16	0.44
1:C:1:FME:H	1:C:2:PRO:CD	2.31	0.44
1:C:538:THR:O	1:C:542:LEU:HD13	2.18	0.44
1:C:586:ARG:O	1:C:589:LYS:HB3	2.16	0.44
2:D:30:VAL:HG21	2:D:62:ILE:CD1	2.47	0.44
1:A:509:LYS:CB	1:A:514:GLY:CA	2.96	0.44
1:A:542:LEU:HD22	1:A:542:LEU:H	1.83	0.44
1:B:99:ASP:OD1	1:B:101:ASP:HB2	2.18	0.44
1:B:905:VAL:N	1:B:906:PRO:HD2	2.32	0.44
1:C:727:PHE:CE1	1:C:807:SER:HB2	2.53	0.44
2:E:142:GLN:HB3	2:E:146:GLY:HA2	2.00	0.44
1:A:602:GLU:HG3	1:A:605:ASN:HB2	1.99	0.43
1:B:154:ILE:O	1:B:158:VAL:HG23	2.17	0.43
1:B:324:VAL:HG23	1:B:326:PRO:HD3	1.99	0.43
1:C:1:FME:H	1:C:2:PRO:HD2	1.84	0.43
1:C:545:TYR:O	1:C:549:VAL:HG23	2.17	0.43
2:E:77:ASP:C	2:E:79:LEU:N	2.68	0.43
1:A:41:PRO:HD2	1:A:95:GLU:O	2.18	0.43
1:A:992:SER:C	1:A:993:THR:CG2	2.86	0.43
1:C:1016:VAL:HG23	1:C:1017:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:93:LEU:HA	2:E:96:VAL:HG21	1.91	0.43
1:A:984:LEU:O	1:A:984:LEU:HD13	2.18	0.43
1:B:945:ILE:HD12	1:B:1022:VAL:HG21	2.00	0.43
1:C:480:LEU:O	1:C:484:VAL:HG23	2.18	0.43
1:C:717:ARG:HA	1:C:718:PRO:HD3	1.90	0.43
1:A:324:VAL:O	1:A:326:PRO:HD3	2.19	0.43
1:A:456:MET:HG2	1:A:467:TYR:HB3	2.00	0.43
1:A:809:TRP:CD2	2:E:46:THR:HG22	2.53	0.43
1:C:23:GLY:O	1:C:27:ILE:HG12	2.19	0.43
1:C:298:ASN:HB3	1:C:301:ASP:HB2	2.00	0.43
1:C:534:ILE:HB	1:C:541:TYR:CE2	2.54	0.43
2:D:62:ILE:HG23	2:D:62:ILE:HD13	1.78	0.43
1:A:939:ALA:O	1:A:943:ILE:HG13	2.18	0.43
1:B:240:LEU:HD12	1:B:240:LEU:N	2.32	0.43
1:B:395:MET:CE	1:B:395:MET:HA	2.49	0.43
1:B:454:VAL:N	1:B:455:PRO:CD	2.81	0.43
1:B:489:THR:HB	1:B:490:PRO:HD3	1.99	0.43
1:C:1032:ARG:C	1:C:1033:PHE:HD1	2.21	0.43
1:C:509:LYS:HB2	1:C:510:LYS:CB	2.49	0.43
1:C:76:MET:HG2	1:C:95:GLU:HG3	2.01	0.43
2:D:31:ARG:O	2:D:34:MET:HB2	2.19	0.43
2:E:60:LEU:HD12	2:E:60:LEU:HA	1.70	0.43
1:B:48:SER:HB3	1:B:125:GLN:HG2	2.00	0.43
1:B:577:GLN:O	1:B:661:ALA:HB1	2.18	0.43
1:B:702:LEU:HD21	1:B:844:MET:HE1	2.01	0.43
1:A:239:ARG:NE	3:A:1113:HOH:O	2.33	0.43
1:A:767:ARG:HA	1:B:63:GLN:HE22	1.82	0.43
1:B:149:MET:HB2	1:B:153:ASP:HB2	2.01	0.43
1:B:223:PRO:HG3	1:C:275:TYR:CD1	2.53	0.43
1:B:683:GLU:HG2	1:B:819:TYR:CG	2.54	0.43
1:B:997:SER:O	1:B:998:GLY:C	2.56	0.43
1:C:876:LEU:HD13	1:C:932:LEU:HD21	2.01	0.43
2:E:14:LEU:C	2:E:16:LYS:N	2.63	0.43
1:A:166:ILE:HD11	1:A:310:LEU:CD1	2.46	0.43
1:A:919:ARG:HD2	1:A:921:LEU:HD13	2.01	0.43
1:B:401:ALA:O	1:B:405:LEU:HG	2.19	0.43
1:B:559:LEU:HD12	1:B:560:PRO:HD3	2.01	0.43
1:B:897:ILE:N	1:B:898:PRO:HD2	2.34	0.43
1:C:189:ASN:O	1:C:193:LEU:HD13	2.19	0.43
1:C:314:GLU:N	1:C:315:PRO:CD	2.81	0.43
2:E:117:LEU:HD21	2:E:129:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:151:ASP:CA	2:E:154:ILE:HG13	2.47	0.43
1:A:181:GLN:HE22	1:A:767:ARG:NH1	2.07	0.43
1:A:741:VAL:HA	3:A:1150:HOH:O	2.18	0.43
1:A:901:VAL:O	1:A:904:VAL:HG12	2.18	0.43
1:C:878:ALA:O	1:C:882:ILE:HG12	2.19	0.43
2:D:134:LYS:HG3	2:D:135:ASN:HD22	1.83	0.43
1:A:314:GLU:HB2	1:A:315:PRO:HD3	2.00	0.42
1:A:712:MET:HA	1:A:832:ALA:CB	2.42	0.42
1:A:892:TYR:O	1:A:950:LYS:HE3	2.19	0.42
1:C:358:PHE:CG	1:C:977:MET:HG2	2.54	0.42
1:A:537:SER:OG	1:A:538:THR:CA	2.67	0.42
1:C:735:LYS:O	1:C:739:LEU:HD13	2.19	0.42
1:A:767:ARG:HA	1:B:63:GLN:HE21	1.80	0.42
1:A:801:PHE:O	1:A:805:SER:OG	2.34	0.42
1:B:332:PHE:CZ	1:B:569:GLN:HA	2.53	0.42
1:B:194:ASN:ND2	1:B:798:MET:HG3	2.34	0.42
1:B:897:ILE:N	1:B:898:PRO:CD	2.82	0.42
1:C:69:MET:CE	1:C:107:VAL:HG13	2.50	0.42
1:C:235:ILE:HG22	1:C:236:ALA:H	1.84	0.42
1:C:505:HIS:H	1:C:505:HIS:CD2	2.35	0.42
1:C:194:ASN:ND2	1:C:798:MET:HG3	2.34	0.42
2:E:18:LEU:HD22	2:E:18:LEU:HA	1.77	0.42
2:E:82:THR:O	2:E:85:HIS:N	2.49	0.42
1:A:293:LEU:CD2	1:A:297:ALA:HB3	2.49	0.42
1:A:568:ASP:CG	1:A:637:ARG:HH22	2.23	0.42
1:A:753:ALA:O	1:A:775:SER:HB3	2.20	0.42
1:C:933:THR:O	1:C:937:LEU:HG	2.19	0.42
2:E:43:ARG:HB3	2:E:47:GLY:HA2	2.01	0.42
2:E:58:GLY:HA3	2:E:92:HIS:CE1	2.55	0.42
1:A:314:GLU:HA	1:A:317:PHE:CD2	2.55	0.42
1:A:300:LEU:CD2	1:A:330:THR:HG23	2.45	0.42
1:A:407:ASP:OD1	1:A:407:ASP:C	2.56	0.42
1:A:682:PHE:HD1	1:A:859:TRP:CH2	2.37	0.42
1:C:413:VAL:O	1:C:417:GLU:HG2	2.19	0.42
1:C:239:ARG:HG2	1:C:762:PHE:HA	2.01	0.42
2:E:60:LEU:C	2:E:62:ILE:N	2.72	0.42
1:A:234:ILE:HD13	1:A:234:ILE:HG21	1.70	0.42
1:A:263:ARG:H	1:A:263:ARG:HG3	1.62	0.42
1:A:459:PHE:O	1:A:464:GLY:HA3	2.19	0.42
1:A:585:GLU:HB2	3:C:1123:HOH:O	2.20	0.42
1:B:892:TYR:O	1:B:950:LYS:HE3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:VAL:O	1:C:18:ILE:HG13	2.19	0.42
1:C:40:PRO:HA	1:C:41:PRO:HD3	1.85	0.42
1:C:736:ALA:O	1:C:741:VAL:HG22	2.19	0.42
1:A:1021:PHE:HB3	1:A:1025:PHE:CE1	2.55	0.42
1:A:23:GLY:HA3	1:A:377:LEU:O	2.19	0.42
1:A:509:LYS:CB	1:A:514:GLY:HA2	2.49	0.42
1:B:27:ILE:HG12	1:B:27:ILE:O	2.19	0.42
1:C:583:THR:HB	3:C:1072:HOH:O	2.19	0.42
1:C:355:MET:SD	1:C:368:PRO:HB2	2.60	0.42
2:E:138:ASP:OD1	2:E:140:ASN:N	2.53	0.42
1:A:111:LEU:HD23	1:A:111:LEU:O	2.19	0.42
1:A:298:ASN:HB3	1:A:301:ASP:HB2	2.01	0.42
1:A:564:LEU:HA	1:A:565:PRO:HD2	1.89	0.42
1:A:80:SER:HA	1:A:89:GLN:O	2.20	0.42
1:A:726:GLN:CD	1:A:812:GLY:HA3	2.40	0.42
1:A:892:TYR:O	1:A:893:GLU:HB2	2.20	0.42
1:A:932:LEU:HA	1:A:935:ILE:HG22	2.01	0.42
1:B:355:MET:HE3	3:B:1109:HOH:O	2.20	0.42
1:A:410:ILE:HG22	1:A:411:VAL:N	2.26	0.42
1:A:717:ARG:HA	1:A:718:PRO:HD3	1.93	0.42
1:B:222:THR:HG23	1:C:622:GLN:NE2	2.35	0.42
1:C:1013:THR:O	1:C:1017:LEU:HB2	2.20	0.42
1:C:893:GLU:HG3	1:C:893:GLU:O	2.20	0.42
2:D:89:ARG:HB2	2:D:119:LEU:HB3	2.01	0.42
1:A:1019:ILE:HA	1:A:1019:ILE:HD13	1.87	0.41
1:A:62:THR:HB	1:A:88:VAL:HG11	2.02	0.41
1:B:719:ASN:HD22	1:B:826:GLU:CD	2.24	0.41
1:C:314:GLU:HA	1:C:317:PHE:CD2	2.55	0.41
2:E:100:LEU:HA	2:E:104:ALA:HB3	2.02	0.41
2:E:139:VAL:CG1	2:E:139:VAL:O	2.67	0.41
1:A:70:ASN:C	1:A:70:ASN:HD22	2.23	0.41
1:A:759:VAL:H	1:A:759:VAL:HG23	1.63	0.41
1:B:143:ILE:HG22	1:B:286:ALA:HB2	2.01	0.41
1:B:420:MET:HE2	3:B:1156:HOH:O	2.19	0.41
2:D:139:VAL:HG12	2:D:140:ASN:N	2.33	0.41
1:A:238:THR:HG22	1:A:239:ARG:N	2.36	0.41
1:B:224:PRO:HA	1:C:781:MET:HE3	2.01	0.41
1:B:446:ALA:HB2	1:B:482:VAL:HG21	2.01	0.41
1:B:939:ALA:O	1:B:943:ILE:HG13	2.21	0.41
1:A:583:THR:HG21	1:C:228:GLN:O	2.21	0.41
2:D:89:ARG:NH1	3:D:172:HOH:O	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:77:ASP:O	2:E:78:SER:C	2.58	0.41
1:A:14:VAL:HG13	1:B:886:LEU:HB3	2.01	0.41
1:C:369:THR:O	1:C:373:PRO:HD3	2.20	0.41
1:A:66:GLU:HG2	1:A:78:MET:CE	2.49	0.41
1:A:987:MET:N	1:A:988:PRO:CD	2.83	0.41
1:B:200:PRO:O	1:B:204:ILE:HG13	2.21	0.41
1:B:676:THR:O	1:B:676:THR:CG2	2.66	0.41
1:C:632:LYS:HG2	1:C:632:LYS:H	1.72	0.41
1:C:780:ARG:HD2	3:C:1089:HOH:O	2.20	0.41
2:E:60:LEU:O	2:E:62:ILE:N	2.54	0.41
1:A:1007:VAL:O	1:A:1011:MET:HB2	2.20	0.41
1:C:85:THR:OG1	1:C:87:THR:HG22	2.21	0.41
1:A:567:GLU:OE1	1:A:996:GLY:HA2	2.21	0.41
1:B:396:PHE:HA	1:B:399:VAL:HG22	2.03	0.41
1:B:682:PHE:CZ	1:B:857:TYR:HB2	2.55	0.41
1:C:445:ILE:O	1:C:448:VAL:HG12	2.21	0.41
2:D:134:LYS:HG3	2:D:135:ASN:ND2	2.35	0.41
2:D:59:HIS:H	2:D:59:HIS:CD2	2.39	0.41
1:B:223:PRO:HG3	1:C:275:TYR:CD2	2.55	0.41
1:C:420:MET:HG3	1:C:425:LEU:O	2.20	0.41
1:C:64:VAL:HG12	1:C:114:ALA:HB1	2.03	0.41
1:C:775:SER:OG	1:C:789:TRP:HZ2	2.03	0.41
2:E:115:THR:O	2:E:116:PRO:C	2.57	0.41
1:A:165:ALA:O	1:A:169:THR:HG23	2.20	0.41
1:B:643:LYS:O	1:B:647:ILE:HG13	2.21	0.41
1:B:799:VAL:HA	1:B:800:PRO:HD3	1.87	0.41
1:B:415:ASN:HB3	3:B:1119:HOH:O	2.20	0.41
1:B:493:CYS:O	1:B:497:LEU:HB2	2.21	0.41
1:B:764:ASP:OD1	1:B:765:ARG:HD3	2.21	0.41
1:A:781:MET:CE	1:C:224:PRO:HA	2.50	0.41
1:C:509:LYS:C	1:C:510:LYS:CG	2.88	0.41
1:C:903:LEU:O	1:C:906:PRO:HD2	2.21	0.41
1:C:960:LEU:HD22	1:C:1027:VAL:HG22	2.03	0.41
1:A:448:VAL:HG12	1:A:887:CYS:HB3	2.03	0.41
1:A:897:ILE:N	1:A:898:PRO:CD	2.84	0.41
1:B:187:TRP:HA	1:B:774:MET:O	2.21	0.41
1:C:443:VAL:O	1:C:447:MET:HB2	2.20	0.41
1:A:535:LEU:HD22	1:A:1027:VAL:HG21	2.03	0.40
1:A:953:MET:SD	1:A:960:LEU:HA	2.61	0.40
1:B:207:ILE:O	1:B:211:ASN:HB3	2.21	0.40
1:C:135:SER:CB	1:C:672:VAL:HG12	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:LEU:HB2	1:C:246:PHE:CE1	2.56	0.40
1:C:564:LEU:HA	1:C:565:PRO:HD3	1.94	0.40
1:C:573:MET:HE3	1:C:626:ILE:HD11	2.02	0.40
1:C:681:ASP:CB	3:C:1143:HOH:O	2.65	0.40
1:C:876:LEU:HD22	1:C:876:LEU:O	2.20	0.40
2:D:49:THR:HB	2:D:50:PRO:HD2	2.03	0.40
1:A:101:ASP:O	1:A:105:VAL:HG23	2.20	0.40
1:A:185:ARG:HA	1:A:185:ARG:HD2	1.99	0.40
1:B:218:GLN:NE2	1:B:231:ASN:HD21	2.20	0.40
1:B:919:ARG:CD	1:B:1005:THR:HG21	2.52	0.40
1:C:23:GLY:HA3	1:C:377:LEU:O	2.21	0.40
1:C:75:LEU:HA	1:C:75:LEU:HD23	1.91	0.40
1:C:897:ILE:N	1:C:898:PRO:CD	2.82	0.40
1:A:454:VAL:HB	1:A:455:PRO:HD3	2.03	0.40
1:A:498:LYS:HA	1:A:499:PRO:HD3	1.94	0.40
1:B:293:LEU:HD22	1:B:297:ALA:HB3	2.02	0.40
1:B:927:PHE:CE2	1:B:931:LEU:HD11	2.56	0.40
1:C:189:ASN:HA	1:C:190:PRO:HD2	1.83	0.40
1:C:243:THR:HG23	3:C:1194:HOH:O	2.20	0.40
1:C:330:THR:N	1:C:331:PRO:CD	2.85	0.40
1:A:983:ILE:HD13	1:A:1012:VAL:HG22	2.02	0.40
1:A:57:VAL:CG1	1:A:88:VAL:HG22	2.52	0.40
1:B:217:GLY:HA3	1:C:754:TRP:O	2.22	0.40
1:B:446:ALA:HA	1:B:478:MET:SD	2.62	0.40
1:B:459:PHE:O	1:B:464:GLY:HA3	2.22	0.40
1:B:681:ASP:HB3	1:B:860:THR:HG23	2.03	0.40
1:C:404:LEU:HG	1:C:449:LEU:HD13	2.03	0.40
1:B:194:ASN:HD22	1:B:798:MET:HG3	1.86	0.40
1:B:420:MET:HE1	1:B:499:PRO:HA	2.02	0.40
1:B:69:MET:HB2	1:B:78:MET:HE1	2.04	0.40
1:C:892:TYR:CG	1:C:897:ILE:HD11	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1020/1049 (97%)	981 (96%)	39 (4%)	0	100	100
1	B	1020/1049 (97%)	985 (97%)	34 (3%)	1 (0%)	51	78
1	C	1032/1049 (98%)	993 (96%)	39 (4%)	0	100	100
2	D	152/169 (90%)	150 (99%)	2 (1%)	0	100	100
2	E	150/169 (89%)	141 (94%)	9 (6%)	0	100	100
All	All	3374/3485 (97%)	3250 (96%)	123 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	677	ALA

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	766/854 (90%)	719 (94%)	47 (6%)	18	41
1	B	780/854 (91%)	749 (96%)	31 (4%)	31	60
1	C	792/854 (93%)	761 (96%)	31 (4%)	32	61
2	D	108/133 (81%)	95 (88%)	13 (12%)	5	11
2	E	104/133 (78%)	90 (86%)	14 (14%)	4	9
All	All	2550/2828 (90%)	2414 (95%)	136 (5%)	22	48

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	TYR
1	A	58	GLN
1	A	62	THR
1	A	70	ASN

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Mol	Chain	Res	Type
1	A	92	LEU
1	A	98	THR
1	A	110	LYS
1	A	130	GLU
1	A	143	ILE
1	A	146	ASP
1	A	148	THR
1	A	151	GLN
1	A	240	LEU
1	A	244	GLU
1	A	258	SER
1	A	259	ARG
1	A	262	LEU
1	A	263	ARG
1	A	274	ASN
1	A	293	LEU
1	A	310	LEU
1	A	321	LEU
1	A	348	ILE
1	A	376	LEU
1	A	537	SER
1	A	538	THR
1	A	577	GLN
1	A	587	THR
1	A	612	VAL
1	A	659	LYS
1	A	668	LEU
1	A	695	LEU
1	A	712	MET
1	A	713	LEU
1	A	714	THR
1	A	729	ILE
1	A	749	THR
1	A	758	TYR
1	A	828	LEU
1	A	923	ASN
1	A	953	MET
1	A	960	LEU
1	A	961	ILE
1	A	971	ARG
1	A	984	LEU
1	A	990	VAL

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Mol	Chain	Res	Type
1	A	997	SER
1	B	11	PHE
1	B	49	TYR
1	B	70	ASN
1	B	163	LYS
1	B	172	VAL
1	B	197	GLN
1	B	224	PRO
1	B	225	VAL
1	B	243	THR
1	B	259	ARG
1	B	267	LYS
1	B	274	ASN
1	B	293	LEU
1	B	355	MET
1	B	366	LEU
1	B	429	GLU
1	B	471	SER
1	B	497	LEU
1	B	578	LEU
1	B	687	GLN
1	B	695	LEU
1	B	716	VAL
1	B	765	ARG
1	B	825	MET
1	B	837	THR
1	B	844	MET
1	B	860	THR
1	B	914	LEU
1	B	956	GLU
1	B	972	LEU
1	B	980	LEU
1	C	10	ILE
1	C	11	PHE
1	C	49	TYR
1	C	81	ASN
1	C	83	ASP
1	C	125	GLN
1	C	127	VAL
1	C	182	TYR
1	C	239	ARG
1	C	274	ASN

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Mol	Chain	Res	Type
1	C	289	LEU
1	C	310	LEU
1	C	394	THR
1	C	404	LEU
1	C	415	ASN
1	C	510	LYS
1	C	544	LEU
1	C	571	VAL
1	C	587	THR
1	C	626	ILE
1	C	632	LYS
1	C	695	LEU
1	C	799	VAL
1	C	860	THR
1	C	876	LEU
1	C	891	LEU
1	C	897	ILE
1	C	901	VAL
1	C	960	LEU
1	C	968	VAL
1	C	1011	MET
2	D	17	LYS
2	D	26	GLN
2	D	34	MET
2	D	51	LEU
2	D	59	HIS
2	D	77	ASP
2	D	84	LEU
2	D	93	LEU
2	D	110	ASP
2	D	117	LEU
2	D	123	ARG
2	D	139	VAL
2	D	140	ASN
2	E	14	LEU
2	E	59	HIS
2	E	64	GLU
2	E	77	ASP
2	E	89	ARG
2	E	93	LEU
2	E	95	ILE
2	E	100	LEU

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Mol	Chain	Res	Type
2	E	122	LYS
2	E	138	ASP
2	E	140	ASN
2	E	152	ILE
2	E	154	ILE
2	E	164	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	63	GLN
1	A	70	ASN
1	A	125	GLN
1	A	151	GLN
1	A	181	GLN
1	A	191	ASN
1	A	194	ASN
1	A	229	GLN
1	A	338	HIS
1	A	361	ASN
1	A	577	GLN
1	A	687	GLN
1	A	923	ASN
1	A	1000	GLN
1	A	1001	ASN
1	B	3	ASN
1	B	63	GLN
1	B	70	ASN
1	B	123	GLN
1	B	124	GLN
1	B	194	ASN
1	B	197	GLN
1	B	218	GLN
1	B	274	ASN
1	B	284	GLN
1	B	360	GLN
1	B	517	ASN
1	B	577	GLN
1	B	592	ASN
1	B	687	GLN
1	B	701	GLN

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Mol	Chain	Res	Type
1	B	719	ASN
1	B	733	GLN
1	B	744	ASN
1	B	871	ASN
1	B	941	ASN
1	B	1000	GLN
1	B	1001	ASN
1	C	3	ASN
1	C	34	GLN
1	C	67	GLN
1	C	68	ASN
1	C	81	ASN
1	C	125	GLN
1	C	194	ASN
1	C	197	GLN
1	C	213	GLN
1	C	229	GLN
1	C	237	GLN
1	C	274	ASN
1	C	298	ASN
1	C	360	GLN
1	C	437	GLN
1	C	517	ASN
1	C	525	HIS
1	C	569	GLN
1	C	604	ASN
1	C	701	GLN
1	C	744	ASN
1	C	830	GLN
1	C	871	ASN
1	C	1001	ASN
2	D	36	ASN
2	D	52	HIS
2	D	59	HIS
2	D	135	ASN
2	D	140	ASN
2	D	142	GLN
2	D	156	ASN
2	E	26	GLN
2	E	41	ASN
2	E	59	HIS
2	E	85	HIS

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Mol	Chain	Res	Type
2	E	92	HIS
2	E	102	ASN
2	E	112	HIS
2	E	118	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	FME	B	1	1	8,9,10	0.34	0	7,9,11	8.82	2 (28%)
1	FME	C	1	1	8,9,10	0.34	0	7,9,11	1.16	1 (14%)
1	FME	A	1	1	8,9,10	0.34	0	7,9,11	12.64	2 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FME	B	1	1	-	1/7/9/11	-
1	FME	C	1	1	-	1/7/9/11	-
1	FME	A	1	1	-	1/7/9/11	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	FME	CA-N-CN	27.93	165.77	122.82
1	A	1	FME	O1-CN-N	18.30	173.45	125.27
1	B	1	FME	CA-N-CN	17.80	150.20	122.82
1	B	1	FME	O1-CN-N	14.96	164.66	125.27
1	C	1	FME	C-CA-N	2.04	113.41	109.73

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1	FME	O1-CN-N-CA
1	C	1	FME	O1-CN-N-CA
1	A	1	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	1	FME	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	1026/1049 (97%)	0.07	36 (3%) 44 44	26, 61, 114, 188	0
1	B	1025/1049 (97%)	-0.06	8 (0%) 86 87	22, 57, 89, 154	1 (0%)
1	C	1033/1049 (98%)	-0.07	24 (2%) 60 62	27, 53, 88, 168	0
2	D	154/169 (91%)	0.20	14 (9%) 9 7	33, 64, 105, 162	0
2	E	152/169 (89%)	1.60	48 (31%) 0 0	57, 97, 140, 200	2 (1%)
All	All	3390/3485 (97%)	0.06	130 (3%) 40 39	22, 57, 107, 200	3 (0%)

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	38	ALA	16.4
2	E	34	MET	8.2
2	E	66	LEU	7.8
2	E	31	ARG	6.9
2	E	30	VAL	6.7
2	E	35	ALA	6.6
2	E	68	LYS	6.1
2	D	150	PHE	5.9
2	E	51	LEU	5.8
1	A	833	PRO	5.2
1	A	1035	ARG	5.1
1	A	515	TRP	5.0
2	E	32	ILE	5.0
1	B	672	VAL	4.9
1	A	865	GLN	4.7
2	D	139	VAL	4.7
1	C	918	PHE	4.6
2	E	67	LEU	4.6
2	E	99	LEU	4.6
2	E	33	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	C	513	PHE	4.5
2	D	149	ALA	4.5
1	A	518	ARG	4.2
2	E	65	VAL	4.2
2	E	37	GLY	4.0
2	E	64	GLU	3.9
2	D	126	LEU	3.9
2	E	137	ALA	3.9
2	D	164	ILE	3.9
2	E	40	VAL	3.9
2	E	69	ASN	3.8
1	C	786	ILE	3.7
2	E	63	VAL	3.7
1	A	425	LEU	3.7
1	C	509	LYS	3.7
2	E	28	ASP	3.7
2	E	29	GLU	3.7
1	C	501	ALA	3.5
2	E	139	VAL	3.5
1	B	600	THR	3.5
2	E	62	ILE	3.4
1	A	538	THR	3.4
2	E	101	LYS	3.3
1	A	1033	PHE	3.2
1	A	386	PHE	3.2
1	A	513	PHE	3.1
2	D	166	GLN	3.1
2	E	36	ASN	3.1
2	E	70	GLY	3.1
1	C	425	LEU	3.1
2	E	60	LEU	3.1
1	A	408	ASP	3.1
2	E	138	ASP	3.1
2	E	140	ASN	3.0
2	D	158	ASN	3.0
1	C	796	GLY	3.0
2	D	156	ASN	3.0
2	D	162	ALA	3.0
2	E	100	LEU	3.0
1	C	793	ALA	3.0
2	E	141	ALA	3.0
2	E	95	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	28	LEU	2.9
1	A	254	ASN	2.9
2	E	154	ILE	2.9
1	C	510	LYS	2.9
1	A	256	ASP	2.9
1	B	424	GLY	2.8
1	C	511	GLY	2.8
1	A	712	MET	2.8
1	A	504	ASP	2.7
1	B	631	LEU	2.7
2	E	45	PHE	2.7
1	C	514	GLY	2.7
1	A	1043	SER	2.7
1	C	499	PRO	2.7
1	A	834	GLY	2.7
2	E	18	LEU	2.7
1	B	407	ASP	2.5
1	B	638	PRO	2.5
1	A	535	LEU	2.5
1	C	1034	SER	2.5
1	A	500	ILE	2.5
1	B	832	ALA	2.5
2	E	156	ASN	2.5
1	C	809	TRP	2.4
1	A	514	GLY	2.4
1	A	618	ALA	2.4
1	C	363	ARG	2.4
1	A	836	SER	2.4
2	D	159	GLU	2.4
1	C	792	ARG	2.3
2	E	27	ASP	2.3
2	E	81	VAL	2.3
1	A	874	PRO	2.3
1	A	503	GLY	2.3
2	E	165	LEU	2.3
1	C	508	GLY	2.3
2	E	108	ALA	2.3
2	E	58	GLY	2.2
1	A	542	LEU	2.2
1	A	508	GLY	2.2
2	D	153	SER	2.2
2	D	141	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	E	106	VAL	2.2
2	D	163	GLU	2.2
1	A	961	ILE	2.2
1	C	798	MET	2.2
1	A	832	ALA	2.2
1	A	426	PRO	2.1
2	E	61	GLU	2.1
1	A	11	PHE	2.1
1	C	500	ILE	2.1
1	C	512	PHE	2.1
1	C	791	VAL	2.1
1	A	516	PHE	2.1
1	A	554	TYR	2.1
2	E	164	ILE	2.1
1	A	423	GLU	2.1
1	A	506	GLY	2.1
1	C	515	TRP	2.1
1	C	702	LEU	2.0
2	E	93	LEU	2.0
2	E	59	HIS	2.0
1	A	432	ARG	2.0
2	D	154	ILE	2.0
1	B	833	PRO	2.0
1	A	258	SER	2.0
2	E	155	ASP	2.0
2	E	117	LEU	2.0

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

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(\AA^2)	Q<0.9
1	FME	A	1	10/11	0.86	0.16	47,80,97,110	0
1	FME	C	1	10/11	0.89	0.20	65,71,86,87	0
1	FME	B	1	10/11	0.92	0.14	42,74,88,109	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.