Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:04 am BST

PDB ID	:	4B2T
Title	:	The crystal structures of the eukaryotic chaperonin CCT reveal its functional partitioning
Authors	:	Kalisman, N.; Schroeder, G.F.; Levitt, M.
Deposited on	:	2012-07-17
Resolution	:	5.50 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:

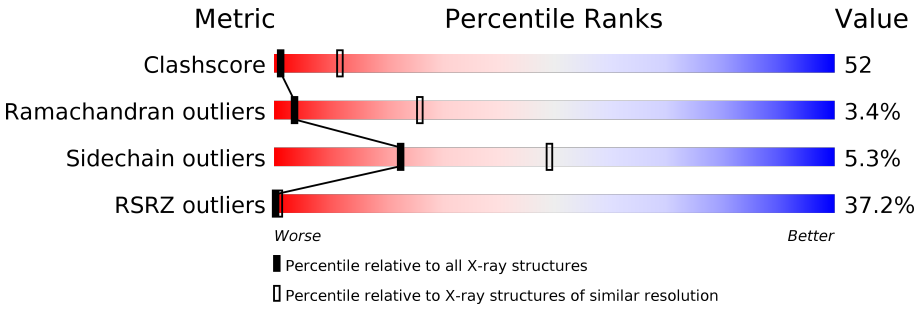
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 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))
Clashscore	141614	1010 (7.10-3.90)
Ramachandran outliers	138981	1014 (7.12-3.82)
Sidechain outliers	138945	1191 (7.20-3.80)
RSRZ outliers	127900	1023 (7.08-3.76)

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 <=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	556	26% 29% 51% 6% 13%
1	a	556	27% 57% 6% 35%
2	B	535	43% 35% 52% 10%
2	b	535	30% 62% 5% 33%
3	D	542	29% 28% 55% 5% 11%
3	d	542	25% 61% 5% 34%
4	E	541	20% 32% 50% 7% 11%

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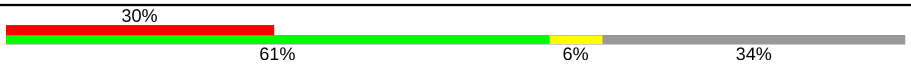
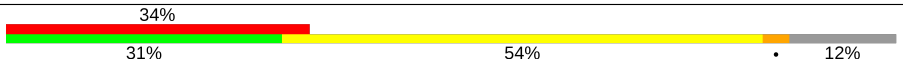
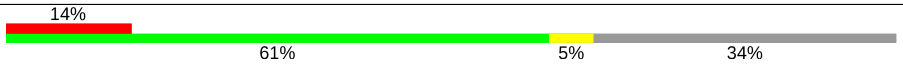
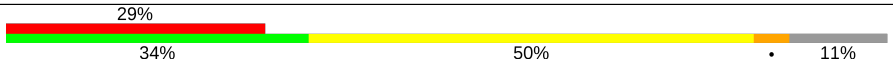
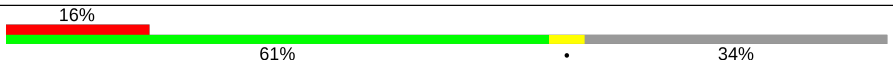
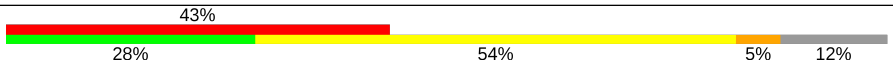
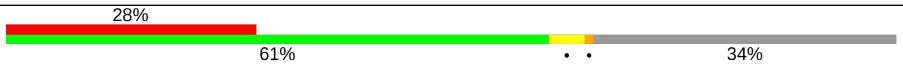
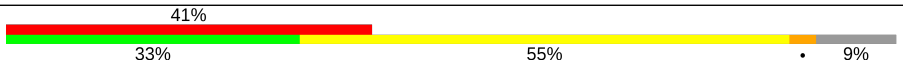
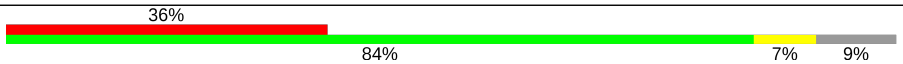
Mol	Chain	Length	Quality of chain
4	e	541	
5	G	545	
5	g	545	
6	H	543	
6	h	543	
7	Q	548	
7	q	548	
8	Z	531	
8	z	531	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 51877 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 T-COMPLEX PROTEIN 1 SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	0	0
			3625	2280	633	692	20			
1	a	359	Total	C	N	O	S	0	0	0
			2705	1703	469	520	13			

- Molecule 2 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	481	Total	C	N	O	S	0	0	0
			3602	2258	629	696	19			
2	b	359	Total	C	N	O	S	0	0	0
			2658	1652	469	524	13			

- Molecule 3 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT DELTA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	481	Total	C	N	O	S	0	0	0
			3610	2259	627	703	21			
3	d	359	Total	C	N	O	S	0	0	0
			2690	1671	473	532	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	158	VAL	GLU	conflict	UNP Q2T9X2
D	510	LEU	GLN	conflict	UNP Q2T9X2
d	1158	VAL	GLU	conflict	UNP Q2T9X2
d	1510	LEU	GLN	conflict	UNP Q2T9X2

- Molecule 4 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT EPSILON.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	481	Total	C	N	O	S	0	0	0
			3674	2299	644	703	28			
4	e	359	Total	C	N	O	S	0	0	0
			2724	1688	486	528	22			

- Molecule 5 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT GAMMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	481	Total	C	N	O	S	0	0	0
			3719	2326	661	705	27			
5	g	359	Total	C	N	O	S	0	0	0
			2735	1711	480	523	21			

- Molecule 6 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT ETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	481	Total	C	N	O	S	0	0	0
			3671	2320	633	693	25			
6	h	359	Total	C	N	O	S	0	0	0
			2724	1719	472	517	16			

- Molecule 7 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT THETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	Q	481	Total	C	N	O	S	0	0	0
			3673	2317	628	703	25			
7	q	359	Total	C	N	O	S	0	0	0
			2739	1729	467	526	17			

- Molecule 8 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT ZETA.

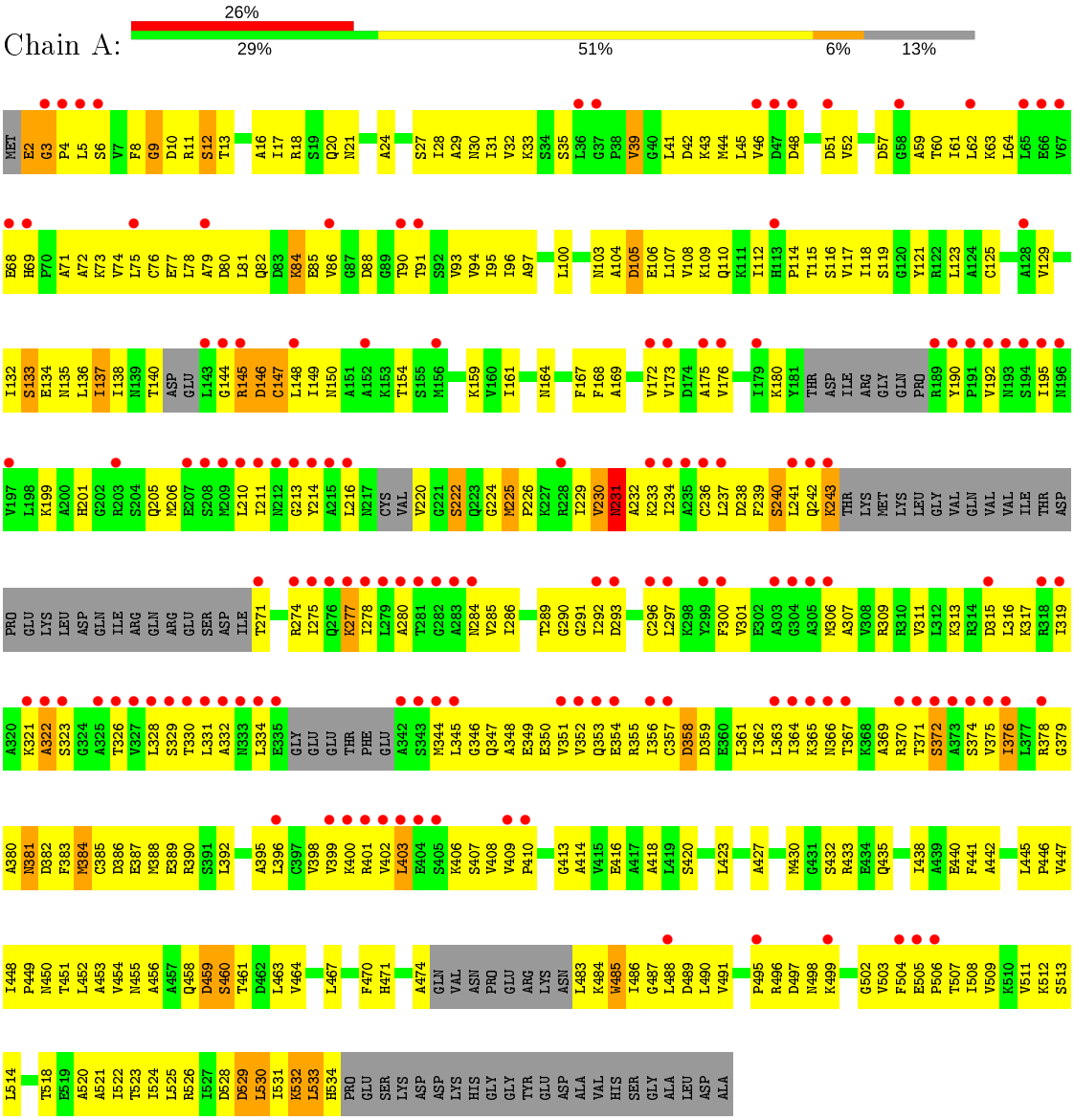
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	Z	481	Total	C	N	O	S	0	0	0
			3664	2310	638	697	19			
8	z	481	Total	C	N	O	S	0	0	0
			3664	2310	638	697	19			

3 Residue-property plots (i)

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

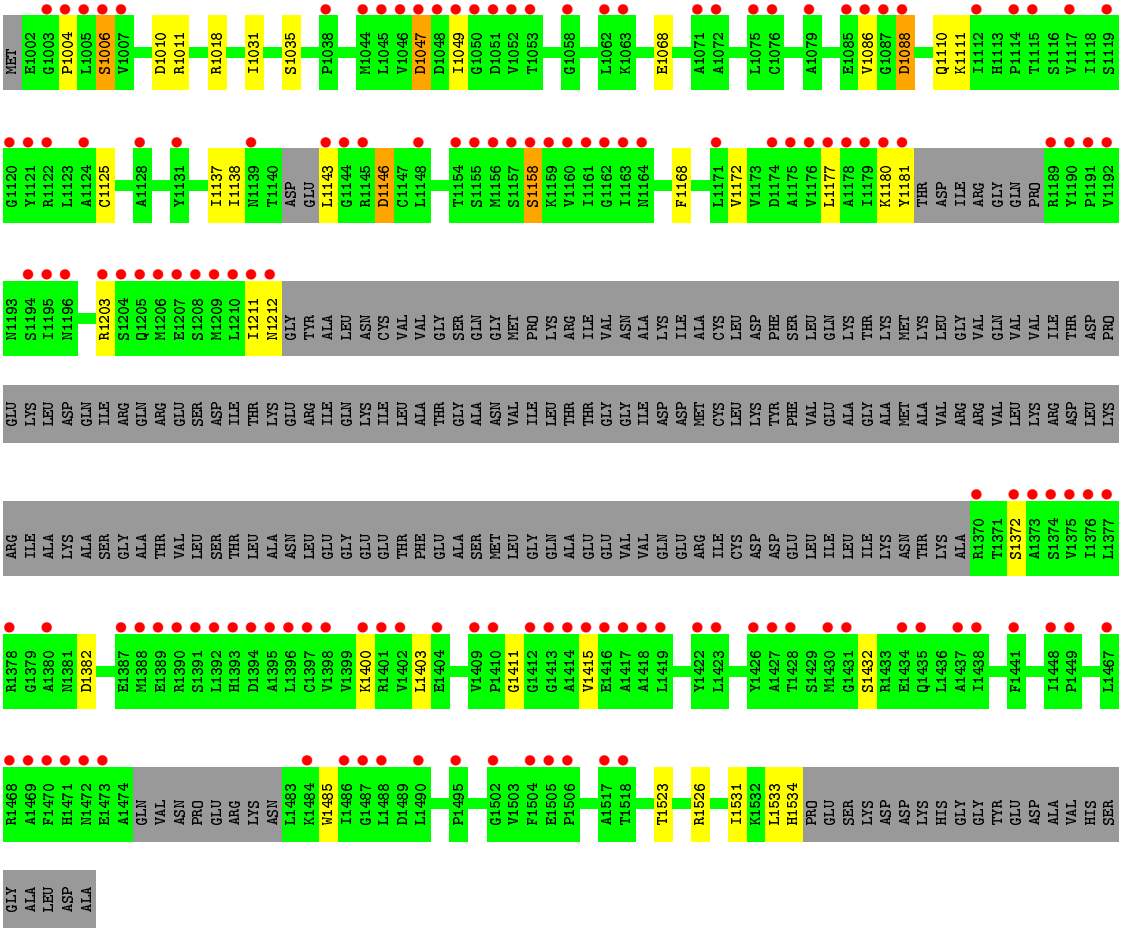
- Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT ALPHA

Chain A:



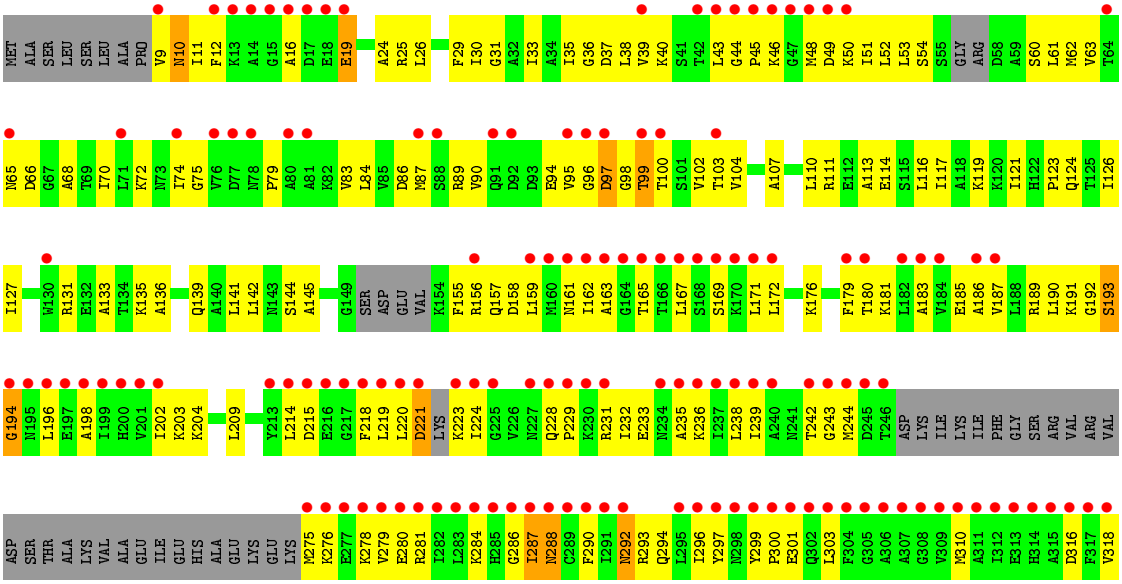
- Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT ALPHA

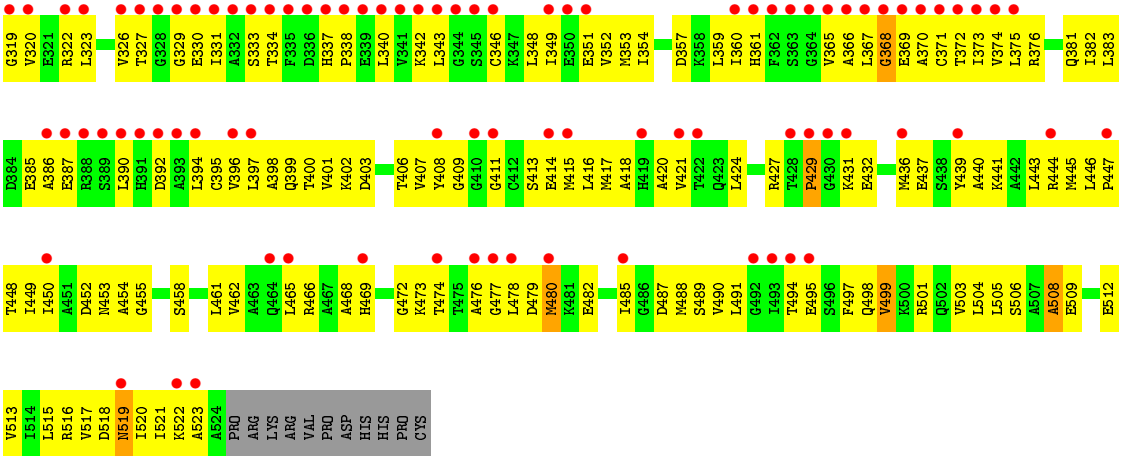
Chain a:



• Molecule 2: T-COMPLEX PROTEIN 1 SUBUNIT BETA

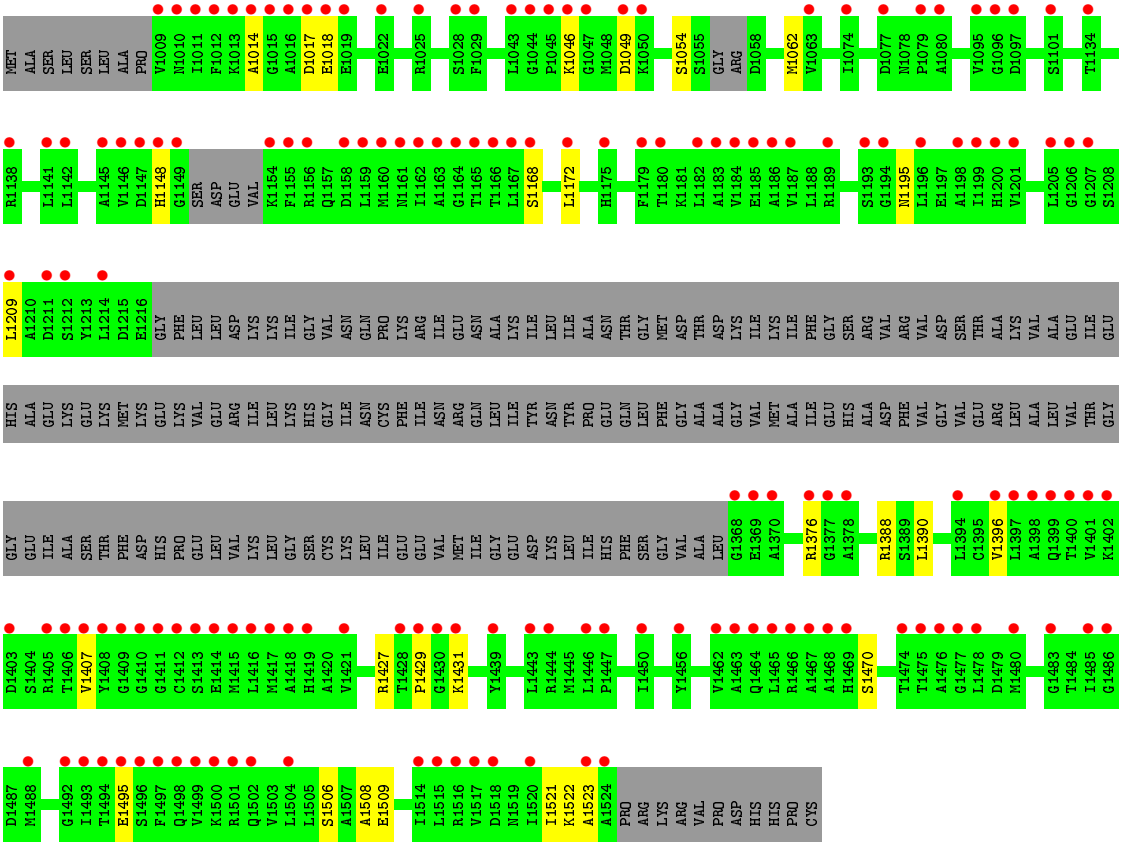
Chain B:





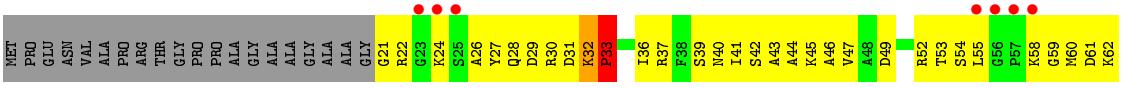
- Molecule 2: T-COMPLEX PROTEIN 1 SUBUNIT BETA

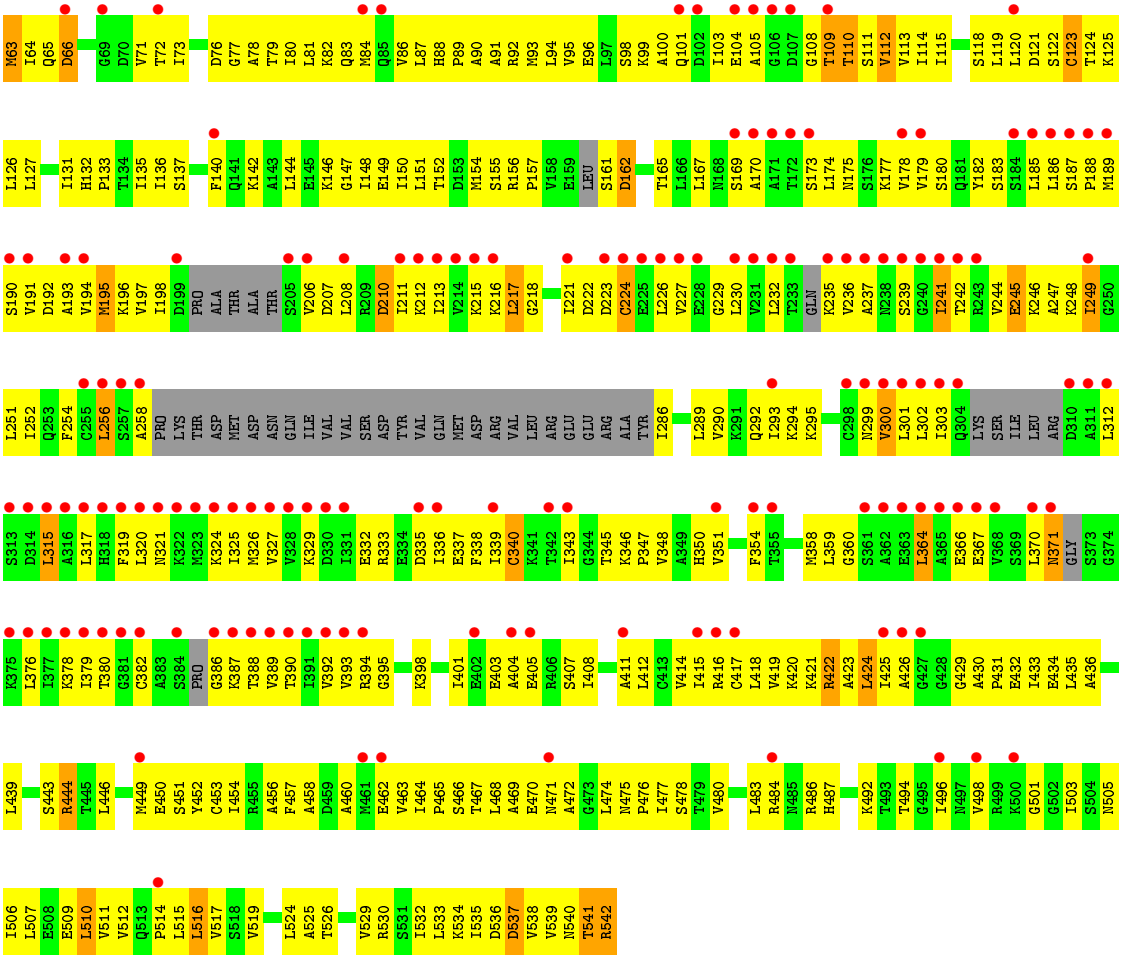
Chain b:



- Molecule 3: T-COMPLEX PROTEIN 1 SUBUNIT DELTA

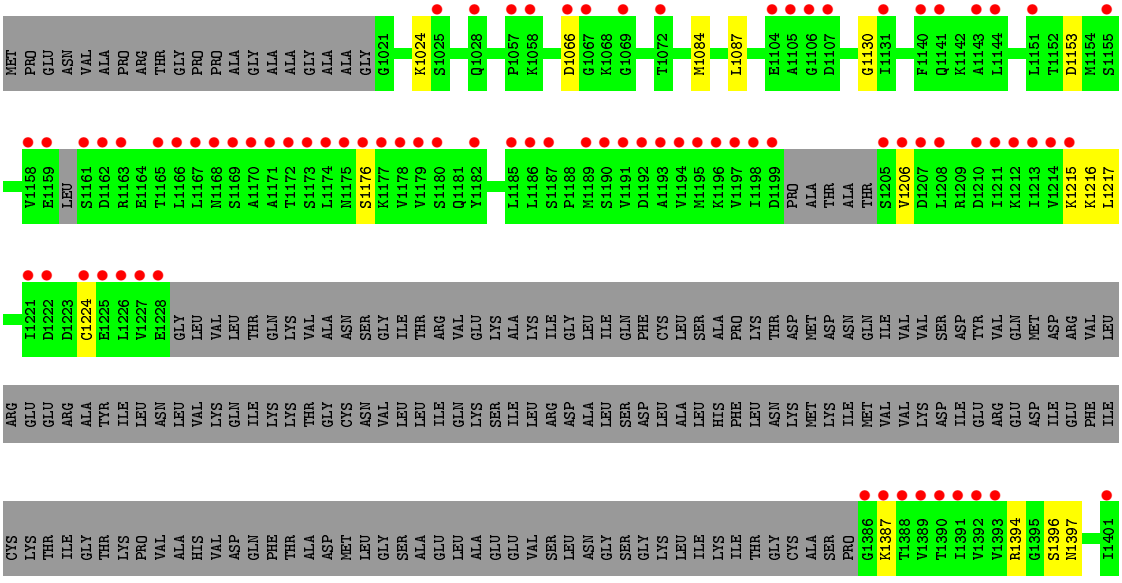
Chain D:

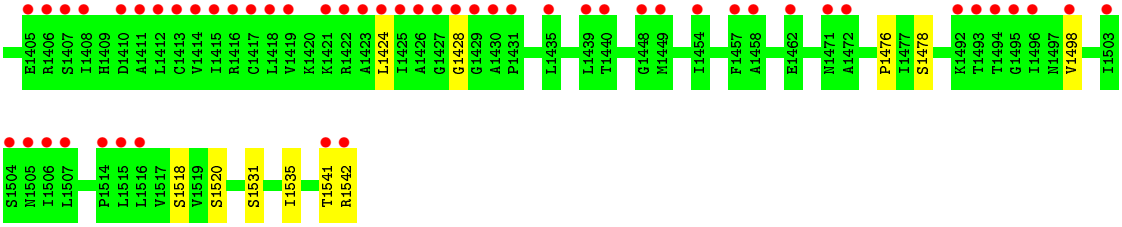




• Molecule 3: T-COMPLEX PROTEIN 1 SUBUNIT DELTA

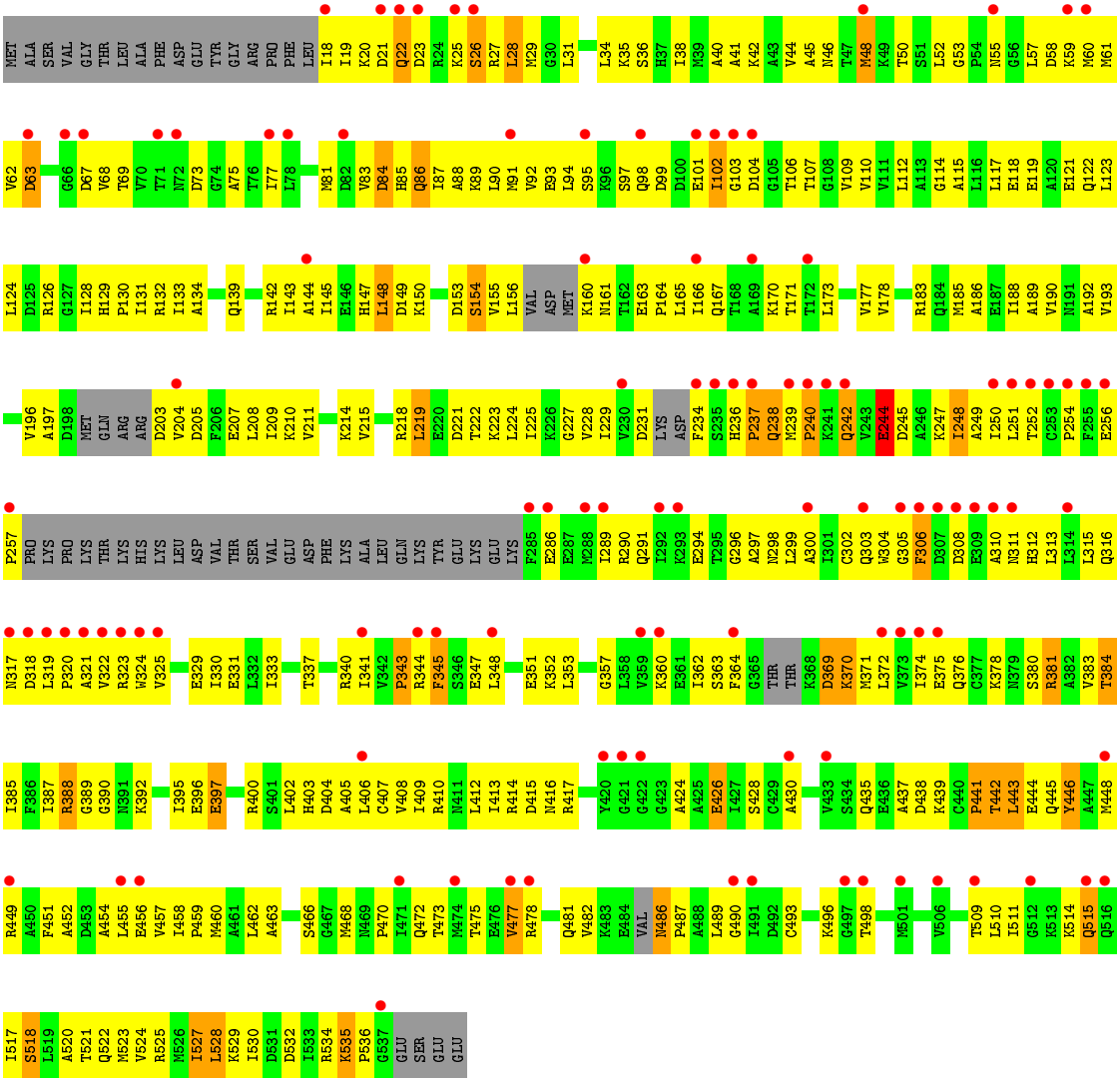
Chain d:





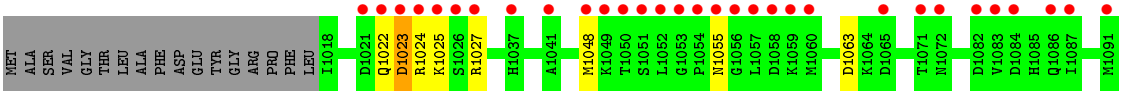
• Molecule 4: T-COMPLEX PROTEIN 1 SUBUNIT EPSILON

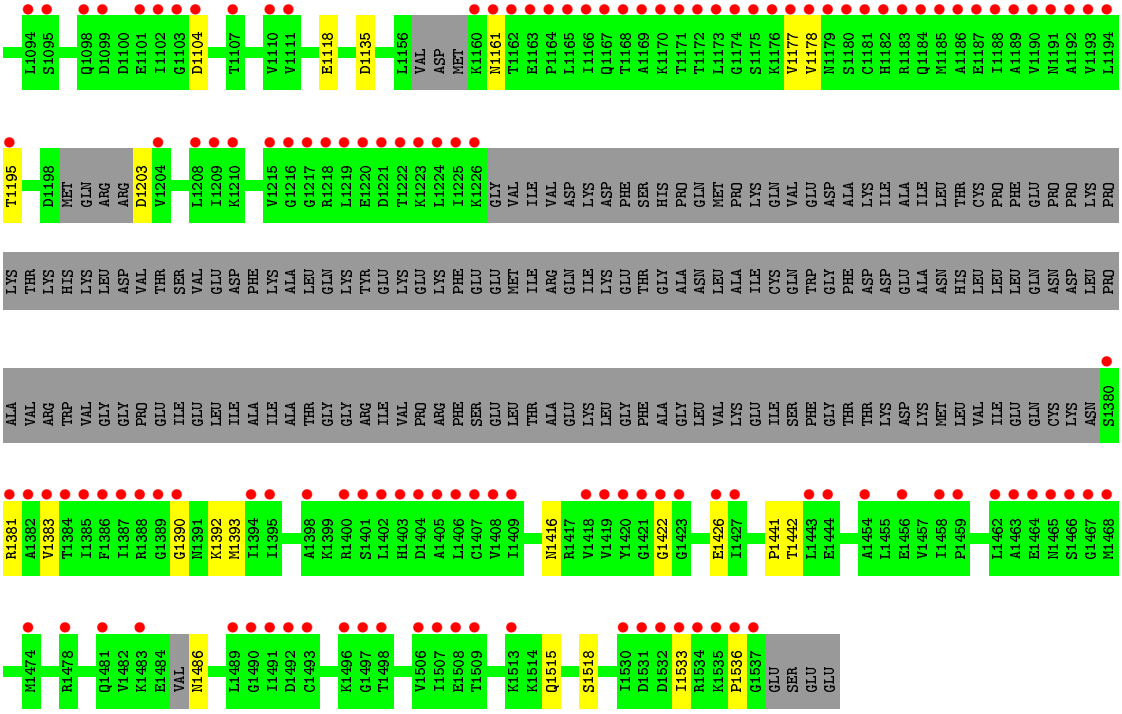
Chain E:



• Molecule 4: T-COMPLEX PROTEIN 1 SUBUNIT EPSILON

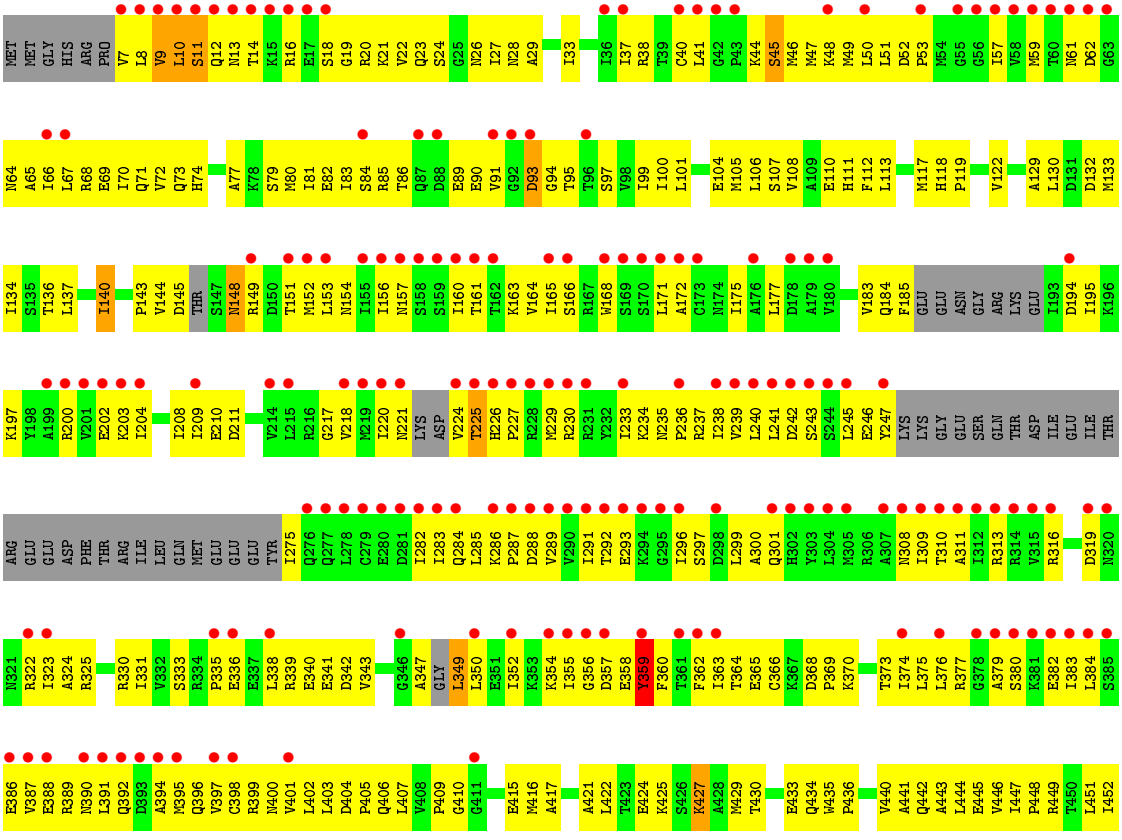
Chain e:

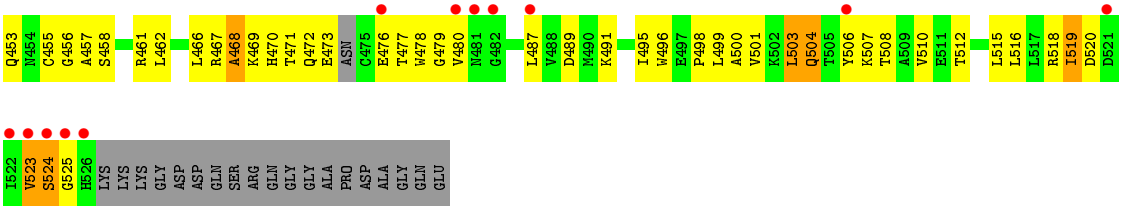




• Molecule 5: T-COMPLEX PROTEIN 1 SUBUNIT GAMMA

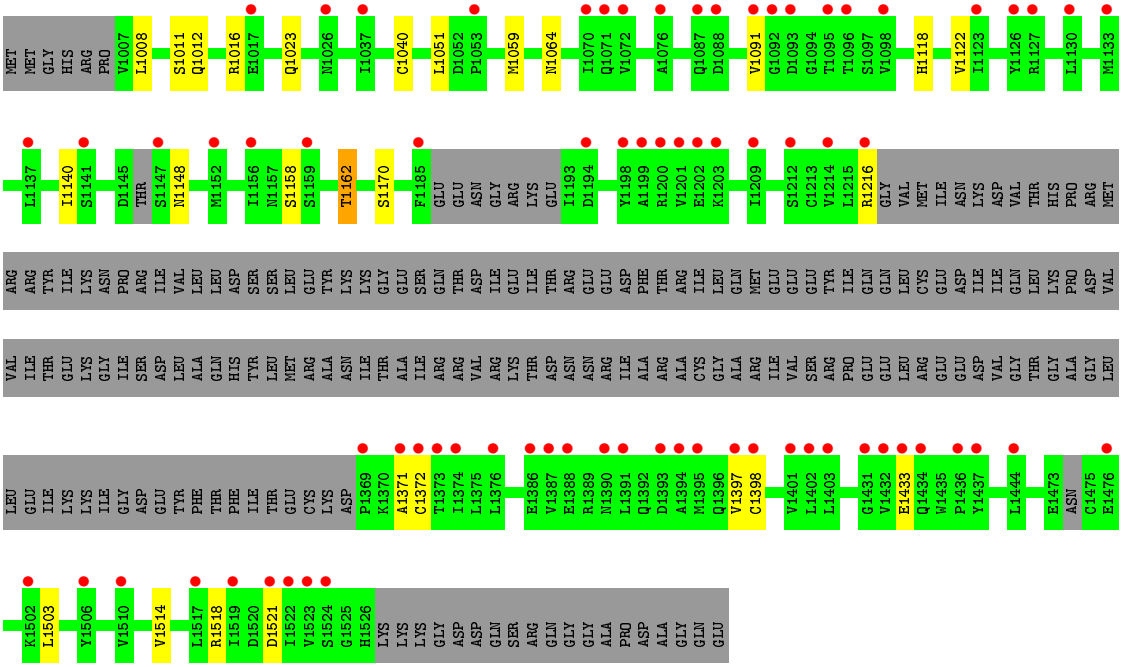
Chain G:





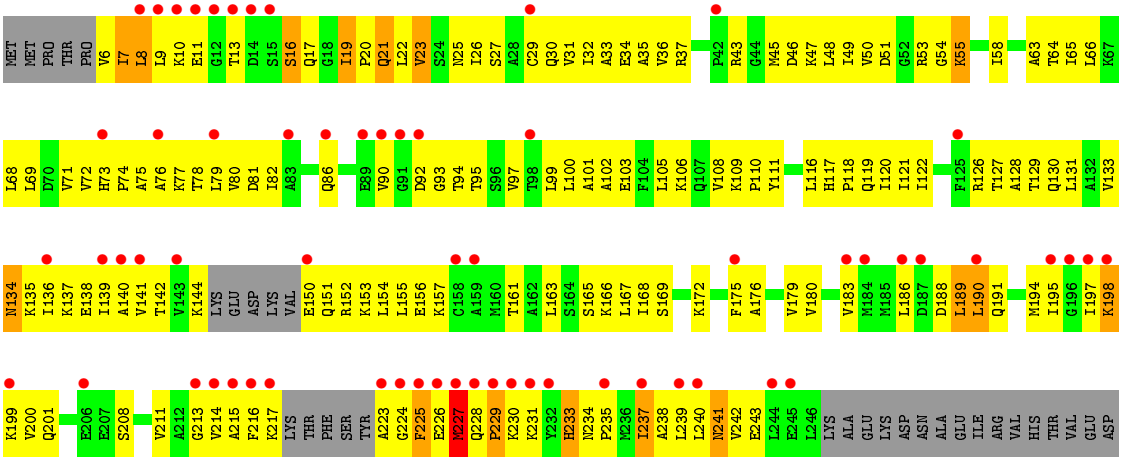
• Molecule 5: T-COMPLEX PROTEIN 1 SUBUNIT GAMMA

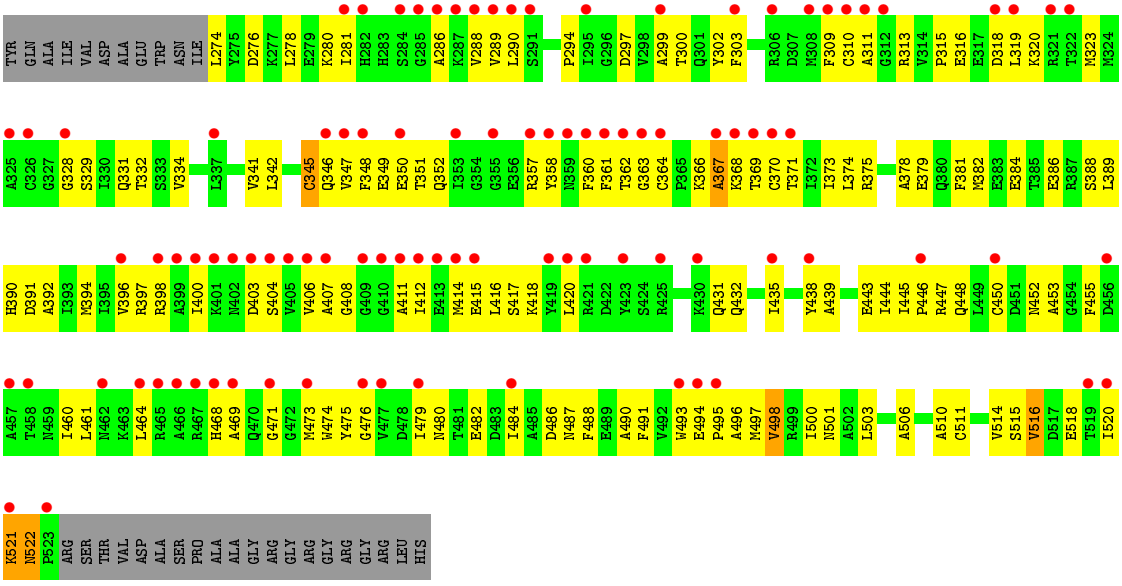
Chain g:



• Molecule 6: T-COMPLEX PROTEIN 1 SUBUNIT ETA

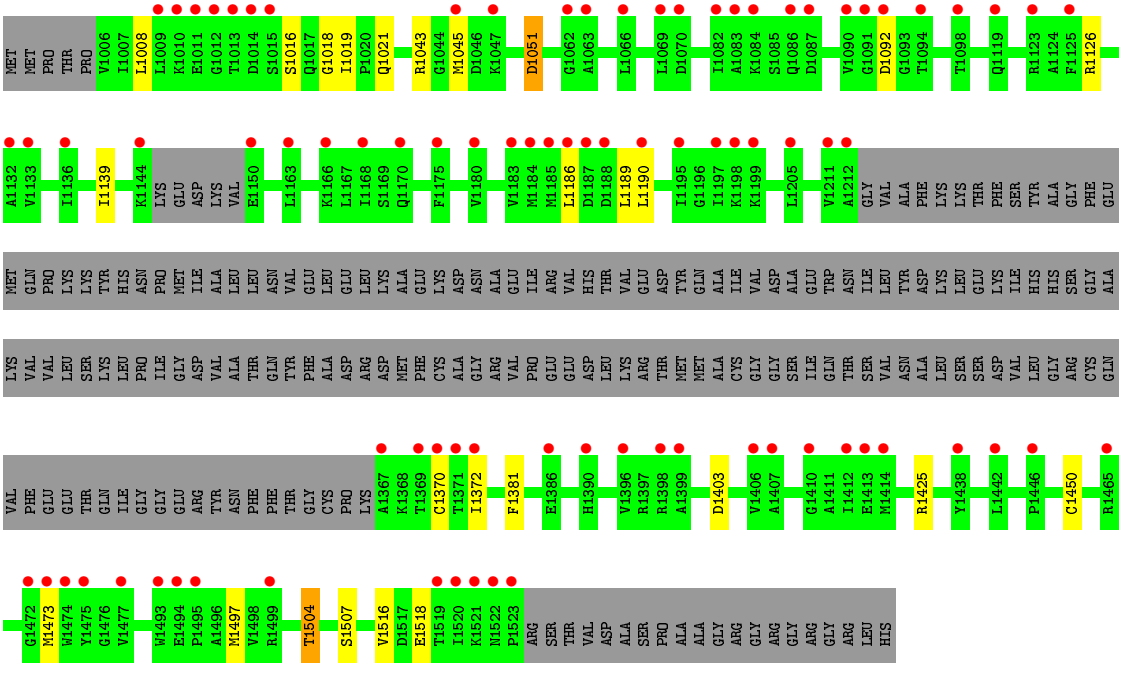
Chain H:





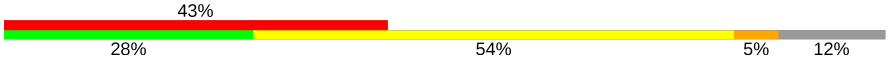
• Molecule 6: T-COMPLEX PROTEIN 1 SUBUNIT ETA

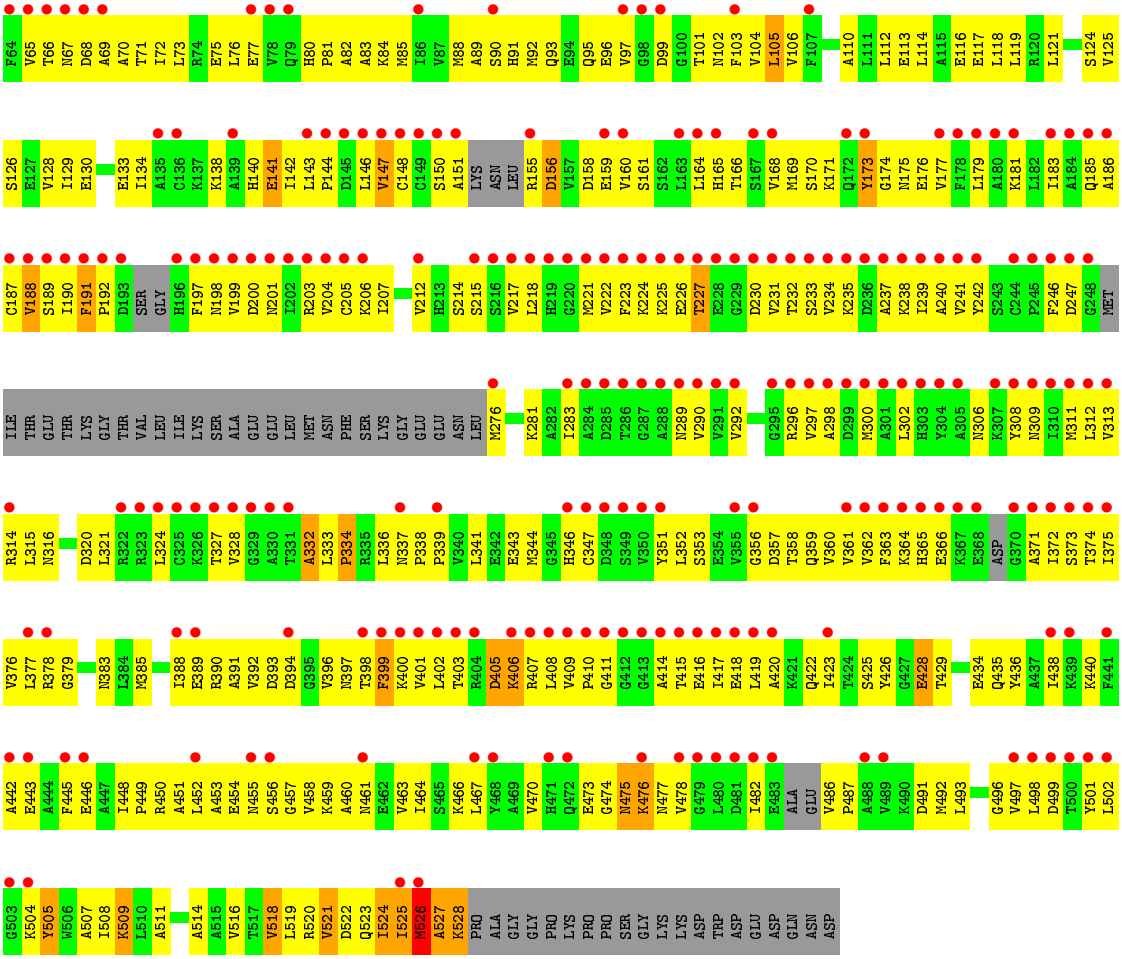
Chain h:



• Molecule 7: T-COMPLEX PROTEIN 1 SUBUNIT THETA

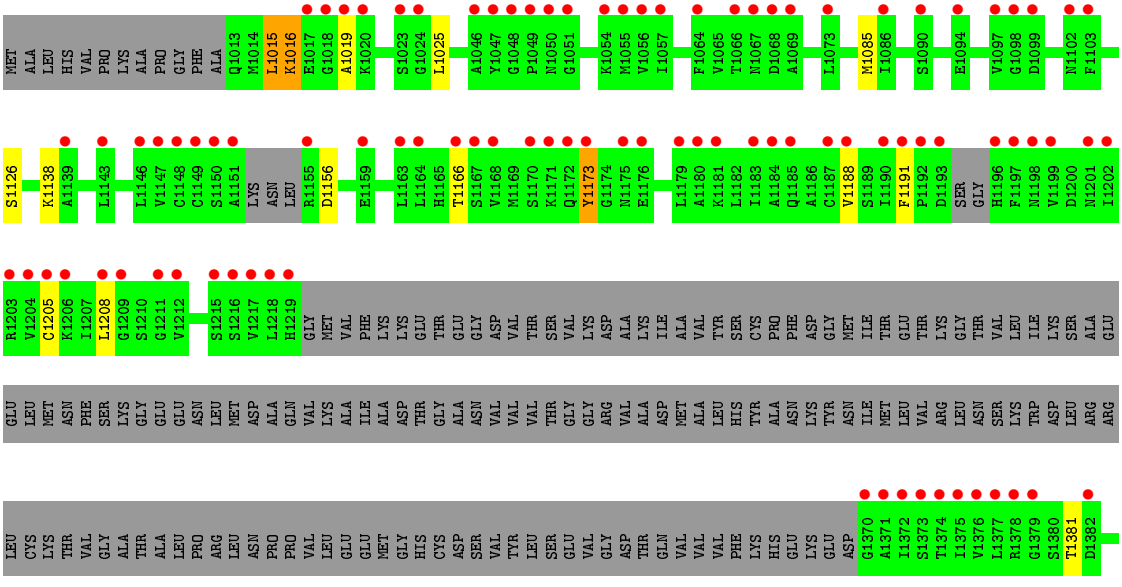
Chain Q:

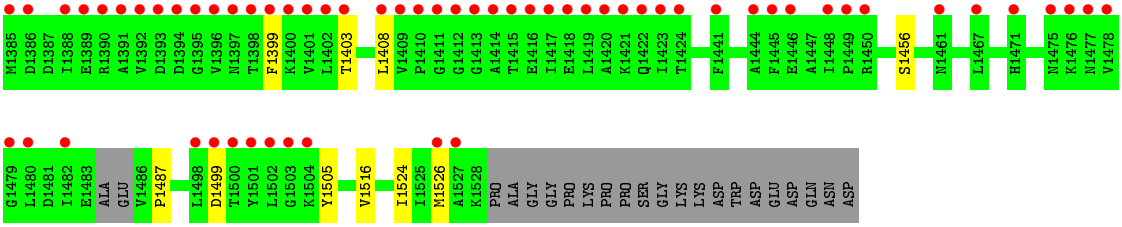




• Molecule 7: T-COMPLEX PROTEIN 1 SUBUNIT THETA

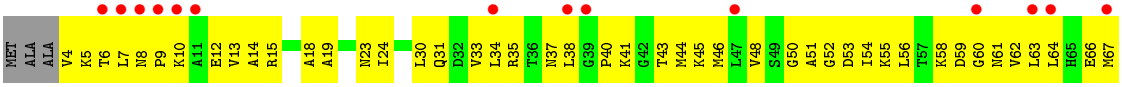
Chain q:

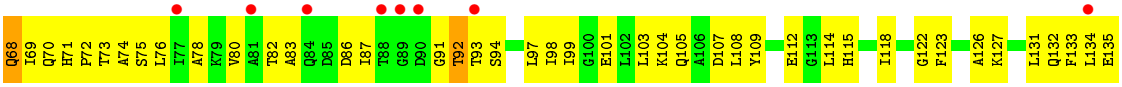


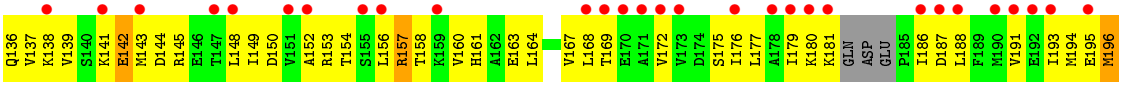


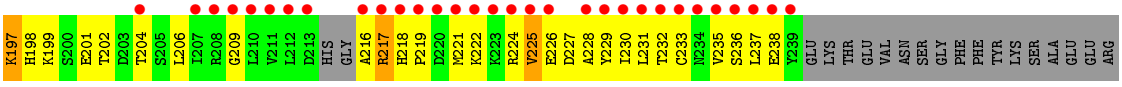
• Molecule 8: T-COMPLEX PROTEIN 1 SUBUNIT ZETA

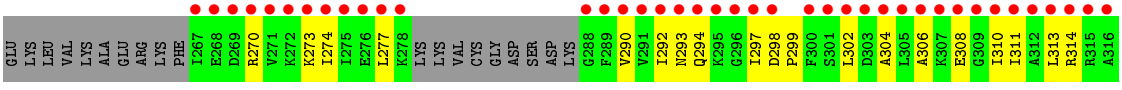
Chain Z:

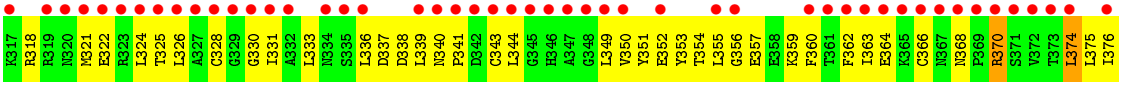


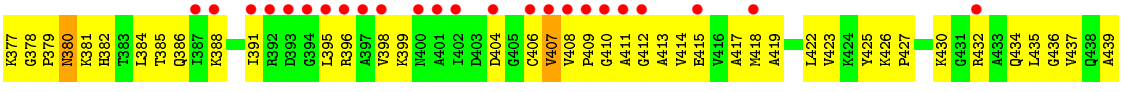


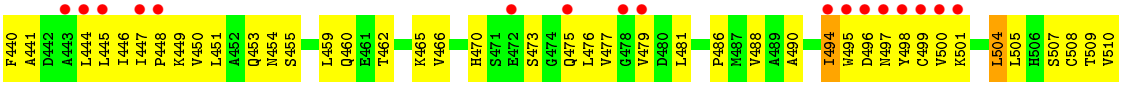


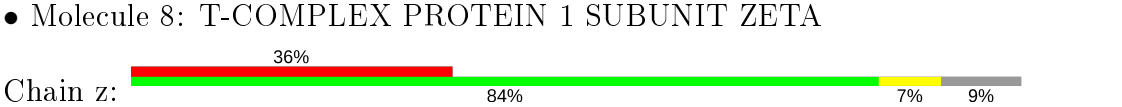






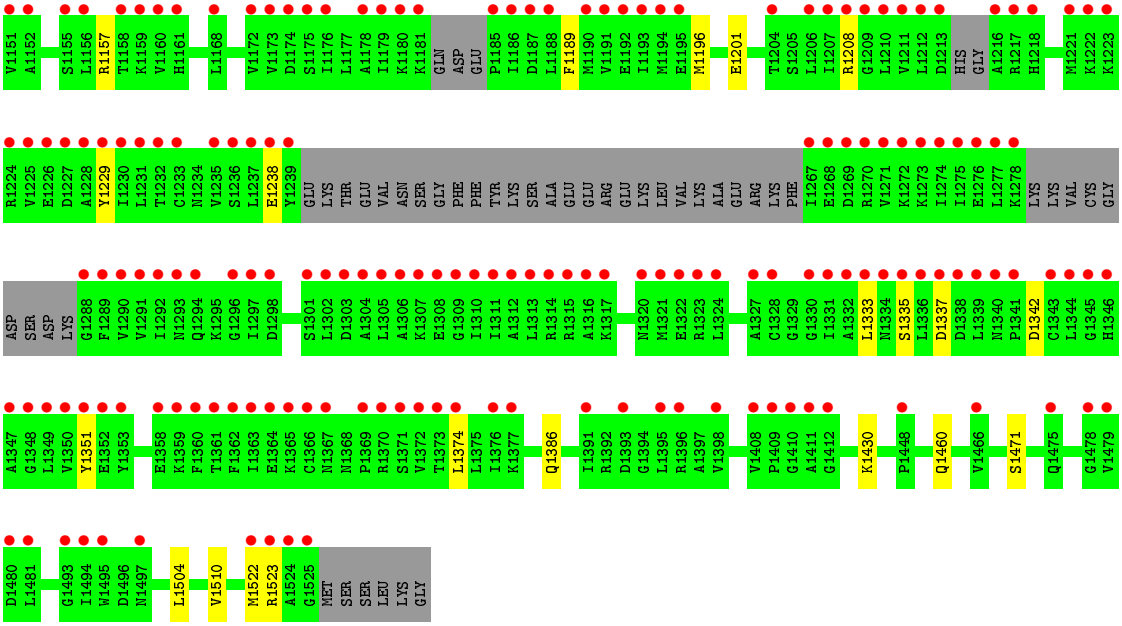






• Molecule 8: T-COMPLEX PROTEIN 1 SUBUNIT ZETA

Chain z:


V1151 A1152 S1155 L1156 R1157 T1158 K1159 V1160 H1161 L1168 V1172 V1173 D1174 S1175 I1176 L1177 A1178 I1179 K1180 K1181 GLN ASP GLU P1185 I1186 D1187 L1188 F1189 M1190 V1191 E1192 I1193 M1194 E1195 M1196 E1201 T1204 S1205 L1206 I1207 R1208 G1209 L1210 V1211 L1212 D1213 HIS GLY A1216 R1217 H1218 M1221 K1222 K1223
R1224 V1225 E1226 D1227 A1228 Y1229 I1230 L1231 T1232 C1233 N1234 V1235 S1236 L1237 E1238 Y1239 GLU LYS THR GLU VAL ASN SER GLY PHE PHE TYR LYS SER ALA GLU GLU ARG GLU LYS LEU VAL LYS ALA GLU ARG LYS PHE I1267 E1268 D1269 R1270 V1271 K1272 K1273 I1274 I1275 E1276 L1277 K1278 LYS LYS VAL CYS GLY
ASP SER ASP LYS G1288 F1289 V1290 V1291 I1292 N1293 Q1294 K1295 G1296 I1297 D1298 S1301 L1302 D1303 A1304 L1305 A1306 K1307 E1308 G1309 I1310 I1311 A1312 L1313 R1314 R1315 A1316 K1317 N1320 M1321 E1322 R1323 L1324 A1327 C1328 G1329 G1330 I1331 A1332 L1333 M1334 S1335 L1336 D1337 D1338 L1339 M1340 P1341 D1342 C1343 L1344 G1345 H1346
A1347 G1348 L1349 V1350 Y1351 E1352 Y1353 E1358 K1359 F1360 T1361 F1362 I1363 E1364 K1365 C1366 N1367 N1368 P1369 R1370 S1371 V1372 T1373 L1374 L1375 I1376 K1377 Q1386 I1391 R1392 D1393 G1394 L1395 R1396 A1397 V1398 V1408 P1409 G1410 A1411 G1412 K1430 P1448 Q1460 V1466 S1471 Q1475 G1478 V1479
D1480 L1481 G1493 I1494 W1495 D1496 N1497 L1504 V1510 M1522 R1523 A1524 G1525 MET SER SER LEU LYS GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	272.70Å 313.50Å 158.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	200.00 – 5.50 97.58 – 5.44	Depositor EDS
% Data completeness (in resolution range)	99.1 (200.00-5.50) 98.4 (97.58-5.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 5.41Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.340 , 0.399 0.345 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	257.8	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 427.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.32$, $< L^2 > = 0.16$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.75	EDS
Total number of atoms	51877	wwPDB-VP
Average B, all atoms (Å^2)	277.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.22	0/3657	0.44	0/4934
1	a	0.22	0/2733	0.46	0/3695
2	B	0.22	0/3638	0.43	0/4903
2	b	0.21	0/2680	0.44	0/3615
3	D	0.21	0/3632	0.46	0/4891
3	d	0.21	0/2707	0.45	0/3650
4	E	0.22	0/3712	0.44	0/4997
4	e	0.21	0/2743	0.44	0/3687
5	G	0.21	0/3758	0.45	0/5073
5	g	0.21	0/2763	0.46	0/3733
6	H	0.23	0/3716	0.43	0/5008
6	h	0.22	0/2751	0.45	0/3711
7	Q	0.23	0/3724	0.44	0/5032
7	q	0.23	0/2774	0.43	0/3746
8	Z	0.22	0/3702	0.44	0/4995
8	z	0.21	0/3702	0.45	0/4995
All	All	0.22	0/52392	0.44	0/70665

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3625	0	3783	380	0
1	a	2705	0	2799	0	0
2	B	3602	0	3705	353	0
2	b	2658	0	2733	0	0
3	D	3610	0	3810	456	0
3	d	2690	0	2818	0	0
4	E	3674	0	3781	382	0
4	e	2724	0	2822	0	0
5	G	3719	0	3870	398	0
5	g	2735	0	2851	0	0
6	H	3671	0	3783	366	0
6	h	2724	0	2842	0	0
7	Q	3673	0	3719	383	0
7	q	2739	0	2777	0	0
8	Z	3664	0	3820	413	0
8	z	3664	0	3820	0	0
All	All	51877	0	53733	2912	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 52.

All (2912) 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)
5:G:456:GLY:HA3	8:Z:118:ILE:HD11	1.37	1.06
1:A:211:ILE:HG22	1:A:213:GLY:H	1.21	1.04
3:D:540:ASN:HB3	3:D:542:ARG:HD3	1.36	1.03
4:E:94:LEU:HD21	4:E:523:MET:HB2	1.39	1.03
3:D:31:ASP:HB3	3:D:36:ILE:HB	1.39	1.03
7:Q:525:ILE:HG23	7:Q:526:MET:H	1.22	1.03
6:H:8:LEU:HA	7:Q:80:HIS:HB2	1.38	1.02
1:A:140:THR:HB	1:A:144:GLY:HA3	1.39	1.01
8:Z:206:LEU:HD13	8:Z:374:LEU:HD12	1.43	1.01
7:Q:225:LYS:HE3	7:Q:361:VAL:HG22	1.42	1.00
7:Q:33:ILE:HG13	7:Q:112:LEU:HB3	1.41	1.00
1:A:532:LYS:HD2	3:D:63:MET:HG2	1.39	0.99
4:E:31:LEU:HA	4:E:34:LEU:HD23	1.45	0.99
3:D:126:LEU:HB3	3:D:131:ILE:HD12	1.46	0.97
4:E:55:ASN:HD22	4:E:466:SER:HA	1.24	0.97
8:Z:231:LEU:HD11	8:Z:339:LEU:HB3	1.43	0.97
3:D:211:ILE:HG23	3:D:389:VAL:HG23	1.46	0.97
4:E:87:ILE:HD13	4:E:527:ILE:HG21	1.43	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:352:LEU:HD11	7:Q:359:GLN:HB3	1.42	0.97
4:E:228:VAL:HG23	4:E:374:ILE:HB	1.44	0.96
5:G:51:LEU:HG	5:G:57:ILE:HG12	1.48	0.96
6:H:19:ILE:H	6:H:20:PRO:HD2	1.27	0.96
1:A:12:SER:HB2	1:A:17:ILE:HB	1.47	0.96
6:H:25:ASN:HD22	6:H:75:ALA:HB2	1.28	0.95
7:Q:428:GLU:HA	7:Q:435:GLN:HE21	1.28	0.95
6:H:30:GLN:HA	6:H:102:ALA:HB1	1.48	0.95
7:Q:104:VAL:HG23	7:Q:511:ALA:HB2	1.49	0.95
6:H:329:SER:HB3	6:H:341:VAL:HG13	1.49	0.95
2:B:326:VAL:HG12	2:B:365:VAL:HG11	1.49	0.94
2:B:218:PHE:HB2	2:B:326:VAL:HG11	1.48	0.94
2:B:33:ILE:HA	2:B:107:ALA:HB1	1.50	0.94
8:Z:225:VAL:HB	8:Z:228:ALA:HB2	1.50	0.94
5:G:466:LEU:HA	5:G:487:LEU:HD22	1.48	0.93
5:G:72:VAL:HG13	8:Z:6:THR:HA	1.50	0.93
3:D:315:LEU:H	3:D:315:LEU:HD22	1.32	0.92
5:G:23:GLN:HE21	5:G:113:LEU:HD13	1.34	0.92
3:D:245:GLU:HG3	3:D:246:LYS:HD2	1.52	0.92
8:Z:41:LYS:HD2	8:Z:455:SER:HA	1.49	0.92
3:D:197:VAL:HG12	3:D:387:LYS:HA	1.51	0.92
8:Z:101:GLU:HB2	8:Z:446:ILE:HD12	1.52	0.91
2:B:121:ILE:HG23	2:B:431:LYS:HD2	1.49	0.91
5:G:204:ILE:HD13	5:G:355:ILE:HG21	1.50	0.91
1:A:106:GLU:HA	1:A:109:LYS:HD2	1.50	0.90
3:D:210:ASP:O	3:D:388:THR:HA	1.70	0.90
4:E:204:VAL:HB	4:E:410:ARG:HG3	1.51	0.90
1:A:351:VAL:HG13	1:A:364:ILE:HG12	1.54	0.90
1:A:408:VAL:HG21	1:A:504:PHE:HB3	1.50	0.90
7:Q:241:VAL:HG13	7:Q:321:LEU:HD22	1.54	0.90
1:A:220:VAL:HG13	1:A:306:MET:HG3	1.52	0.90
6:H:190:LEU:HD11	6:H:195:ILE:HD11	1.52	0.90
7:Q:90:SER:HB3	7:Q:105:LEU:HD21	1.54	0.90
5:G:152:MET:SD	5:G:402:LEU:HD11	2.11	0.90
5:G:241:LEU:HD13	5:G:338:LEU:HD11	1.54	0.90
5:G:239:VAL:HG22	5:G:343:VAL:HG22	1.53	0.89
4:E:50:THR:HB	4:E:57:LEU:HD12	1.54	0.89
6:H:215:ALA:HB3	6:H:373:ILE:HD11	1.53	0.89
5:G:74:HIS:HB2	8:Z:5:LYS:HB2	1.55	0.89
6:H:17:GLN:HB3	6:H:518:GLU:HG3	1.54	0.89
7:Q:247:ASP:HA	7:Q:298:ALA:HB2	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:26:ASN:HD21	5:G:519:ILE:HD12	1.37	0.89
1:A:349:GLU:HB3	1:A:366:ASN:HB3	1.54	0.89
7:Q:199:VAL:HG12	7:Q:396:VAL:HG12	1.53	0.89
1:A:31:ILE:HG22	1:A:43:LYS:HE2	1.54	0.89
5:G:203:LYS:HD2	5:G:384:LEU:HG	1.54	0.88
8:Z:230:ILE:HG21	8:Z:324:LEU:HD21	1.54	0.88
1:A:10:ASP:O	1:A:531:ILE:HA	1.72	0.88
3:D:178:VAL:HB	3:D:403:GLU:HG2	1.55	0.88
2:B:144:SER:HB2	2:B:474:THR:HG21	1.55	0.88
8:Z:237:LEU:HG	8:Z:336:LEU:HD11	1.56	0.88
6:H:183:VAL:HG13	6:H:190:LEU:HD22	1.56	0.88
3:D:119:LEU:HD12	3:D:529:VAL:HG21	1.56	0.88
2:B:229:PRO:HG2	2:B:310:MET:HB2	1.56	0.87
7:Q:199:VAL:HG13	7:Q:400:LYS:HD2	1.53	0.87
6:H:23:VAL:HG22	6:H:109:LYS:HE3	1.54	0.87
8:Z:466:VAL:HG22	8:Z:486:PRO:HB3	1.55	0.87
3:D:208:LEU:HG	3:D:416:ARG:HD3	1.56	0.87
3:D:152:THR:HG22	3:D:515:LEU:HD21	1.53	0.87
3:D:101:GLN:HE22	3:D:105:ALA:HB3	1.37	0.86
4:E:99:ASP:HA	4:E:103:GLY:HA2	1.56	0.86
8:Z:224:ARG:HH11	8:Z:351:TYR:HB3	1.38	0.86
1:A:530:LEU:HD12	1:A:531:ILE:N	1.90	0.86
1:A:2:GLU:HG3	3:D:43:ALA:HB3	1.56	0.86
7:Q:142:ILE:HG22	7:Q:146:LEU:HD23	1.57	0.86
2:B:158:ASP:HA	2:B:161:ASN:HD22	1.41	0.85
3:D:239:SER:HB2	3:D:321:ASN:HB3	1.57	0.85
4:E:156:LEU:HB3	4:E:161:ASN:HB3	1.56	0.85
6:H:33:ALA:HB1	6:H:99:LEU:HA	1.58	0.85
1:A:180:LYS:HD3	1:A:403:LEU:HD23	1.58	0.85
7:Q:112:LEU:HD22	7:Q:519:LEU:HD21	1.55	0.85
4:E:188:ILE:HG23	4:E:224:LEU:HB2	1.59	0.85
6:H:26:ILE:HG23	6:H:105:LEU:HB3	1.58	0.85
6:H:120:ILE:HD11	7:Q:457:GLY:HA3	1.57	0.85
8:Z:199:LYS:HZ1	8:Z:377:LYS:HD3	1.41	0.85
6:H:48:LEU:HG	6:H:58:ILE:HG12	1.59	0.84
8:Z:277:LEU:HD22	8:Z:340:ASN:HA	1.58	0.84
4:E:247:LYS:HB3	4:E:353:LEU:HD13	1.57	0.84
1:A:137:ILE:HD12	1:A:410:PRO:HD3	1.57	0.84
6:H:154:LEU:HD23	6:H:157:LYS:HZ3	1.41	0.84
3:D:167:LEU:HD23	3:D:191:VAL:HG21	1.56	0.84
3:D:247:ALA:HA	3:D:299:ASN:HD21	1.43	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:103:LEU:HD22	8:Z:516:LEU:HD21	1.59	0.84
7:Q:183:ILE:HG23	7:Q:217:VAL:HG22	1.58	0.84
4:E:209:ILE:HA	4:E:383:VAL:HG22	1.59	0.84
1:A:506:PRO:HB2	1:A:509:VAL:HG23	1.59	0.83
3:D:421:LYS:HE2	3:D:515:LEU:HD23	1.60	0.83
4:E:458:ILE:HB	4:E:459:PRO:HD3	1.61	0.83
5:G:238:ILE:HD13	5:G:323:ILE:HG21	1.59	0.83
4:E:163:GLU:HB3	4:E:164:PRO:HD3	1.60	0.83
6:H:227:MET:HA	6:H:230:LYS:NZ	1.93	0.83
1:A:112:ILE:HG23	1:A:433:ARG:HD3	1.58	0.83
4:E:98:GLN:HE21	4:E:102:ILE:HD11	1.41	0.83
1:A:237:LEU:HD13	1:A:331:LEU:HG	1.61	0.83
2:B:239:ILE:HG21	2:B:331:ILE:HG12	1.61	0.82
4:E:25:LYS:HG2	4:E:536:PRO:HA	1.60	0.82
7:Q:205:CYS:SG	7:Q:376:VAL:HA	2.19	0.82
1:A:356:ILE:HD13	1:A:361:LEU:HD22	1.61	0.82
5:G:407:LEU:HD13	5:G:496:TRP:HB3	1.61	0.82
7:Q:390:ARG:HH11	7:Q:390:ARG:HG2	1.45	0.82
1:A:351:VAL:HG22	1:A:364:ILE:HG23	1.62	0.82
1:A:199:LYS:HB2	1:A:385:CYS:HB3	1.61	0.82
7:Q:297:VAL:HG21	7:Q:312:LEU:HD21	1.61	0.82
8:Z:201:GLU:HA	8:Z:377:LYS:O	1.80	0.82
5:G:130:LEU:HD23	5:G:510:VAL:HG21	1.61	0.82
6:H:313:ARG:HG3	6:H:313:ARG:HH11	1.42	0.82
8:Z:448:PRO:HA	8:Z:451:LEU:HD12	1.61	0.82
1:A:85:GLU:HB3	1:A:512:LYS:HE2	1.62	0.82
2:B:421:VAL:HA	2:B:424:LEU:HD12	1.61	0.81
1:A:532:LYS:HG3	3:D:63:MET:O	1.80	0.81
4:E:20:LYS:NZ	6:H:31:VAL:HB	1.94	0.81
5:G:491:LYS:HA	5:G:496:TRP:HE1	1.45	0.81
2:B:95:VAL:HG23	2:B:96:GLY:H	1.44	0.81
5:G:156:ILE:HG23	5:G:394:ALA:HB1	1.62	0.81
7:Q:151:ALA:HB3	7:Q:159:GLU:HG3	1.60	0.81
6:H:346:GLN:HB3	6:H:363:GLY:HA3	1.62	0.81
7:Q:238:LYS:NZ	7:Q:341:LEU:HD11	1.96	0.81
7:Q:240:ALA:HB2	7:Q:344:MET:SD	2.20	0.81
4:E:510:LEU:HG	4:E:514:LYS:NZ	1.94	0.81
2:B:209:LEU:HD21	2:B:382:ILE:HG22	1.63	0.81
3:D:443:SER:OG	3:D:454:ILE:HB	1.80	0.81
2:B:454:ALA:HB2	2:B:480:MET:SD	2.20	0.81
8:Z:168:LEU:HD21	8:Z:391:ILE:HG12	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:406:CYS:HB3	8:Z:498:TYR:HB2	1.62	0.81
2:B:520:ILE:HD12	4:E:60:MET:HB3	1.60	0.81
5:G:238:ILE:HD11	5:G:291:ILE:HG13	1.62	0.81
4:E:161:ASN:HD22	4:E:164:PRO:HB2	1.46	0.80
7:Q:276:MET:SD	7:Q:300:MET:HB2	2.20	0.80
2:B:354:ILE:HD12	2:B:359:LEU:HD22	1.63	0.80
4:E:527:ILE:HA	4:E:530:ILE:HD12	1.63	0.80
2:B:53:LEU:HA	2:B:60:SER:O	1.81	0.80
8:Z:231:LEU:HG	8:Z:339:LEU:HD13	1.61	0.80
3:D:236:VAL:HG21	3:D:329:LYS:HG2	1.64	0.80
4:E:234:PHE:HE1	4:E:372:LEU:HD13	1.47	0.80
6:H:6:VAL:HG12	6:H:7:ILE:HG13	1.62	0.80
1:A:530:LEU:HD12	1:A:531:ILE:H	1.46	0.80
4:E:489:LEU:HD21	4:E:498:THR:HB	1.64	0.80
2:B:214:LEU:HG	2:B:373:ILE:HG12	1.62	0.80
6:H:25:ASN:ND2	6:H:75:ALA:HB2	1.95	0.80
6:H:190:LEU:HD23	6:H:397:ARG:HB2	1.63	0.80
4:E:21:ASP:HB3	4:E:25:LYS:HD2	1.61	0.79
4:E:97:SER:O	4:E:101:GLU:HG2	1.82	0.79
2:B:465:LEU:HA	2:B:485:ILE:HD12	1.64	0.79
8:Z:228:ALA:HB1	8:Z:290:VAL:HG21	1.65	0.79
1:A:27:SER:O	1:A:31:ILE:HG13	1.83	0.79
1:A:27:SER:HB2	5:G:9:VAL:HG11	1.65	0.79
6:H:49:ILE:HD11	6:H:65:ILE:HG23	1.65	0.79
6:H:522:ASN:HB3	7:Q:77:GLU:HB2	1.63	0.79
4:E:298:ASN:HA	4:E:319:LEU:HG	1.63	0.79
6:H:23:VAL:HG13	6:H:109:LYS:HZ1	1.47	0.79
1:A:237:LEU:HD21	1:A:334:LEU:HD22	1.62	0.79
4:E:251:LEU:HD21	4:E:348:LEU:HD22	1.65	0.78
5:G:347:ALA:HB3	5:G:365:GLU:HB3	1.65	0.78
3:D:93:MET:HA	3:D:96:GLU:OE1	1.83	0.78
1:A:418:ALA:HB2	1:A:471:HIS:NE2	1.98	0.78
3:D:64:ILE:HD11	3:D:80:ILE:HG23	1.65	0.78
2:B:136:ALA:HB1	2:B:424:LEU:HD13	1.65	0.78
2:B:97:ASP:CG	2:B:98:GLY:H	1.87	0.78
6:H:211:VAL:HG13	6:H:362:THR:HB	1.64	0.78
1:A:190:TYR:HD2	1:A:400:LYS:HB2	1.48	0.77
4:E:177:VAL:HB	4:E:397:GLU:HG2	1.65	0.77
6:H:239:LEU:HD22	6:H:319:LEU:HD12	1.65	0.77
5:G:49:MET:HE2	5:G:51:LEU:HD11	1.65	0.77
1:A:234:ILE:HG21	1:A:319:ILE:HG21	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:33:PRO:HA	3:D:536:ASP:CG	2.04	0.77
1:A:408:VAL:CG2	1:A:504:PHE:HB3	2.14	0.77
4:E:98:GLN:NE2	4:E:102:ILE:HD11	1.98	0.77
7:Q:333:LEU:HD13	7:Q:339:PRO:HB3	1.65	0.77
7:Q:524:ILE:HG21	8:Z:46:MET:H	1.50	0.77
2:B:196:LEU:HD22	2:B:394:LEU:HB3	1.67	0.77
6:H:231:LYS:HA	6:H:348:PHE:O	1.84	0.77
8:Z:118:ILE:H	8:Z:118:ILE:HD12	1.50	0.77
1:A:530:LEU:HD13	3:D:62:LYS:HB3	1.65	0.77
7:Q:225:LYS:HA	7:Q:313:VAL:HG22	1.66	0.77
2:B:513:VAL:HA	2:B:516:ARG:NH1	1.99	0.77
4:E:404:ASP:HA	4:E:407:CYS:SG	2.25	0.76
8:Z:48:VAL:HG22	8:Z:54:ILE:HG12	1.65	0.76
4:E:20:LYS:HZ2	6:H:31:VAL:HB	1.51	0.76
6:H:97:VAL:HG23	6:H:506:ALA:HB2	1.68	0.76
2:B:50:LYS:HA	3:D:538:VAL:HG22	1.66	0.76
4:E:193:VAL:HG13	4:E:204:VAL:HG11	1.65	0.76
6:H:238:ALA:HB3	6:H:289:VAL:HG22	1.68	0.76
5:G:130:LEU:HD11	5:G:507:LYS:HD3	1.65	0.76
2:B:11:ILE:HA	4:E:85:HIS:H	1.51	0.76
2:B:299:TYR:HB3	2:B:300:PRO:HD3	1.67	0.76
5:G:388:GLU:O	5:G:392:GLN:HG3	1.86	0.76
1:A:68:GLU:HB2	5:G:11:SER:HA	1.68	0.76
6:H:235:PRO:HD2	6:H:345:CYS:O	1.86	0.76
6:H:238:ALA:HB2	6:H:286:ALA:HB1	1.66	0.76
8:Z:440:PHE:O	8:Z:444:LEU:HG	1.86	0.76
3:D:24:LYS:HD3	3:D:28:GLN:HE22	1.50	0.76
4:E:35:LYS:HA	4:E:38:ILE:HD12	1.68	0.76
5:G:416:MET:HG2	5:G:466:LEU:HD22	1.66	0.76
1:A:356:ILE:HG23	1:A:378:ARG:NH2	2.00	0.76
5:G:86:THR:O	5:G:90:GLU:HG2	1.86	0.76
8:Z:46:MET:HB2	8:Z:56:LEU:HD13	1.68	0.76
5:G:466:LEU:HG	5:G:487:LEU:HD13	1.67	0.75
6:H:157:LYS:O	6:H:161:THR:HG23	1.86	0.75
8:Z:118:ILE:HG21	8:Z:432:ARG:HB2	1.68	0.75
8:Z:228:ALA:HB1	8:Z:290:VAL:CG2	2.17	0.75
8:Z:293:ASN:HD22	8:Z:297:ILE:HD11	1.51	0.75
1:A:17:ILE:HG23	1:A:18:ARG:H	1.52	0.75
3:D:237:ALA:HB1	3:D:321:ASN:OD1	1.86	0.75
3:D:433:ILE:HD11	3:D:465:PRO:HG3	1.68	0.75
4:E:236:HIS:HB3	4:E:239:MET:HG3	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:29:CYS:HA	6:H:79:LEU:HD11	1.66	0.75
6:H:19:ILE:N	6:H:20:PRO:HD2	2.01	0.75
8:Z:114:LEU:HD23	8:Z:432:ARG:HD3	1.68	0.75
7:Q:20:LYS:NZ	8:Z:68:GLN:HB3	2.02	0.75
5:G:70:ILE:HG23	8:Z:7:LEU:HD23	1.68	0.75
4:E:466:SER:HB3	4:E:493:CYS:SG	2.26	0.74
8:Z:216:ALA:HB1	8:Z:221:MET:HB2	1.69	0.74
7:Q:521:VAL:HG13	8:Z:45:LYS:HA	1.69	0.74
8:Z:466:VAL:HG21	8:Z:479:VAL:HG22	1.68	0.74
2:B:407:VAL:HG23	2:B:495:GLU:HB2	1.70	0.74
3:D:477:ILE:H	3:D:477:ILE:HD12	1.52	0.74
6:H:51:ASP:OD2	6:H:55:LYS:HB3	1.88	0.74
5:G:73:GLN:HB2	8:Z:5:LYS:HB3	1.67	0.74
3:D:529:VAL:O	3:D:533:LEU:HG	1.87	0.74
6:H:394:MET:HE3	6:H:397:ARG:HH21	1.51	0.74
7:Q:129:ILE:HD12	7:Q:516:VAL:HG13	1.68	0.74
7:Q:58:ASN:HD21	7:Q:62:LYS:HB2	1.53	0.74
1:A:33:LYS:HA	1:A:95:ILE:HD11	1.68	0.74
2:B:33:ILE:HG21	2:B:111:ARG:HD3	1.70	0.74
3:D:244:VAL:HG11	3:D:299:ASN:OD1	1.88	0.74
6:H:200:VAL:HG11	6:H:358:TYR:HE2	1.50	0.74
6:H:414:MET:HG2	6:H:464:LEU:HG	1.67	0.74
3:D:101:GLN:NE2	3:D:105:ALA:HB3	2.02	0.74
7:Q:234:VAL:HG11	7:Q:289:ASN:OD1	1.87	0.74
3:D:32:LYS:O	3:D:36:ILE:HG22	1.87	0.74
4:E:306:PHE:HB2	4:E:323:ARG:HB3	1.69	0.74
7:Q:104:VAL:HG13	7:Q:105:LEU:HD23	1.70	0.74
2:B:51:ILE:HD12	2:B:63:VAL:HG22	1.69	0.74
7:Q:49:PRO:HA	7:Q:170:SER:HA	1.70	0.74
2:B:190:LEU:HD11	2:B:371:CYS:SG	2.28	0.74
4:E:413:ILE:HG23	4:E:414:ARG:HG3	1.69	0.74
5:G:238:ILE:HA	5:G:289:VAL:HG23	1.69	0.73
1:A:180:LYS:HZ1	1:A:403:LEU:HB3	1.53	0.73
4:E:511:ILE:H	4:E:511:ILE:HD12	1.53	0.73
5:G:64:ASN:HB2	5:G:95:THR:HG21	1.68	0.73
6:H:135:LYS:O	6:H:139:ILE:HG12	1.87	0.73
4:E:236:HIS:CD2	4:E:315:LEU:HD12	2.24	0.73
5:G:240:LEU:HD12	5:G:331:ILE:HG12	1.69	0.73
5:G:74:HIS:H	8:Z:5:LYS:HB2	1.52	0.73
3:D:193:ALA:HB1	3:D:389:VAL:HG21	1.69	0.73
3:D:94:LEU:HD22	3:D:113:VAL:HG13	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ASP:HB3	1:A:329:SER:HA	1.69	0.73
5:G:89:GLU:HA	5:G:389:ARG:NH2	2.03	0.73
6:H:227:MET:HA	6:H:230:LYS:HZ1	1.53	0.73
7:Q:17:GLU:HA	8:Z:70:GLN:CD	2.09	0.73
1:A:43:LYS:HG2	5:G:520:ASP:OD1	1.88	0.73
3:D:256:LEU:N	3:D:256:LEU:HD12	2.03	0.73
8:Z:115:HIS:HB3	8:Z:118:ILE:HD13	1.68	0.73
2:B:43:LEU:HD12	2:B:44:GLY:H	1.54	0.73
7:Q:402:LEU:HD12	7:Q:406:LYS:HA	1.70	0.73
8:Z:131:LEU:HD23	8:Z:505:LEU:HD12	1.69	0.73
3:D:217:LEU:HD11	3:D:398:LYS:HG3	1.71	0.72
2:B:12:PHE:HB3	2:B:16:ALA:HB3	1.70	0.72
3:D:235:LYS:HE3	3:D:367:GLU:HB2	1.69	0.72
8:Z:176:ILE:HD13	8:Z:179:ILE:HD11	1.71	0.72
1:A:136:LEU:HD22	1:A:407:SER:HB3	1.69	0.72
3:D:32:LYS:NZ	3:D:33:PRO:HD2	2.03	0.72
6:H:188:ASP:O	6:H:189:LEU:HB2	1.88	0.72
4:E:331:GLU:OE1	6:H:297:ASP:HB3	1.89	0.72
3:D:290:VAL:HG21	3:D:319:PHE:HB2	1.70	0.72
2:B:79:PRO:HD3	2:B:522:LYS:HD2	1.70	0.72
5:G:220:ILE:HD11	5:G:323:ILE:HD11	1.72	0.72
1:A:121:TYR:HB3	1:A:518:THR:HG23	1.71	0.72
6:H:19:ILE:H	6:H:20:PRO:CD	2.02	0.72
1:A:135:ASN:HB3	1:A:484:LYS:HD3	1.70	0.72
3:D:421:LYS:HG2	3:D:515:LEU:HB3	1.71	0.71
5:G:49:MET:HG3	5:G:59:MET:HG2	1.72	0.71
7:Q:233:SER:HA	7:Q:351:TYR:HA	1.72	0.71
3:D:78:ALA:HB2	3:D:109:THR:HG21	1.72	0.71
7:Q:230:ASP:HB3	7:Q:311:MET:HA	1.71	0.71
1:A:2:GLU:CG	3:D:43:ALA:HB3	2.20	0.71
8:Z:97:LEU:HD23	8:Z:450:VAL:HG21	1.72	0.71
4:E:55:ASN:ND2	4:E:466:SER:HA	2.02	0.71
8:Z:222:LYS:HB2	8:Z:311:ILE:HD11	1.71	0.71
4:E:510:LEU:HG	4:E:514:LYS:HZ2	1.52	0.71
4:E:534:ARG:HH21	6:H:35:ALA:CB	2.03	0.71
5:G:399:ARG:O	5:G:403:LEU:HD13	1.91	0.71
7:Q:289:ASN:OD1	7:Q:290:VAL:HG23	1.89	0.71
1:A:8:PHE:O	1:A:533:LEU:HD22	1.91	0.71
7:Q:526:MET:HG2	8:Z:48:VAL:O	1.90	0.71
2:B:124:GLN:HG2	4:E:55:ASN:ND2	2.06	0.71
8:Z:414:VAL:HA	8:Z:475:GLN:HE22	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:167:LEU:HB3	6:H:384:GLU:HG2	1.72	0.71
6:H:43:ARG:NH2	6:H:480:ASN:HA	2.05	0.71
2:B:231:ARG:HH21	2:B:348:LEU:HD11	1.55	0.71
3:D:187:SER:HB2	3:D:188:PRO:HD3	1.73	0.71
3:D:252:ILE:HB	3:D:303:ILE:HD13	1.71	0.71
5:G:407:LEU:HB3	5:G:498:PRO:HA	1.72	0.71
7:Q:176:GLU:HG3	7:Q:212:VAL:HG13	1.73	0.71
6:H:19:ILE:HA	6:H:22:LEU:HD23	1.73	0.71
6:H:366:LYS:HD3	6:H:368:LYS:NZ	2.06	0.71
8:Z:193:ILE:HG21	8:Z:388:LYS:HG3	1.71	0.71
2:B:518:ASP:CG	4:E:59:LYS:HZ3	1.94	0.70
5:G:27:ILE:HG23	5:G:106:LEU:HB3	1.73	0.70
7:Q:113:GLU:O	7:Q:116:GLU:HG2	1.91	0.70
7:Q:452:LEU:HG	7:Q:482:ILE:HD11	1.73	0.70
7:Q:524:ILE:CG2	8:Z:46:MET:H	2.03	0.70
2:B:187:VAL:HG21	2:B:397:LEU:HD13	1.72	0.70
3:D:210:ASP:HB3	3:D:387:LYS:O	1.92	0.70
4:E:222:THR:HG22	4:E:387:ILE:HA	1.73	0.70
5:G:401:VAL:HA	5:G:405:PRO:HB3	1.72	0.70
6:H:313:ARG:HG3	6:H:313:ARG:NH1	2.04	0.70
7:Q:232:THR:O	7:Q:351:TYR:HA	1.91	0.70
6:H:278:LEU:HD23	6:H:302:TYR:HB2	1.73	0.70
1:A:532:LYS:HG2	3:D:65:GLN:CB	2.20	0.70
3:D:299:ASN:OD1	3:D:300:VAL:HG23	1.91	0.70
4:E:209:ILE:HA	4:E:383:VAL:CG2	2.21	0.70
7:Q:525:ILE:HG23	7:Q:526:MET:N	2.01	0.70
8:Z:138:LYS:HA	8:Z:408:VAL:HG12	1.74	0.70
5:G:47:MET:O	8:Z:518:VAL:HG22	1.91	0.70
8:Z:455:SER:HB3	8:Z:481:LEU:HD13	1.73	0.70
2:B:279:VAL:HG11	2:B:303:LEU:HB3	1.73	0.70
3:D:192:ASP:O	3:D:195:MET:HG3	1.91	0.70
4:E:362:ILE:HB	4:E:364:PHE:CE1	2.27	0.70
1:A:458:GLN:HB3	1:A:463:LEU:HD11	1.72	0.70
4:E:247:LYS:O	4:E:353:LEU:HD22	1.91	0.70
8:Z:105:GLN:HA	8:Z:108:LEU:HD12	1.72	0.70
4:E:468:MET:SD	4:E:496:LYS:HB3	2.31	0.70
6:H:161:THR:HG21	6:H:491:PHE:HB3	1.72	0.70
7:Q:70:ALA:H	7:Q:101:THR:HG21	1.56	0.70
7:Q:523:GLN:HB3	8:Z:45:LYS:NZ	2.07	0.70
8:Z:135:GLU:HA	8:Z:138:LYS:HD3	1.74	0.70
4:E:87:ILE:CD1	4:E:527:ILE:HG21	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:337:ASN:H	7:Q:338:PRO:HD2	1.55	0.70
7:Q:417:ILE:HD11	7:Q:449:PRO:HG3	1.73	0.70
2:B:416:LEU:HD22	2:B:474:THR:HG23	1.74	0.70
2:B:427:ARG:O	2:B:429:PRO:HD3	1.91	0.70
3:D:144:LEU:HB2	3:D:526:THR:HG21	1.71	0.70
5:G:238:ILE:HD11	5:G:291:ILE:CG1	2.22	0.70
5:G:200:ARG:HE	5:G:322:ARG:HH11	1.40	0.70
4:E:85:HIS:O	4:E:89:LYS:HG3	1.92	0.69
5:G:73:GLN:NE2	8:Z:9:PRO:HD3	2.07	0.69
6:H:239:LEU:HD23	6:H:290:LEU:HB2	1.74	0.69
8:Z:222:LYS:HD2	8:Z:311:ILE:HD11	1.74	0.69
7:Q:17:GLU:HA	8:Z:70:GLN:OE1	1.92	0.69
3:D:178:VAL:CB	3:D:403:GLU:HG2	2.22	0.69
7:Q:221:MET:HA	7:Q:374:THR:OG1	1.92	0.69
7:Q:103:PHE:HE1	7:Q:448:ILE:HG12	1.57	0.69
8:Z:30:LEU:HD22	8:Z:74:ALA:HB1	1.74	0.69
1:A:2:GLU:HA	3:D:88:HIS:HB3	1.74	0.69
4:E:286:GLU:HA	4:E:313:LEU:HD13	1.74	0.69
5:G:156:ILE:HD11	5:G:398:CYS:SG	2.33	0.69
5:G:14:THR:HG23	5:G:525:GLY:HA3	1.74	0.69
6:H:154:LEU:HD23	6:H:157:LYS:NZ	2.07	0.69
7:Q:80:HIS:HB3	7:Q:83:ALA:HB3	1.72	0.69
1:A:172:VAL:O	1:A:176:VAL:HG23	1.92	0.69
2:B:187:VAL:O	2:B:191:LYS:HB2	1.93	0.69
3:D:146:LYS:O	3:D:149:GLU:HG2	1.93	0.69
5:G:397:VAL:HA	5:G:400:ASN:HD22	1.57	0.69
6:H:200:VAL:HG11	6:H:358:TYR:CE2	2.27	0.69
7:Q:161:SER:HB2	7:Q:181:LYS:HD2	1.74	0.69
1:A:348:ALA:HA	1:A:367:THR:HA	1.74	0.69
2:B:186:ALA:HA	2:B:189:ARG:HH12	1.57	0.69
2:B:280:GLU:HG2	2:B:284:LYS:HE3	1.75	0.69
4:E:161:ASN:HB2	4:E:164:PRO:HD2	1.73	0.69
7:Q:237:ALA:HA	7:Q:289:ASN:HD21	1.55	0.69
8:Z:224:ARG:CZ	8:Z:349:LEU:HD11	2.23	0.69
4:E:166:ILE:HG22	4:E:170:LYS:HE2	1.75	0.69
8:Z:197:LYS:HE2	8:Z:381:LYS:HG3	1.75	0.69
1:A:328:LEU:HD21	1:A:344:MET:HB3	1.73	0.69
3:D:193:ALA:CB	3:D:389:VAL:HG21	2.23	0.69
3:D:237:ALA:HB2	3:D:327:VAL:HG12	1.75	0.69
7:Q:410:PRO:O	7:Q:414:ALA:HB3	1.93	0.69
2:B:398:ALA:O	2:B:402:LYS:HD2	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:294:GLN:NE2	8:Z:318:ARG:HD3	2.08	0.69
8:Z:409:PRO:O	8:Z:413:ALA:HB3	1.93	0.69
1:A:31:ILE:HG12	5:G:16:ARG:HH12	1.58	0.68
2:B:30:ILE:HA	2:B:33:ILE:HD12	1.74	0.68
6:H:406:VAL:HB	6:H:412:ILE:HD11	1.75	0.68
7:Q:337:ASN:C	7:Q:339:PRO:HD2	2.13	0.68
7:Q:85:MET:HA	7:Q:88:MET:SD	2.33	0.68
3:D:256:LEU:HD21	3:D:301:LEU:HD21	1.74	0.68
3:D:416:ARG:HH11	3:D:420:LYS:NZ	1.91	0.68
6:H:133:VAL:HG12	6:H:137:LYS:NZ	2.09	0.68
1:A:145:ARG:HG2	1:A:149:ILE:HD11	1.76	0.68
1:A:211:ILE:HG12	1:A:376:ILE:HG12	1.76	0.68
4:E:218:ARG:HA	4:E:389:GLY:HA2	1.76	0.68
6:H:412:ILE:O	6:H:416:LEU:HG	1.94	0.68
3:D:415:ILE:O	3:D:419:VAL:HG13	1.94	0.68
1:A:69:HIS:HB2	5:G:8:LEU:O	1.94	0.68
2:B:516:ARG:HG2	4:E:58:ASP:H	1.57	0.68
7:Q:53:ASN:HB3	7:Q:67:ASN:OD1	1.94	0.68
8:Z:414:VAL:HA	8:Z:475:GLN:NE2	2.08	0.68
7:Q:239:ILE:HD12	7:Q:328:VAL:HG11	1.76	0.68
2:B:25:ARG:HD2	2:B:117:ILE:HD13	1.76	0.68
3:D:41:ILE:HG23	3:D:120:LEU:HB3	1.75	0.68
3:D:505:ASN:O	3:D:509:GLU:HG2	1.94	0.68
3:D:52:ARG:HA	3:D:114:ILE:HD11	1.76	0.68
5:G:112:PHE:HE2	5:G:436:PRO:HA	1.59	0.68
3:D:177:LYS:HD3	3:D:407:SER:HB3	1.76	0.68
7:Q:225:LYS:NZ	7:Q:352:LEU:HB2	2.09	0.68
8:Z:44:MET:SD	8:Z:56:LEU:HG	2.34	0.68
6:H:21:GLN:NE2	6:H:22:LEU:HD13	2.09	0.67
7:Q:174:GLY:HA2	7:Q:177:VAL:HG13	1.76	0.67
7:Q:203:ARG:HH22	7:Q:223:PHE:HD1	1.41	0.67
1:A:234:ILE:HG21	1:A:319:ILE:CG2	2.24	0.67
4:E:27:ARG:HH22	4:E:534:ARG:NH2	1.92	0.67
5:G:23:GLN:NE2	5:G:113:LEU:HB3	2.10	0.67
5:G:246:GLU:HA	5:G:297:SER:HB3	1.75	0.67
5:G:29:ALA:HA	8:Z:4:VAL:HG13	1.76	0.67
6:H:198:LYS:HZ3	6:H:217:LYS:HG3	1.59	0.67
6:H:30:GLN:O	6:H:34:GLU:HG2	1.94	0.67
5:G:140:ILE:HG13	5:G:476:GLU:OE1	1.93	0.67
4:E:204:VAL:CG2	4:E:413:ILE:HG21	2.24	0.67
8:Z:12:GLU:O	8:Z:522:MET:HA	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:181:LYS:HE2	8:Z:370:ARG:HH12	1.57	0.67
1:A:530:LEU:HD21	3:D:63:MET:H	1.59	0.67
4:E:94:LEU:HD11	4:E:523:MET:HB3	1.76	0.67
5:G:33:ILE:HD11	5:G:67:LEU:HD22	1.76	0.67
6:H:153:LYS:HG2	6:H:157:LYS:HZ2	1.59	0.67
1:A:241:LEU:HG	1:A:331:LEU:HD21	1.77	0.67
1:A:2:GLU:CA	3:D:88:HIS:HB3	2.25	0.67
3:D:249:ILE:HG21	3:D:345:THR:HG21	1.76	0.67
3:D:256:LEU:HD11	3:D:303:ILE:CD1	2.25	0.67
5:G:64:ASN:ND2	5:G:68:ARG:HD2	2.10	0.67
6:H:22:LEU:HD22	6:H:22:LEU:H	1.60	0.67
8:Z:504:LEU:HD23	8:Z:505:LEU:N	2.10	0.67
4:E:344:ARG:HE	4:E:345:PHE:H	1.40	0.67
5:G:129:ALA:HA	5:G:132:ASP:OD2	1.95	0.67
5:G:359:TYR:HD1	5:G:359:TYR:H	1.42	0.67
5:G:498:PRO:HB2	5:G:501:VAL:HG23	1.77	0.67
5:G:70:ILE:HG22	8:Z:6:THR:O	1.95	0.67
4:E:536:PRO:HD2	6:H:50:VAL:O	1.94	0.67
6:H:198:LYS:NZ	6:H:217:LYS:HG3	2.10	0.67
6:H:417:SER:HA	6:H:439:ALA:HB1	1.77	0.67
6:H:450:CYS:SG	6:H:460:ILE:HG21	2.35	0.67
8:Z:197:LYS:O	8:Z:198:HIS:HB2	1.95	0.67
2:B:279:VAL:HG21	2:B:303:LEU:HB2	1.75	0.67
2:B:461:LEU:HD21	2:B:478:LEU:HD13	1.76	0.67
1:A:20:GLN:HB2	5:G:7:VAL:N	2.10	0.67
6:H:118:PRO:HA	6:H:121:ILE:HD12	1.77	0.66
3:D:256:LEU:HD11	3:D:303:ILE:HG13	1.76	0.66
3:D:241:ILE:O	3:D:326:MET:HB2	1.95	0.66
4:E:227:GLY:HA3	4:E:375:GLU:HA	1.77	0.66
5:G:19:GLY:O	5:G:23:GLN:HG2	1.94	0.66
6:H:237:ILE:O	6:H:342:LEU:HA	1.95	0.66
8:Z:199:LYS:NZ	8:Z:377:LYS:HD3	2.11	0.66
7:Q:397:ASN:O	7:Q:401:VAL:HG23	1.94	0.66
7:Q:523:GLN:O	8:Z:45:LYS:HD2	1.95	0.66
1:A:313:LYS:HE2	1:A:317:LYS:HE3	1.76	0.66
2:B:194:GLY:HA3	2:B:401:VAL:HG21	1.77	0.66
3:D:175:ASN:HA	3:D:180:SER:HB3	1.78	0.66
4:E:118:GLU:O	4:E:121:GLU:HG2	1.96	0.66
5:G:144:VAL:O	5:G:405:PRO:HB2	1.95	0.66
8:Z:230:ILE:HD13	8:Z:290:VAL:HB	1.77	0.66
2:B:111:ARG:HH11	2:B:111:ARG:HG2	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:379:ALA:HB3	5:G:383:ILE:HD12	1.76	0.66
5:G:469:LYS:HA	5:G:472:GLN:OE1	1.96	0.66
7:Q:72:ILE:O	7:Q:76:LEU:HG	1.94	0.66
8:Z:417:ALA:HB2	8:Z:470:HIS:HE2	1.61	0.66
3:D:232:LEU:HD21	3:D:339:ILE:HD11	1.76	0.66
3:D:474:LEU:HD11	3:D:501:GLY:HA2	1.78	0.66
3:D:137:SER:HB3	3:D:530:ARG:HG3	1.78	0.66
7:Q:239:ILE:HD13	7:Q:324:LEU:HD11	1.78	0.66
7:Q:328:VAL:HG12	7:Q:366:GLU:HG2	1.75	0.66
8:Z:118:ILE:CG2	8:Z:432:ARG:HB2	2.26	0.66
2:B:72:LYS:NZ	2:B:89:ARG:HG3	2.10	0.66
4:E:156:LEU:HD23	4:E:161:ASN:HB3	1.77	0.66
5:G:104:GLU:HG2	5:G:446:VAL:HG11	1.78	0.66
5:G:10:LEU:HD12	5:G:10:LEU:H	1.60	0.66
6:H:453:ALA:HB3	6:H:479:ILE:HD11	1.78	0.66
7:Q:206:LYS:HB3	7:Q:385:MET:HG2	1.76	0.66
2:B:51:ILE:HG23	2:B:63:VAL:HG22	1.78	0.66
6:H:141:VAL:HG21	6:H:474:TRP:HE1	1.60	0.66
7:Q:44:ARG:NE	7:Q:451:ALA:HB2	2.11	0.66
7:Q:55:MET:SD	7:Q:63:LEU:HD11	2.36	0.66
5:G:240:LEU:HD12	5:G:324:ALA:HB2	1.77	0.66
8:Z:7:LEU:HD11	8:Z:522:MET:SD	2.35	0.66
1:A:86:VAL:HG13	1:A:512:LYS:NZ	2.10	0.65
3:D:126:LEU:HD11	3:D:453:CYS:HA	1.78	0.65
4:E:170:LYS:NZ	4:E:183:ARG:HA	2.11	0.65
4:E:437:ALA:O	4:E:445:GLN:HG3	1.96	0.65
5:G:422:LEU:HD23	5:G:441:ALA:HB2	1.77	0.65
8:Z:13:VAL:HG22	8:Z:522:MET:HG2	1.78	0.65
8:Z:270:ARG:HB3	8:Z:336:LEU:HD13	1.78	0.65
4:E:435:GLN:O	4:E:439:LYS:HG3	1.95	0.65
8:Z:218:HIS:ND1	8:Z:219:PRO:HD2	2.11	0.65
2:B:337:HIS:H	2:B:338:PRO:HD2	1.60	0.65
3:D:105:ALA:HA	3:D:417:CYS:SG	2.37	0.65
4:E:248:ILE:O	4:E:353:LEU:HA	1.97	0.65
5:G:376:LEU:HD21	5:G:391:LEU:HD22	1.78	0.65
8:Z:94:SER:O	8:Z:98:ILE:HG12	1.95	0.65
2:B:141:LEU:HG	2:B:417:MET:SD	2.36	0.65
2:B:411:GLY:HA2	2:B:446:LEU:HD23	1.77	0.65
5:G:137:LEU:HD11	5:G:506:TYR:CE2	2.31	0.65
7:Q:411:GLY:HA3	7:Q:499:ASP:OD2	1.97	0.65
5:G:72:VAL:HG21	5:G:81:ILE:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:197:ILE:HG21	6:H:386:GLU:HG3	1.78	0.65
8:Z:152:ALA:HB3	8:Z:169:THR:HG23	1.77	0.65
3:D:248:LYS:HD2	3:D:359:LEU:HD13	1.78	0.65
3:D:30:ARG:HG3	3:D:539:VAL:HG22	1.78	0.65
4:E:20:LYS:HZ3	6:H:32:ILE:CD1	2.09	0.65
4:E:221:ASP:HB3	4:E:388:ARG:HD2	1.78	0.65
4:E:437:ALA:HA	4:E:448:MET:SD	2.37	0.65
4:E:90:LEU:O	4:E:523:MET:HE3	1.96	0.65
6:H:23:VAL:HA	6:H:109:LYS:NZ	2.11	0.65
7:Q:44:ARG:HA	7:Q:102:ASN:HD21	1.61	0.65
7:Q:24:GLY:HA2	7:Q:522:ASP:O	1.97	0.65
1:A:233:LYS:HA	1:A:346:GLY:O	1.96	0.65
1:A:445:LEU:N	1:A:446:PRO:HD2	2.12	0.65
2:B:221:ASP:OD1	2:B:359:LEU:HG	1.97	0.65
3:D:251:LEU:HD12	3:D:336:ILE:HG23	1.78	0.65
1:A:192:VAL:HG13	1:A:400:LYS:HD2	1.77	0.65
3:D:235:LYS:HZ2	3:D:242:THR:HA	1.61	0.65
7:Q:238:LYS:HZ2	7:Q:341:LEU:HD11	1.61	0.65
3:D:194:VAL:HA	3:D:197:VAL:HG22	1.78	0.65
3:D:232:LEU:HD22	3:D:335:ASP:HB3	1.78	0.65
5:G:221:ASN:HD22	5:G:316:ARG:HH22	1.44	0.65
6:H:364:CYS:HB2	6:H:367:ALA:HB2	1.79	0.65
8:Z:145:ARG:O	8:Z:149:ILE:HG13	1.96	0.65
3:D:293:ILE:HD13	3:D:301:LEU:HD22	1.80	0.65
3:D:232:LEU:HD11	3:D:339:ILE:HD11	1.79	0.65
4:E:161:ASN:ND2	4:E:164:PRO:HB2	2.11	0.65
6:H:6:VAL:CG2	7:Q:21:HIS:HB2	2.27	0.65
3:D:446:LEU:HD23	3:D:454:ILE:HD11	1.79	0.64
5:G:46:MET:HG2	8:Z:517:LEU:HD22	1.77	0.64
5:G:130:LEU:HD23	5:G:510:VAL:CG2	2.28	0.64
8:Z:273:LYS:O	8:Z:277:LEU:HG	1.97	0.64
8:Z:374:LEU:HD23	8:Z:391:ILE:HD13	1.77	0.64
1:A:487:GLY:HA3	1:A:498:ASN:HD21	1.63	0.64
3:D:179:VAL:CG1	3:D:404:ALA:HA	2.26	0.64
4:E:224:LEU:HD13	4:E:385:ILE:HG12	1.78	0.64
5:G:149:ARG:HG3	5:G:177:LEU:HD11	1.78	0.64
7:Q:226:GLU:HG3	7:Q:314:ARG:HG2	1.78	0.64
3:D:154:MET:HB3	3:D:492:LYS:HD3	1.79	0.64
8:Z:154:THR:HA	8:Z:157:ARG:HD2	1.79	0.64
8:Z:176:ILE:HD11	8:Z:395:LEU:HB3	1.79	0.64
7:Q:173:TYR:HB3	7:Q:388:ILE:HG12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:ALA:HB1	1:A:95:ILE:HA	1.80	0.64
2:B:236:LYS:NZ	2:B:288:ASN:HD21	1.96	0.64
2:B:97:ASP:CG	2:B:98:GLY:N	2.48	0.64
3:D:227:VAL:HG11	3:D:378:LYS:HE3	1.79	0.64
4:E:90:LEU:HA	4:E:93:GLU:OE1	1.97	0.64
8:Z:415:GLU:HG2	8:Z:447:ILE:HB	1.79	0.64
8:Z:31:GLN:CG	8:Z:97:LEU:HA	2.27	0.64
1:A:112:ILE:HA	1:A:433:ARG:CZ	2.27	0.64
8:Z:426:LYS:N	8:Z:427:PRO:HD2	2.13	0.64
2:B:287:ILE:HG22	2:B:343:LEU:HD21	1.79	0.64
3:D:213:ILE:HD11	3:D:412:LEU:HD11	1.78	0.64
4:E:204:VAL:HG21	4:E:413:ILE:HG21	1.80	0.64
4:E:410:ARG:HA	4:E:413:ILE:HG22	1.79	0.64
4:E:460:MET:HG2	4:E:470:PRO:HB3	1.77	0.64
6:H:128:ALA:HB1	6:H:438:TYR:CD2	2.33	0.64
1:A:117:VAL:HG12	1:A:121:TYR:CE2	2.33	0.64
5:G:240:LEU:CD1	5:G:324:ALA:HB2	2.28	0.64
6:H:119:GLN:HB2	7:Q:52:MET:HE2	1.79	0.64
8:Z:417:ALA:CB	8:Z:470:HIS:HE2	2.11	0.64
1:A:2:GLU:HB3	3:D:90:ALA:HB3	1.79	0.64
1:A:148:LEU:HD13	1:A:399:VAL:HG13	1.79	0.64
4:E:31:LEU:HD12	4:E:34:LEU:HB2	1.80	0.63
5:G:225:THR:HG21	5:G:301:GLN:HG2	1.80	0.63
5:G:33:ILE:HG21	5:G:80:MET:HG3	1.79	0.63
5:G:49:MET:O	8:Z:521:ILE:HG23	1.98	0.63
1:A:356:ILE:HG23	1:A:378:ARG:HH21	1.64	0.63
1:A:190:TYR:OH	1:A:396:LEU:HD22	1.98	0.63
1:A:85:GLU:HB3	1:A:512:LYS:CE	2.27	0.63
3:D:41:ILE:HD12	3:D:120:LEU:HB3	1.80	0.63
5:G:160:ILE:HG23	5:G:165:ILE:HG23	1.80	0.63
6:H:407:ALA:HB1	6:H:487:ASN:HD22	1.60	0.63
1:A:210:LEU:CD1	1:A:375:VAL:HG22	2.28	0.63
1:A:448:ILE:O	1:A:452:LEU:HG	1.98	0.63
4:E:481:GLN:HE21	4:E:487:PRO:CA	2.11	0.63
5:G:62:ASP:O	5:G:66:ILE:HG13	1.98	0.63
7:Q:138:LYS:HE3	7:Q:142:ILE:HD11	1.80	0.63
8:Z:476:LEU:HB3	8:Z:488:VAL:HG13	1.81	0.63
7:Q:20:LYS:HZ3	8:Z:68:GLN:HB3	1.60	0.63
1:A:238:ASP:CB	1:A:329:SER:HA	2.27	0.63
2:B:219:LEU:HB3	2:B:372:THR:HG21	1.81	0.63
4:E:223:LYS:HD3	4:E:388:ARG:NH2	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:221:ASN:HD22	5:G:316:ARG:NH2	1.96	0.63
5:G:435:TRP:HB2	5:G:436:PRO:HD3	1.80	0.63
5:G:46:MET:HA	8:Z:517:LEU:HB3	1.80	0.63
1:A:118:ILE:HG23	1:A:522:ILE:HG12	1.80	0.63
3:D:515:LEU:HG	3:D:519:VAL:CG2	2.28	0.63
3:D:417:CYS:HA	3:D:516:LEU:HD12	1.80	0.63
4:E:234:PHE:HA	4:E:322:VAL:HG22	1.79	0.63
6:H:23:VAL:HA	6:H:109:LYS:HZ1	1.64	0.63
6:H:73:HIS:CD2	6:H:74:PRO:HD2	2.34	0.63
7:Q:338:PRO:N	7:Q:339:PRO:HD2	2.13	0.63
2:B:497:PHE:CE2	2:B:501:ARG:HD3	2.33	0.63
4:E:291:GLN:HA	4:E:294:GLU:OE1	1.98	0.63
4:E:41:ALA:O	4:E:44:VAL:HG12	1.98	0.63
7:Q:17:GLU:HB2	8:Z:68:GLN:HG2	1.80	0.63
6:H:522:ASN:CB	7:Q:77:GLU:HB2	2.27	0.63
8:Z:224:ARG:NH2	8:Z:349:LEU:HD11	2.12	0.63
2:B:238:LEU:HB2	2:B:343:LEU:CD2	2.29	0.63
5:G:237:ARG:HB3	5:G:343:VAL:CG1	2.29	0.63
6:H:453:ALA:CB	6:H:479:ILE:HD11	2.29	0.63
4:E:118:GLU:HA	4:E:121:GLU:OE2	1.98	0.63
5:G:424:GLU:HA	5:G:427:LYS:NZ	2.14	0.63
6:H:226:GLU:O	6:H:227:MET:HB2	1.99	0.63
7:Q:171:LYS:HB2	7:Q:173:TYR:CE1	2.34	0.63
3:D:218:GLY:O	3:D:394:ARG:HB3	1.99	0.63
3:D:514:PRO:HG2	3:D:517:VAL:HG23	1.81	0.63
7:Q:191:PHE:N	7:Q:192:PRO:CD	2.62	0.63
7:Q:324:LEU:O	7:Q:328:VAL:HG22	1.99	0.63
7:Q:91:HIS:O	7:Q:95:GLN:HG2	1.98	0.63
8:Z:376:ILE:HD11	8:Z:391:ILE:HD12	1.81	0.63
1:A:137:ILE:HD13	1:A:499:LYS:HG3	1.80	0.62
6:H:133:VAL:HA	6:H:136:ILE:HD12	1.81	0.62
8:Z:105:GLN:HB3	8:Z:439:ALA:HB1	1.81	0.62
3:D:63:MET:HG3	3:D:71:VAL:HG13	1.80	0.62
4:E:424:ALA:HB1	4:E:487:PRO:O	1.98	0.62
4:E:145:ILE:HD11	4:E:514:LYS:HA	1.81	0.62
1:A:103:ASN:HB3	1:A:440:GLU:HB3	1.81	0.62
1:A:467:LEU:HD22	1:A:488:LEU:HG	1.80	0.62
6:H:100:LEU:HD21	6:H:445:ILE:HD11	1.80	0.62
8:Z:224:ARG:NH1	8:Z:351:TYR:HB3	2.10	0.62
1:A:68:GLU:HB2	5:G:11:SER:CA	2.29	0.62
2:B:513:VAL:HA	2:B:516:ARG:HH12	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:72:THR:HG21	3:D:83:GLN:HE21	1.64	0.62
5:G:285:LEU:O	5:G:340:GLU:HG3	1.99	0.62
5:G:130:LEU:HB2	5:G:510:VAL:HG11	1.80	0.62
8:Z:470:HIS:HA	8:Z:477:VAL:HG21	1.82	0.62
5:G:53:PRO:HD2	8:Z:525:GLY:HA2	1.81	0.62
1:A:46:VAL:HA	1:A:51:ASP:O	1.99	0.62
3:D:540:ASN:O	3:D:541:THR:HG22	1.99	0.62
4:E:360:LYS:HE2	4:E:362:ILE:HG12	1.82	0.62
1:A:206:MET:HA	1:A:206:MET:CE	2.30	0.62
1:A:138:ILE:HB	1:A:406:LYS:HE2	1.81	0.62
2:B:468:ALA:HB3	2:B:485:ILE:HD13	1.82	0.62
3:D:119:LEU:HB2	3:D:529:VAL:HG11	1.80	0.62
7:Q:20:LYS:HD3	7:Q:527:ALA:N	2.15	0.62
8:Z:233:CYS:HB3	8:Z:293:ASN:OD1	1.99	0.62
8:Z:230:ILE:HA	8:Z:290:VAL:O	2.00	0.62
1:A:225:MET:SD	1:A:306:MET:HA	2.40	0.62
5:G:10:LEU:HD22	5:G:523:VAL:HG11	1.81	0.62
5:G:245:LEU:HB2	5:G:296:ILE:HG23	1.82	0.62
7:Q:198:ASN:ND2	7:Q:200:ASP:HB2	2.13	0.62
8:Z:122:GLY:HA3	8:Z:436:GLY:HA3	1.81	0.62
2:B:232:ILE:CG2	2:B:235:ALA:HB2	2.29	0.62
3:D:82:LYS:NZ	3:D:99:LYS:HZ3	1.97	0.62
5:G:433:GLU:C	5:G:436:PRO:HD2	2.20	0.62
6:H:78:THR:O	6:H:82:ILE:HG13	2.00	0.62
7:Q:166:THR:HG21	7:Q:496:GLY:O	1.99	0.62
1:A:180:LYS:HZ2	1:A:403:LEU:HG	1.65	0.62
2:B:38:LEU:HG	2:B:50:LYS:HE2	1.81	0.62
7:Q:230:ASP:OD1	7:Q:306:ASN:HA	2.00	0.62
7:Q:390:ARG:NH1	7:Q:390:ARG:HG2	2.13	0.62
8:Z:156:LEU:HD21	8:Z:168:LEU:HD22	1.81	0.62
8:Z:447:ILE:O	8:Z:451:LEU:HG	2.00	0.62
1:A:211:ILE:HG22	1:A:213:GLY:N	2.04	0.62
3:D:416:ARG:O	3:D:419:VAL:HG22	1.99	0.62
7:Q:388:ILE:O	7:Q:392:VAL:HG23	2.00	0.62
7:Q:45:THR:O	7:Q:51:GLY:HA2	2.00	0.62
2:B:244:MET:HB2	2:B:296:ILE:HG23	1.81	0.61
3:D:256:LEU:HD11	3:D:303:ILE:CG1	2.29	0.61
3:D:244:VAL:HG11	3:D:299:ASN:CG	2.20	0.61
5:G:218:VAL:HG21	5:G:323:ILE:HG12	1.82	0.61
7:Q:337:ASN:N	7:Q:338:PRO:HD2	2.15	0.61
3:D:112:VAL:HG13	3:D:113:VAL:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:200:ARG:NE	5:G:322:ARG:HH11	1.97	0.61
8:Z:218:HIS:HB3	8:Z:221:MET:HG3	1.82	0.61
1:A:284:ASN:OD1	1:A:285:VAL:HG23	2.00	0.61
2:B:337:HIS:N	2:B:338:PRO:HD2	2.15	0.61
3:D:147:GLY:HA2	3:D:150:ILE:HD12	1.81	0.61
3:D:215:LYS:HB3	3:D:405:GLU:OE2	2.01	0.61
3:D:348:VAL:HG21	3:D:354:PHE:HD1	1.65	0.61
2:B:520:ILE:HD12	4:E:60:MET:H	1.65	0.61
8:Z:61:ASN:HB2	8:Z:92:THR:HG21	1.81	0.61
1:A:2:GLU:OE1	3:D:44:ALA:HB2	2.00	0.61
4:E:385:ILE:HG21	4:E:402:LEU:HD21	1.82	0.61
6:H:166:LYS:HD2	6:H:388:SER:OG	2.00	0.61
6:H:136:ILE:HD11	6:H:503:LEU:HD12	1.81	0.61
7:Q:40:ALA:HB1	7:Q:106:VAL:HA	1.82	0.61
5:G:74:HIS:N	8:Z:5:LYS:HB2	2.16	0.61
6:H:366:LYS:HD3	6:H:368:LYS:HZ1	1.65	0.61
7:Q:33:ILE:O	7:Q:37:LYS:HG3	2.00	0.61
1:A:216:LEU:HB3	1:A:362:ILE:HB	1.82	0.61
2:B:281:ARG:HH11	2:B:281:ARG:HG2	1.65	0.61
3:D:112:VAL:HG13	3:D:113:VAL:H	1.65	0.61
3:D:434:GLU:HG3	3:D:492:LYS:HD2	1.81	0.61
6:H:201:GLN:OE1	6:H:379:GLU:HG2	2.00	0.61
4:E:534:ARG:HH21	6:H:35:ALA:HB2	1.66	0.61
6:H:175:PHE:HB3	6:H:389:LEU:HD21	1.82	0.61
3:D:55:LEU:HD22	3:D:114:ILE:HD12	1.83	0.61
3:D:348:VAL:HG11	3:D:354:PHE:N	2.16	0.61
3:D:80:ILE:O	3:D:84:MET:HG2	2.01	0.61
4:E:94:LEU:HD21	4:E:523:MET:CB	2.24	0.61
4:E:481:GLN:HE21	4:E:487:PRO:HA	1.65	0.61
2:B:520:ILE:CD1	4:E:60:MET:H	2.14	0.61
5:G:229:MET:SD	5:G:310:THR:HA	2.41	0.61
6:H:278:LEU:HG	6:H:303:PHE:CE1	2.35	0.61
6:H:515:SER:O	7:Q:52:MET:HB3	2.00	0.61
1:A:489:ASP:OD1	1:A:491:VAL:HB	2.00	0.61
5:G:48:LYS:HD2	8:Z:520:GLU:HG3	1.82	0.61
2:B:158:ASP:HA	2:B:161:ASN:ND2	2.15	0.60
8:Z:101:GLU:OE2	8:Z:104:LYS:HD3	2.00	0.60
3:D:432:GLU:HG2	3:D:464:ILE:HB	1.83	0.60
4:E:437:ALA:HB2	4:E:448:MET:HB2	1.83	0.60
4:E:486:ASN:HB3	4:E:487:PRO:HD2	1.83	0.60
5:G:134:ILE:HD11	5:G:507:LYS:HE2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:352:GLN:HG2	6:H:357:ARG:HG2	1.83	0.60
7:Q:29:VAL:O	7:Q:33:ILE:HD13	2.01	0.60
8:Z:238:GLU:HA	8:Z:298:ASP:HB2	1.82	0.60
8:Z:426:LYS:HD2	8:Z:434:GLN:HG2	1.83	0.60
1:A:222:SER:OG	1:A:301:VAL:HG22	2.00	0.60
1:A:28:ILE:HA	1:A:31:ILE:HD12	1.83	0.60
3:D:509:GLU:O	3:D:510:LEU:HB2	2.01	0.60
5:G:165:ILE:HD12	5:G:387:VAL:HG13	1.83	0.60
4:E:20:LYS:HZ3	6:H:32:ILE:HD13	1.66	0.60
7:Q:477:ASN:HB3	7:Q:491:ASP:CG	2.22	0.60
1:A:20:GLN:NE2	5:G:7:VAL:HG23	2.16	0.60
1:A:458:GLN:HB3	1:A:463:LEU:CD1	2.31	0.60
2:B:236:LYS:HZ3	2:B:288:ASN:HD21	1.47	0.60
3:D:146:LYS:O	3:D:150:ILE:HG13	2.01	0.60
3:D:235:LYS:NZ	3:D:242:THR:HA	2.17	0.60
5:G:134:ILE:CD1	5:G:507:LYS:HE2	2.30	0.60
5:G:23:GLN:O	5:G:27:ILE:HD13	2.02	0.60
8:Z:34:LEU:HD12	8:Z:37:ASN:HD21	1.67	0.60
5:G:49:MET:O	8:Z:521:ILE:HG13	2.01	0.60
1:A:175:ALA:HB1	1:A:195:ILE:HD12	1.83	0.60
4:E:41:ALA:HA	4:E:44:VAL:HG12	1.84	0.60
4:E:85:HIS:ND1	4:E:87:ILE:HG22	2.16	0.60
4:E:88:ALA:O	4:E:92:VAL:HG23	2.02	0.60
5:G:452:ILE:HD11	5:G:457:ALA:HB3	1.84	0.60
6:H:352:GLN:CG	6:H:357:ARG:HG2	2.32	0.60
6:H:407:ALA:O	6:H:411:ALA:HB3	2.00	0.60
7:Q:147:VAL:HG21	7:Q:407:ARG:HB3	1.84	0.60
8:Z:419:ALA:O	8:Z:423:VAL:HG23	2.02	0.60
1:A:351:VAL:CG1	1:A:364:ILE:HG12	2.31	0.60
3:D:24:LYS:NZ	3:D:539:VAL:HG11	2.16	0.60
4:E:458:ILE:O	4:E:462:LEU:HG	2.01	0.60
6:H:392:ALA:O	6:H:396:VAL:HG23	2.01	0.60
7:Q:17:GLU:HB2	8:Z:68:GLN:CG	2.32	0.60
5:G:72:VAL:HG22	8:Z:6:THR:HG23	1.83	0.60
1:A:24:ALA:O	1:A:28:ILE:HG12	2.01	0.60
1:A:401:ARG:HH21	1:A:506:PRO:HG2	1.65	0.60
4:E:98:GLN:HE21	4:E:102:ILE:CD1	2.13	0.60
5:G:500:ALA:HA	5:G:503:LEU:HB3	1.83	0.60
8:Z:48:VAL:HA	8:Z:53:ASP:O	2.01	0.60
5:G:137:LEU:HB3	5:G:499:LEU:HD11	1.84	0.60
5:G:51:LEU:O	8:Z:523:ARG:HG3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:190:LEU:HD23	6:H:397:ARG:CB	2.32	0.60
8:Z:118:ILE:HG21	8:Z:432:ARG:HD2	1.83	0.60
4:E:210:LYS:HB3	4:E:383:VAL:O	2.01	0.60
5:G:156:ILE:CG2	5:G:394:ALA:HB1	2.29	0.60
8:Z:354:THR:HG22	8:Z:359:LYS:HG3	1.82	0.60
1:A:145:ARG:O	1:A:147:CYS:N	2.35	0.60
1:A:180:LYS:NZ	1:A:403:LEU:HB3	2.17	0.60
2:B:229:PRO:HG2	2:B:232:ILE:HD11	1.84	0.60
5:G:50:LEU:O	5:G:51:LEU:HD12	2.02	0.60
6:H:347:VAL:HB	6:H:362:THR:HG23	1.83	0.60
7:Q:57:ILE:HA	7:Q:62:LYS:O	2.02	0.60
8:Z:109:TYR:CE2	8:Z:435:LEU:HB3	2.36	0.60
8:Z:153:ARG:O	8:Z:157:ARG:HG3	2.02	0.60
2:B:416:LEU:HD22	2:B:474:THR:CG2	2.32	0.59
6:H:21:GLN:HE22	6:H:22:LEU:HD13	1.67	0.59
6:H:6:VAL:HG21	7:Q:21:HIS:HB2	1.84	0.59
8:Z:411:ALA:HB2	8:Z:494:ILE:HG21	1.82	0.59
1:A:450:ASN:OD1	1:A:460:SER:HB2	2.02	0.59
2:B:86:ASP:O	2:B:90:VAL:HG23	2.02	0.59
3:D:433:ILE:HG13	3:D:483:LEU:HD23	1.84	0.59
3:D:120:LEU:HD23	3:D:529:VAL:HG13	1.83	0.59
3:D:63:MET:SD	3:D:73:ILE:HD11	2.42	0.59
5:G:374:ILE:HG21	5:G:391:LEU:HD21	1.83	0.59
6:H:23:VAL:HG13	6:H:109:LYS:NZ	2.17	0.59
1:A:12:SER:O	1:A:529:ASP:HA	2.02	0.59
2:B:327:THR:HG22	2:B:365:VAL:HG12	1.82	0.59
3:D:408:ILE:O	3:D:412:LEU:HG	2.03	0.59
4:E:234:PHE:CE1	4:E:372:LEU:HD13	2.34	0.59
4:E:28:LEU:O	4:E:532:ASP:HA	2.02	0.59
5:G:137:LEU:O	5:G:140:ILE:HD13	2.02	0.59
5:G:275:ILE:HG21	5:G:299:LEU:HB2	1.85	0.59
6:H:37:ARG:HG3	6:H:99:LEU:HD22	1.84	0.59
6:H:495:PRO:HB2	6:H:498:VAL:HG23	1.83	0.59
1:A:243:LYS:HE2	1:A:271:THR:OG1	2.01	0.59
1:A:232:ALA:HB3	1:A:348:ALA:HB3	1.84	0.59
1:A:532:LYS:HG2	3:D:65:GLN:HB2	1.82	0.59
2:B:408:TYR:CE1	2:B:494:THR:HG22	2.38	0.59
2:B:49:ASP:HB3	2:B:65:ASN:OD1	2.02	0.59
3:D:256:LEU:HD11	3:D:303:ILE:HD12	1.83	0.59
5:G:398:CYS:HA	5:G:401:VAL:HG12	1.85	0.59
5:G:469:LYS:HD2	5:G:472:GLN:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:26:ASN:ND2	5:G:519:ILE:HD12	2.14	0.59
6:H:126:ARG:O	6:H:130:GLN:HG3	2.02	0.59
6:H:415:GLU:HB2	6:H:468:HIS:NE2	2.18	0.59
7:Q:402:LEU:HA	7:Q:405:ASP:O	2.02	0.59
7:Q:416:GLU:OE1	7:Q:448:ILE:HG21	2.02	0.59
2:B:399:GLN:OE1	2:B:498:GLN:HG3	2.03	0.59
4:E:308:ASP:HA	4:E:311:ASN:HD22	1.66	0.59
6:H:108:VAL:HG21	6:H:121:ILE:HG21	1.85	0.59
8:Z:108:LEU:O	8:Z:112:GLU:HG3	2.03	0.59
8:Z:181:LYS:CE	8:Z:370:ARG:HH12	2.15	0.59
2:B:519:ASN:O	2:B:520:ILE:HD13	2.03	0.59
3:D:252:ILE:HG21	3:D:351:VAL:HG22	1.84	0.59
4:E:223:LYS:HD3	4:E:388:ARG:HH21	1.67	0.59
5:G:22:VAL:HG11	5:G:520:ASP:O	2.03	0.59
7:Q:238:LYS:HE2	7:Q:346:HIS:HE1	1.67	0.59
1:A:115:THR:HG23	3:D:58:LYS:HE3	1.85	0.59
2:B:403:ASP:OD2	2:B:498:GLN:HG2	2.02	0.59
3:D:436:ALA:HA	3:D:458:ALA:HB1	1.84	0.59
7:Q:356:GLY:O	7:Q:357:ASP:HB2	2.02	0.59
2:B:338:PRO:HA	2:B:342:LYS:HG3	1.85	0.59
2:B:409:GLY:HA2	2:B:495:GLU:OE2	2.03	0.59
4:E:214:LYS:HD3	4:E:215:VAL:H	1.67	0.59
5:G:23:GLN:HE22	5:G:113:LEU:HB3	1.67	0.59
1:A:242:GLN:HA	1:A:293:ASP:HB2	1.84	0.59
2:B:223:LYS:NZ	2:B:351:GLU:HB2	2.18	0.59
2:B:445:MET:O	2:B:449:ILE:HG12	2.03	0.59
2:B:446:LEU:O	2:B:450:ILE:HG13	2.02	0.59
2:B:476:ALA:HB1	2:B:485:ILE:HD11	1.84	0.59
3:D:122:SER:HA	3:D:125:LYS:HE3	1.85	0.59
3:D:223:ASP:HB2	3:D:394:ARG:HD2	1.85	0.59
4:E:154:SER:HB3	4:E:416:ASN:ND2	2.18	0.59
4:E:322:VAL:HG21	4:E:372:LEU:HD22	1.84	0.59
5:G:226:HIS:HB3	5:G:229:MET:HG3	1.84	0.59
5:G:359:TYR:N	5:G:359:TYR:CD1	2.71	0.59
6:H:153:LYS:HG2	6:H:157:LYS:NZ	2.17	0.59
7:Q:394:ASP:O	7:Q:398:THR:HG23	2.03	0.59
8:Z:476:LEU:O	8:Z:488:VAL:HA	2.03	0.59
3:D:178:VAL:CG2	3:D:403:GLU:HG2	2.32	0.59
6:H:37:ARG:HG2	6:H:448:GLN:HG2	1.84	0.59
1:A:172:VAL:HG13	1:A:396:LEU:HD23	1.85	0.58
3:D:33:PRO:HA	3:D:536:ASP:OD1	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:343:ILE:HD11	3:D:379:ILE:HG21	1.85	0.58
4:E:221:ASP:CB	4:E:388:ARG:HD2	2.33	0.58
6:H:165:SER:HB3	6:H:480:ASN:HB3	1.85	0.58
3:D:230:LEU:HD23	3:D:339:ILE:HG12	1.85	0.58
3:D:227:VAL:O	3:D:389:VAL:HA	2.04	0.58
4:E:387:ILE:HG22	4:E:395:ILE:HG23	1.85	0.58
4:E:86:GLN:OE1	4:E:86:GLN:N	2.36	0.58
2:B:186:ALA:HA	2:B:189:ARG:NH1	2.17	0.58
6:H:460:ILE:HG23	6:H:461:LEU:N	2.18	0.58
8:Z:134:LEU:HA	8:Z:137:VAL:HG22	1.84	0.58
8:Z:333:LEU:HD21	8:Z:343:CYS:SG	2.44	0.58
1:A:5:LEU:HD11	1:A:11:ARG:HB2	1.85	0.58
2:B:418:ALA:HA	2:B:440:ALA:HB1	1.83	0.58
2:B:448:THR:HG23	2:B:458:SER:HB2	1.84	0.58
4:E:25:LYS:HZ3	4:E:536:PRO:HB3	1.68	0.58
4:E:511:ILE:N	4:E:511:ILE:HD12	2.18	0.58
6:H:17:GLN:HB3	6:H:518:GLU:CG	2.30	0.58
6:H:278:LEU:HD21	6:H:299:ALA:HA	1.86	0.58
7:Q:47:TYR:HB2	7:Q:102:ASN:HD22	1.67	0.58
7:Q:37:LYS:O	7:Q:41:GLN:HG2	2.04	0.58
2:B:39:VAL:HA	2:B:50:LYS:NZ	2.19	0.58
5:G:237:ARG:HB3	5:G:343:VAL:HG11	1.84	0.58
6:H:233:HIS:O	6:H:235:PRO:HD3	2.03	0.58
6:H:521:LYS:CG	7:Q:57:ILE:HB	2.34	0.58
7:Q:143:LEU:HD21	7:Q:419:LEU:HD11	1.86	0.58
7:Q:84:LYS:O	7:Q:88:MET:HG3	2.02	0.58
8:Z:142:GLU:C	8:Z:144:ASP:H	2.07	0.58
7:Q:523:GLN:HB3	8:Z:45:LYS:HZ1	1.68	0.58
3:D:216:LYS:HE3	3:D:376:LEU:HD11	1.85	0.58
1:A:115:THR:HG23	3:D:58:LYS:NZ	2.18	0.58
3:D:90:ALA:O	3:D:93:MET:HG3	2.04	0.58
4:E:535:LYS:HB2	6:H:50:VAL:HB	1.86	0.58
1:A:42:ASP:CG	5:G:518:ARG:HG2	2.24	0.58
6:H:408:GLY:HA2	6:H:494:GLU:OE2	2.04	0.58
6:H:497:MET:O	6:H:497:MET:HE2	2.03	0.58
7:Q:411:GLY:O	7:Q:492:MET:HG3	2.03	0.58
1:A:530:LEU:HD11	3:D:63:MET:N	2.18	0.58
2:B:155:PHE:CE2	2:B:157:GLN:HB3	2.39	0.58
3:D:206:VAL:CG2	3:D:419:VAL:HG21	2.34	0.58
6:H:186:LEU:HD12	6:H:186:LEU:N	2.19	0.58
6:H:224:GLY:HA2	6:H:310:CYS:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:322:GLU:O	8:Z:326:LEU:HG	2.03	0.58
8:Z:186:ILE:CD1	8:Z:399:LYS:HA	2.34	0.58
1:A:467:LEU:O	1:A:471:HIS:HB2	2.03	0.58
2:B:499:VAL:O	2:B:503:VAL:HG23	2.04	0.58
3:D:346:LYS:HB2	3:D:358:MET:SD	2.44	0.58
4:E:144:ALA:O	4:E:148:LEU:HD12	2.03	0.58
8:Z:118:ILE:HD12	8:Z:118:ILE:N	2.18	0.58
8:Z:308:GLU:HB2	8:Z:310:ILE:HG12	1.86	0.58
8:Z:417:ALA:HB2	8:Z:470:HIS:NE2	2.18	0.58
8:Z:406:CYS:CB	8:Z:498:TYR:HB2	2.34	0.58
8:Z:59:ASP:O	8:Z:63:LEU:HG	2.04	0.58
1:A:416:GLU:H	1:A:416:GLU:CD	2.06	0.58
3:D:32:LYS:HB3	3:D:33:PRO:HD2	1.86	0.58
3:D:364:LEU:HD21	3:D:366:GLU:OE1	2.04	0.58
3:D:474:LEU:O	3:D:476:PRO:HD3	2.03	0.58
4:E:122:GLN:O	4:E:126:ARG:HG3	2.03	0.58
4:E:25:LYS:HA	4:E:535:LYS:O	2.04	0.58
1:A:190:TYR:CD2	1:A:400:LYS:HB2	2.35	0.58
3:D:486:ARG:O	3:D:494:THR:HG21	2.04	0.58
4:E:166:ILE:O	4:E:170:LYS:HG3	2.04	0.58
4:E:438:ASP:HA	4:E:445:GLN:HE21	1.68	0.58
5:G:240:LEU:HB2	5:G:331:ILE:HA	1.84	0.58
5:G:275:ILE:HG23	5:G:300:ALA:HB2	1.86	0.58
7:Q:238:LYS:HZ3	7:Q:341:LEU:HD11	1.69	0.58
7:Q:460:ALA:HA	7:Q:463:VAL:HG12	1.86	0.58
1:A:445:LEU:H	1:A:446:PRO:HD2	1.67	0.57
3:D:81:LEU:HB3	3:D:95:VAL:HG22	1.84	0.57
4:E:40:ALA:HB3	4:E:87:ILE:HG21	1.84	0.57
2:B:520:ILE:HG23	4:E:60:MET:O	2.04	0.57
1:A:42:ASP:OD2	5:G:518:ARG:HG2	2.03	0.57
6:H:109:LYS:N	6:H:110:PRO:HD2	2.19	0.57
6:H:455:PHE:HB2	6:H:482:GLU:OE2	2.04	0.57
8:Z:186:ILE:HD12	8:Z:399:LYS:HA	1.86	0.57
8:Z:204:THR:HG22	8:Z:377:LYS:H	1.68	0.57
5:G:46:MET:HE2	8:Z:517:LEU:HD23	1.86	0.57
1:A:277:LYS:HZ2	1:A:280:ALA:HB3	1.69	0.57
1:A:46:VAL:HG22	1:A:52:VAL:HG22	1.85	0.57
1:A:533:LEU:HD23	1:A:533:LEU:N	2.19	0.57
8:Z:179:ILE:HD12	8:Z:187:ASP:O	2.04	0.57
1:A:45:LEU:HD11	1:A:61:ILE:HA	1.86	0.57
2:B:235:ALA:HB3	2:B:349:ILE:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:473:THR:O	4:E:477:VAL:HG23	2.05	0.57
2:B:516:ARG:O	4:E:57:LEU:HB3	2.04	0.57
5:G:242:ASP:OD2	5:G:331:ILE:HG22	2.03	0.57
5:G:38:ARG:HA	5:G:100:ILE:HD11	1.86	0.57
6:H:73:HIS:HD2	6:H:74:PRO:HD2	1.69	0.57
6:H:37:ARG:HB2	6:H:99:LEU:HD13	1.87	0.57
7:Q:186:ALA:O	7:Q:190:ILE:HG13	2.03	0.57
7:Q:53:ASN:O	7:Q:54:LYS:HD3	2.04	0.57
8:Z:101:GLU:HG2	8:Z:446:ILE:HB	1.86	0.57
8:Z:299:PRO:HA	8:Z:302:LEU:HD12	1.86	0.57
2:B:516:ARG:HD2	4:E:58:ASP:OD2	2.04	0.57
3:D:45:LYS:HD2	3:D:121:ASP:HB2	1.87	0.57
1:A:526:ARG:O	3:D:60:MET:HB3	2.04	0.57
5:G:425:LYS:O	5:G:429:MET:HG2	2.03	0.57
5:G:479:GLY:C	5:G:487:LEU:HD12	2.24	0.57
6:H:510:ALA:O	6:H:514:VAL:HG23	2.03	0.57
7:Q:150:SER:HB2	7:Q:159:GLU:OE1	2.05	0.57
1:A:176:VAL:HG13	1:A:190:TYR:CD1	2.39	0.57
1:A:532:LYS:NZ	3:D:65:GLN:HB2	2.19	0.57
3:D:256:LEU:HD13	3:D:312:LEU:CD1	2.33	0.57
4:E:218:ARG:CA	4:E:389:GLY:HA2	2.33	0.57
4:E:242:GLN:O	4:E:242:GLN:HG2	2.03	0.57
4:E:85:HIS:CG	4:E:87:ILE:HG22	2.39	0.57
6:H:226:GLU:HB3	6:H:227:MET:CE	2.34	0.57
6:H:522:ASN:HD21	7:Q:76:LEU:HA	1.69	0.57
8:Z:407:VAL:O	8:Z:407:VAL:HG13	2.05	0.57
8:Z:446:ILE:O	8:Z:450:VAL:HG23	2.05	0.57
2:B:113:ALA:O	2:B:117:ILE:HG13	2.05	0.57
3:D:256:LEU:H	3:D:256:LEU:HD12	1.68	0.57
4:E:20:LYS:HZ2	6:H:31:VAL:CB	2.17	0.57
4:E:443:LEU:HD23	4:E:444:GLU:N	2.20	0.57
5:G:108:VAL:O	5:G:111:HIS:HB3	2.04	0.57
5:G:195:ILE:HG22	5:G:197:LYS:H	1.69	0.57
7:Q:332:ALA:O	7:Q:334:PRO:HD3	2.04	0.57
7:Q:420:ALA:HA	7:Q:442:ALA:HB1	1.87	0.57
1:A:140:THR:HB	1:A:144:GLY:CA	2.25	0.57
1:A:220:VAL:HG22	1:A:306:MET:SD	2.44	0.57
2:B:172:LEU:HD21	2:B:386:ALA:HA	1.87	0.57
5:G:47:MET:HB3	5:G:61:ASN:ND2	2.20	0.57
4:E:20:LYS:NZ	6:H:32:ILE:HG12	2.20	0.57
7:Q:173:TYR:HD1	7:Q:173:TYR:H	1.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:225:ILE:HG23	4:E:375:GLU:HB3	1.87	0.57
4:E:457:VAL:HG23	4:E:458:ILE:N	2.20	0.57
5:G:240:LEU:HD23	5:G:240:LEU:N	2.18	0.57
6:H:450:CYS:HA	6:H:479:ILE:HD13	1.86	0.57
5:G:50:LEU:HA	8:Z:521:ILE:O	2.03	0.57
1:A:137:ILE:HG23	1:A:499:LYS:HE3	1.87	0.57
1:A:530:LEU:CD2	3:D:63:MET:H	2.17	0.57
2:B:123:PRO:HB3	2:B:515:LEU:HG	1.85	0.57
2:B:349:ILE:HA	2:B:361:HIS:O	2.05	0.57
3:D:217:LEU:HA	3:D:401:ILE:CD1	2.34	0.57
3:D:54:SER:HA	3:D:60:MET:H	1.69	0.57
6:H:320:LYS:O	6:H:323:MET:HB3	2.05	0.57
6:H:407:ALA:HB1	6:H:487:ASN:ND2	2.20	0.57
8:Z:87:ILE:N	8:Z:87:ILE:HD12	2.20	0.57
2:B:297:TYR:HB3	2:B:300:PRO:HD2	1.87	0.57
3:D:33:PRO:HD3	3:D:537:ASP:OD1	2.03	0.57
3:D:371:ASN:HD22	3:D:394:ARG:HE	1.52	0.57
7:Q:405:ASP:HB2	7:Q:502:LEU:HD22	1.87	0.57
8:Z:229:TYR:HB3	8:Z:344:LEU:HB3	1.87	0.57
8:Z:354:THR:CG2	8:Z:359:LYS:HG3	2.35	0.57
2:B:220:LEU:HD13	2:B:319:GLY:HA3	1.87	0.56
3:D:245:GLU:HG3	3:D:246:LYS:CD	2.31	0.56
4:E:186:ALA:O	4:E:190:VAL:HG23	2.05	0.56
5:G:91:VAL:HG11	5:G:501:VAL:HA	1.86	0.56
6:H:225:PHE:HB3	6:H:228:GLN:HG3	1.85	0.56
7:Q:377:LEU:O	7:Q:378:ARG:HD2	2.04	0.56
8:Z:378:GLY:HA3	8:Z:384:LEU:HD21	1.85	0.56
2:B:100:THR:O	2:B:104:VAL:HG23	2.05	0.56
4:E:156:LEU:CB	4:E:161:ASN:HB3	2.34	0.56
5:G:401:VAL:HG13	5:G:402:LEU:HD13	1.87	0.56
7:Q:20:LYS:HD3	7:Q:528:LYS:H	1.70	0.56
7:Q:55:MET:CG	7:Q:63:LEU:HD11	2.35	0.56
2:B:518:ASP:O	2:B:519:ASN:HB2	2.06	0.56
3:D:317:LEU:HG	3:D:321:ASN:HD21	1.71	0.56
3:D:539:VAL:HG12	3:D:541:THR:H	1.70	0.56
4:E:250:ILE:HG21	4:E:341:ILE:HG12	1.87	0.56
5:G:165:ILE:HG21	5:G:390:ASN:CB	2.35	0.56
5:G:433:GLU:CD	5:G:433:GLU:H	2.08	0.56
5:G:479:GLY:O	5:G:487:LEU:HD12	2.05	0.56
6:H:239:LEU:O	6:H:240:LEU:HD23	2.05	0.56
6:H:521:LYS:HG2	7:Q:57:ILE:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:46:MET:HG3	8:Z:54:ILE:HG23	1.86	0.56
1:A:313:LYS:HE2	1:A:317:LYS:CE	2.35	0.56
3:D:487:HIS:CE1	3:D:492:LYS:HA	2.40	0.56
7:Q:205:CYS:HG	7:Q:376:VAL:HA	1.70	0.56
8:Z:139:VAL:HB	8:Z:407:VAL:O	2.04	0.56
1:A:24:ALA:HA	5:G:9:VAL:HG22	1.88	0.56
2:B:111:ARG:NH1	2:B:111:ARG:HG2	2.19	0.56
2:B:411:GLY:HA3	2:B:447:PRO:HB3	1.87	0.56
4:E:208:LEU:O	4:E:383:VAL:HG22	2.04	0.56
4:E:472:GLN:O	4:E:475:THR:HB	2.06	0.56
5:G:491:LYS:HA	5:G:496:TRP:NE1	2.18	0.56
2:B:11:ILE:O	4:E:84:ASP:N	2.33	0.56
3:D:175:ASN:HA	3:D:180:SER:CB	2.36	0.56
3:D:236:VAL:HG11	3:D:329:LYS:HD3	1.86	0.56
3:D:292:GLN:HA	3:D:295:LYS:HE2	1.87	0.56
3:D:29:ASP:HB2	3:D:540:ASN:CG	2.25	0.56
3:D:424:LEU:HD12	3:D:424:LEU:O	2.05	0.56
4:E:156:LEU:HG	4:E:156:LEU:O	2.06	0.56
5:G:74:HIS:HB2	8:Z:5:LYS:CB	2.31	0.56
7:Q:392:VAL:O	7:Q:396:VAL:HG23	2.05	0.56
7:Q:523:GLN:HB3	8:Z:45:LYS:CE	2.36	0.56
1:A:410:PRO:O	1:A:414:ALA:HB3	2.05	0.56
2:B:53:LEU:HB3	3:D:542:ARG:NH1	2.21	0.56
4:E:156:LEU:HB3	4:E:161:ASN:CB	2.32	0.56
4:E:117:LEU:CD2	4:E:524:VAL:HG13	2.36	0.56
4:E:117:LEU:HD21	4:E:524:VAL:HG13	1.88	0.56
6:H:142:THR:HG22	6:H:404:SER:OG	2.05	0.56
8:Z:31:GLN:HG2	8:Z:97:LEU:HA	1.87	0.56
8:Z:407:VAL:CG2	8:Z:495:TRP:HB3	2.36	0.56
3:D:24:LYS:CD	3:D:28:GLN:HE22	2.17	0.56
3:D:249:ILE:HG13	3:D:343:ILE:HD13	1.87	0.56
4:E:98:GLN:HE22	4:E:515:GLN:HG2	1.71	0.56
5:G:137:LEU:HD11	5:G:506:TYR:CD2	2.40	0.56
5:G:20:ARG:O	5:G:20:ARG:HG2	2.05	0.56
5:G:289:VAL:HG11	5:G:350:LEU:HD13	1.88	0.56
8:Z:127:LYS:NZ	8:Z:509:THR:HB	2.21	0.56
1:A:107:LEU:O	1:A:112:ILE:HB	2.05	0.56
3:D:416:ARG:HH11	3:D:420:LYS:HZ1	1.53	0.56
3:D:151:LEU:HD21	3:D:435:LEU:HD11	1.87	0.56
4:E:247:LYS:HE3	4:E:298:ASN:ND2	2.20	0.56
5:G:347:ALA:HB3	5:G:365:GLU:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:52:ASP:HB3	8:Z:525:GLY:O	2.06	0.56
6:H:215:ALA:HB3	6:H:373:ILE:CD1	2.32	0.56
8:Z:476:LEU:HD22	8:Z:490:ALA:CB	2.36	0.56
1:A:456:ALA:HB3	1:A:490:LEU:HD22	1.88	0.56
2:B:29:PHE:HB3	2:B:110:LEU:HB3	1.88	0.56
2:B:52:LEU:HD11	2:B:70:ILE:HA	1.88	0.56
6:H:281:ILE:HG21	6:H:289:VAL:HG21	1.88	0.56
7:Q:410:PRO:HB2	7:Q:492:MET:HB2	1.87	0.56
4:E:18:ILE:HG22	4:E:19:ILE:H	1.70	0.56
4:E:34:LEU:H	4:E:34:LEU:HD22	1.71	0.56
8:Z:333:LEU:HB2	8:Z:339:LEU:HD23	1.88	0.56
8:Z:501:LYS:O	8:Z:504:LEU:HB3	2.06	0.56
2:B:221:ASP:CG	2:B:359:LEU:HG	2.26	0.55
4:E:204:VAL:CB	4:E:410:ARG:HG3	2.32	0.55
5:G:358:GLU:HB3	5:G:360:PHE:CE1	2.41	0.55
5:G:89:GLU:HA	5:G:389:ARG:HH22	1.69	0.55
5:G:445:GLU:O	5:G:449:ARG:HG3	2.05	0.55
5:G:72:VAL:HG12	5:G:73:GLN:N	2.21	0.55
6:H:150:GLU:OE2	6:H:400:ILE:HG23	2.06	0.55
8:Z:109:TYR:HB3	8:Z:114:LEU:HD13	1.86	0.55
1:A:133:SER:HA	1:A:136:LEU:HD21	1.88	0.55
2:B:116:LEU:HA	2:B:119:LYS:HD2	1.88	0.55
3:D:37:ARG:HG3	3:D:536:ASP:OD1	2.06	0.55
4:E:451:PHE:O	4:E:455:LEU:HG	2.07	0.55
5:G:105:MET:CE	5:G:510:VAL:HA	2.36	0.55
5:G:49:MET:HB2	5:G:59:MET:CE	2.36	0.55
6:H:161:THR:HG21	6:H:491:PHE:CB	2.37	0.55
1:A:352:VAL:HG22	1:A:353:GLN:N	2.20	0.55
2:B:229:PRO:CG	2:B:232:ILE:HD11	2.35	0.55
5:G:37:ILE:HD11	5:G:99:ILE:HG21	1.87	0.55
6:H:198:LYS:HZ3	6:H:217:LYS:CE	2.19	0.55
6:H:350:GLU:HA	6:H:358:TYR:O	2.06	0.55
7:Q:143:LEU:N	7:Q:144:PRO:HD2	2.22	0.55
7:Q:17:GLU:HG2	8:Z:70:GLN:NE2	2.20	0.55
8:Z:83:ALA:O	8:Z:87:ILE:HD13	2.05	0.55
3:D:226:LEU:CD1	3:D:389:VAL:HB	2.36	0.55
5:G:168:TRP:CD1	5:G:209:ILE:HB	2.42	0.55
5:G:330:ARG:HD2	5:G:342:ASP:OD1	2.06	0.55
6:H:448:GLN:HG3	6:H:452:ASN:ND2	2.21	0.55
7:Q:117:GLU:O	7:Q:121:LEU:HG	2.07	0.55
8:Z:127:LYS:HD2	8:Z:509:THR:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:135:GLU:HG3	8:Z:138:LYS:NZ	2.21	0.55
8:Z:139:VAL:HB	8:Z:407:VAL:HG13	1.87	0.55
8:Z:150:ASP:O	8:Z:154:THR:HG23	2.06	0.55
1:A:74:VAL:O	1:A:78:LEU:HG	2.06	0.55
3:D:137:SER:OG	3:D:533:LEU:HB2	2.06	0.55
6:H:349:GLU:HG3	6:H:360:PHE:HD2	1.70	0.55
7:Q:206:LYS:HD3	7:Q:389:GLU:OE1	2.07	0.55
7:Q:69:ALA:HB3	7:Q:101:THR:HG22	1.89	0.55
8:Z:376:ILE:HG22	8:Z:384:LEU:HD22	1.89	0.55
1:A:17:ILE:O	1:A:20:GLN:HG2	2.07	0.55
1:A:521:ALA:HA	1:A:524:ILE:HD12	1.89	0.55
2:B:390:LEU:O	2:B:394:LEU:HG	2.06	0.55
2:B:513:VAL:HG13	2:B:516:ARG:NH1	2.20	0.55
4:E:229:ILE:HB	4:E:384:THR:HG21	1.89	0.55
5:G:417:ALA:HB2	5:G:476:GLU:HG3	1.88	0.55
6:H:79:LEU:HA	6:H:82:ILE:HD12	1.89	0.55
7:Q:188:VAL:HG13	7:Q:197:PHE:CE1	2.41	0.55
7:Q:58:ASN:ND2	7:Q:62:LYS:HB2	2.19	0.55
8:Z:459:LEU:HD23	8:Z:460:GLN:N	2.22	0.55
5:G:48:LYS:HA	8:Z:518:VAL:HG13	1.89	0.55
8:Z:98:ILE:HD11	8:Z:447:ILE:HD11	1.88	0.55
1:A:17:ILE:HG13	1:A:21:ASN:HD21	1.71	0.55
1:A:226:PRO:CG	1:A:229:ILE:HD11	2.37	0.55
2:B:292:ASN:HD22	2:B:293:ARG:N	2.05	0.55
4:E:145:ILE:CD1	4:E:514:LYS:HA	2.36	0.55
4:E:444:GLU:O	4:E:448:MET:HG3	2.07	0.55
4:E:83:VAL:HG13	4:E:88:ALA:HB3	1.88	0.55
5:G:118:HIS:CD2	5:G:119:PRO:HD2	2.42	0.55
5:G:224:VAL:HG21	5:G:352:ILE:HG21	1.88	0.55
6:H:341:VAL:O	6:H:341:VAL:HG12	2.07	0.55
8:Z:273:LYS:HD3	8:Z:337:ASP:OD1	2.07	0.55
7:Q:13:GLN:OE1	8:Z:72:PRO:HD2	2.06	0.55
1:A:529:ASP:O	3:D:62:LYS:HD2	2.07	0.55
3:D:178:VAL:HG12	3:D:178:VAL:O	2.07	0.55
3:D:207:ASP:O	3:D:210:ASP:HB2	2.07	0.55
1:A:43:LYS:HE3	5:G:520:ASP:OD2	2.07	0.55
5:G:72:VAL:CG2	5:G:81:ILE:HD11	2.37	0.55
7:Q:242:TYR:OH	7:Q:283:ILE:HG12	2.07	0.55
7:Q:312:LEU:HD23	7:Q:313:VAL:N	2.22	0.55
7:Q:475:ASN:O	7:Q:477:ASN:N	2.40	0.55
1:A:323:SER:HB2	1:A:347:GLN:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:322:ARG:O	2:B:326:VAL:HG23	2.06	0.55
3:D:294:LYS:HD3	3:D:325:ILE:HD11	1.87	0.55
8:Z:355:LEU:HD22	8:Z:377:LYS:HE3	1.87	0.55
1:A:456:ALA:CB	1:A:490:LEU:HD22	2.38	0.55
1:A:96:ILE:O	1:A:100:LEU:HG	2.07	0.55
2:B:497:PHE:CZ	2:B:501:ARG:HD3	2.41	0.55
3:D:124:THR:HA	3:D:127:LEU:HD12	1.89	0.55
4:E:387:ILE:CG2	4:E:395:ILE:HG23	2.37	0.55
5:G:200:ARG:NE	5:G:322:ARG:NH1	2.55	0.55
5:G:359:TYR:N	5:G:359:TYR:HD1	2.02	0.55
1:A:80:ASP:O	1:A:84:LYS:HD3	2.06	0.54
3:D:197:VAL:HG12	3:D:387:LYS:CA	2.33	0.54
3:D:211:ILE:HG23	3:D:389:VAL:CG2	2.28	0.54
3:D:21:GLY:O	3:D:22:ARG:HG2	2.08	0.54
3:D:239:SER:HB2	3:D:321:ASN:CB	2.32	0.54
4:E:130:PRO:HB3	4:E:528:LEU:HD22	1.88	0.54
4:E:215:VAL:HB	4:E:392:LYS:NZ	2.22	0.54
5:G:203:LYS:HB2	5:G:384:LEU:HD11	1.89	0.54
6:H:163:LEU:HD22	6:H:168:ILE:HG21	1.90	0.54
7:Q:118:LEU:HD21	7:Q:440:LYS:HG3	1.89	0.54
7:Q:164:LEU:O	7:Q:168:VAL:HG13	2.07	0.54
7:Q:114:LEU:HD11	7:Q:443:GLU:OE2	2.07	0.54
7:Q:15:LEU:HA	8:Z:71:HIS:ND1	2.22	0.54
1:A:201:HIS:HA	1:A:379:GLY:O	2.08	0.54
2:B:474:THR:O	2:B:474:THR:HG22	2.07	0.54
3:D:251:LEU:HD23	3:D:345:THR:OG1	2.07	0.54
4:E:170:LYS:HZ2	4:E:183:ARG:HA	1.70	0.54
4:E:290:ARG:O	4:E:294:GLU:HG3	2.07	0.54
5:G:136:THR:O	5:G:140:ILE:HG23	2.06	0.54
6:H:156:GLU:HA	6:H:180:VAL:HG21	1.89	0.54
6:H:190:LEU:HD11	6:H:195:ILE:CD1	2.31	0.54
6:H:487:ASN:HA	6:H:490:ALA:HB3	1.89	0.54
7:Q:390:ARG:HA	7:Q:390:ARG:CZ	2.37	0.54
1:A:132:ILE:O	1:A:136:LEU:HG	2.07	0.54
2:B:172:LEU:O	2:B:176:LYS:N	2.40	0.54
2:B:167:LEU:HD13	2:B:179:PHE:HB2	1.90	0.54
2:B:204:LYS:O	2:B:376:ARG:HA	2.07	0.54
3:D:230:LEU:HD13	3:D:338:PHE:HB3	1.89	0.54
3:D:170:ALA:HB2	3:D:415:ILE:HD11	1.89	0.54
4:E:254:PRO:HB3	4:E:304:TRP:HB3	1.89	0.54
5:G:407:LEU:O	5:G:407:LEU:HD12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:160:VAL:O	7:Q:164:LEU:HG	2.07	0.54
7:Q:191:PHE:H	7:Q:192:PRO:CD	2.20	0.54
7:Q:203:ARG:HH11	7:Q:221:MET:HG2	1.73	0.54
7:Q:338:PRO:N	7:Q:339:PRO:CD	2.70	0.54
8:Z:350:VAL:HA	8:Z:362:PHE:O	2.07	0.54
8:Z:37:ASN:HA	8:Z:43:THR:H	1.73	0.54
8:Z:422:LEU:HB3	8:Z:437:VAL:HG12	1.90	0.54
1:A:105:ASP:HA	1:A:108:VAL:HB	1.90	0.54
2:B:131:ARG:O	2:B:135:LYS:HG3	2.06	0.54
2:B:192:GLY:O	2:B:193:SER:HB2	2.07	0.54
2:B:236:LYS:HD2	2:B:286:GLY:O	2.07	0.54
3:D:443:SER:HB3	3:D:451:SER:HA	1.89	0.54
6:H:226:GLU:O	6:H:227:MET:CB	2.55	0.54
7:Q:378:ARG:HH11	7:Q:378:ARG:HG3	1.71	0.54
2:B:203:LYS:HG3	2:B:203:LYS:O	2.07	0.54
2:B:420:ALA:O	2:B:424:LEU:HG	2.08	0.54
2:B:408:TYR:CE2	2:B:489:SER:HB3	2.43	0.54
6:H:488:PHE:HA	6:H:493:TRP:CZ2	2.43	0.54
7:Q:129:ILE:HG22	7:Q:133:GLU:HG3	1.89	0.54
7:Q:477:ASN:HB3	7:Q:491:ASP:OD1	2.07	0.54
1:A:105:ASP:O	1:A:109:LYS:HG3	2.08	0.54
4:E:524:VAL:HA	4:E:527:ILE:CD1	2.38	0.54
2:B:9:VAL:HA	4:E:85:HIS:NE2	2.22	0.54
5:G:209:ILE:HG22	5:G:209:ILE:O	2.07	0.54
6:H:521:LYS:HG2	7:Q:57:ILE:HB	1.89	0.54
1:A:275:ILE:HD11	1:A:296:CYS:HB3	1.90	0.54
2:B:219:LEU:HD21	2:B:359:LEU:HD23	1.90	0.54
4:E:392:LYS:O	4:E:396:GLU:HG3	2.07	0.54
5:G:350:LEU:HG	5:G:363:ILE:HG12	1.90	0.54
5:G:424:GLU:O	5:G:427:LYS:HG2	2.07	0.54
6:H:227:MET:HA	6:H:230:LYS:HZ2	1.68	0.54
7:Q:80:HIS:HB3	7:Q:83:ALA:CB	2.38	0.54
8:Z:445:LEU:O	8:Z:449:LYS:HG3	2.08	0.54
1:A:59:ALA:O	1:A:63:LYS:HG3	2.08	0.54
2:B:141:LEU:HD21	2:B:413:SER:OG	2.08	0.54
3:D:467:THR:O	3:D:470:GLU:HB3	2.07	0.54
3:D:72:THR:HG21	3:D:83:GLN:NE2	2.23	0.54
4:E:236:HIS:CG	4:E:237:PRO:HD2	2.43	0.54
5:G:144:VAL:HG21	5:G:407:LEU:CD2	2.37	0.54
5:G:18:SER:H	5:G:21:LYS:HB2	1.73	0.54
5:G:85:ARG:HA	5:G:85:ARG:NE	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:206:LYS:HB3	7:Q:385:MET:CG	2.36	0.54
7:Q:225:LYS:HD2	7:Q:352:LEU:HD13	1.89	0.54
7:Q:55:MET:HG2	7:Q:65:VAL:HG22	1.90	0.54
8:Z:414:VAL:O	8:Z:418:MET:HG3	2.08	0.54
3:D:29:ASP:HB2	3:D:540:ASN:HB2	1.89	0.54
4:E:121:GLU:HA	4:E:124:LEU:HD12	1.90	0.54
4:E:25:LYS:HE2	4:E:536:PRO:HB3	1.89	0.54
5:G:286:LYS:HD2	5:G:340:GLU:OE2	2.08	0.54
5:G:52:ASP:HB3	8:Z:525:GLY:C	2.28	0.54
6:H:406:VAL:HB	6:H:412:ILE:CD1	2.38	0.54
6:H:9:LEU:HD22	6:H:13:THR:HG21	1.90	0.54
7:Q:104:VAL:HG13	7:Q:105:LEU:N	2.23	0.54
7:Q:146:LEU:HD12	7:Q:147:VAL:N	2.23	0.54
7:Q:327:THR:HG22	7:Q:366:GLU:CD	2.28	0.54
7:Q:523:GLN:HG2	8:Z:33:VAL:HG13	1.90	0.54
8:Z:109:TYR:HB3	8:Z:114:LEU:CD1	2.38	0.54
8:Z:133:PHE:HA	8:Z:136:GLN:OE1	2.07	0.54
2:B:202:ILE:HG12	2:B:372:THR:CG2	2.38	0.53
2:B:43:LEU:HD23	2:B:449:ILE:HB	1.89	0.53
2:B:52:LEU:C	2:B:53:LEU:HD12	2.28	0.53
2:B:97:ASP:C	2:B:99:THR:H	2.10	0.53
4:E:44:VAL:HG11	4:E:91:MET:HG3	1.90	0.53
4:E:149:ASP:OD2	4:E:510:LEU:HD21	2.07	0.53
5:G:112:PHE:CE2	5:G:436:PRO:HA	2.42	0.53
5:G:156:ILE:HG12	5:G:398:CYS:HB2	1.91	0.53
5:G:70:ILE:HG21	8:Z:6:THR:HG22	1.90	0.53
6:H:274:LEU:HD22	6:H:299:ALA:HB2	1.89	0.53
6:H:294:PRO:HG3	6:H:313:ARG:HD3	1.88	0.53
7:Q:191:PHE:HE2	7:Q:373:SER:HG	1.56	0.53
7:Q:436:TYR:O	7:Q:440:LYS:HG2	2.08	0.53
1:A:150:ASN:O	1:A:154:THR:HG23	2.09	0.53
1:A:383:PHE:HA	1:A:386:ASP:OD2	2.07	0.53
1:A:86:VAL:HG11	1:A:509:VAL:HA	1.91	0.53
2:B:508:ALA:O	2:B:512:GLU:HG3	2.08	0.53
3:D:312:LEU:HB3	3:D:329:LYS:HD2	1.90	0.53
8:Z:222:LYS:HB2	8:Z:311:ILE:CD1	2.38	0.53
3:D:36:ILE:CG2	3:D:536:ASP:HA	2.38	0.53
1:A:526:ARG:HG3	3:D:60:MET:HA	1.91	0.53
4:E:289:ILE:HD11	4:E:310:ALA:HB1	1.91	0.53
4:E:318:ASP:C	4:E:319:LEU:HD12	2.29	0.53
4:E:119:GLU:HG3	4:E:454:ALA:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:83:ILE:HG23	5:G:508:THR:CG2	2.39	0.53
7:Q:238:LYS:HB3	7:Q:344:MET:HB3	1.90	0.53
8:Z:294:GLN:HE22	8:Z:318:ARG:HD3	1.71	0.53
1:A:112:ILE:HA	1:A:433:ARG:NH2	2.23	0.53
1:A:60:THR:O	1:A:64:LEU:HG	2.08	0.53
2:B:70:ILE:O	2:B:74:ILE:HG13	2.08	0.53
3:D:224:CYS:SG	3:D:393:VAL:HA	2.49	0.53
5:G:164:VAL:HB	5:G:386:GLU:HG2	1.90	0.53
5:G:225:THR:HB	5:G:311:ALA:O	2.07	0.53
7:Q:222:VAL:CG1	7:Q:360:VAL:HB	2.39	0.53
5:G:50:LEU:HD23	8:Z:521:ILE:O	2.07	0.53
3:D:256:LEU:HD13	3:D:312:LEU:HD13	1.90	0.53
4:E:256:GLU:HB2	4:E:257:PRO:HD2	1.89	0.53
4:E:42:LYS:HG2	4:E:46:ASN:HD21	1.72	0.53
5:G:12:GLN:O	5:G:13:ASN:HB2	2.09	0.53
5:G:217:GLY:HA3	5:G:364:THR:HA	1.91	0.53
5:G:49:MET:HG2	5:G:49:MET:O	2.09	0.53
6:H:111:TYR:HB3	6:H:116:LEU:HD22	1.90	0.53
6:H:238:ALA:N	6:H:288:VAL:O	2.41	0.53
8:Z:179:ILE:HD13	8:Z:191:VAL:CG2	2.38	0.53
8:Z:350:VAL:HG13	8:Z:363:ILE:HG12	1.90	0.53
8:Z:450:VAL:HG12	8:Z:454:ASN:ND2	2.24	0.53
1:A:45:LEU:HD13	1:A:64:LEU:HB2	1.90	0.53
2:B:399:GLN:O	2:B:403:ASP:HB3	2.08	0.53
2:B:432:GLU:O	2:B:436:MET:HG3	2.07	0.53
2:B:43:LEU:HD12	2:B:44:GLY:N	2.22	0.53
3:D:433:ILE:HG13	3:D:483:LEU:CD2	2.39	0.53
3:D:515:LEU:O	3:D:519:VAL:HG23	2.09	0.53
6:H:9:LEU:HD13	6:H:13:THR:CG2	2.38	0.53
6:H:153:LYS:O	6:H:157:LYS:HG3	2.08	0.53
7:Q:225:LYS:HZ2	7:Q:352:LEU:HB2	1.70	0.53
7:Q:204:VAL:HG13	7:Q:377:LEU:HG	1.89	0.53
1:A:17:ILE:HG23	1:A:18:ARG:N	2.21	0.53
1:A:211:ILE:HG12	1:A:376:ILE:CG1	2.38	0.53
1:A:239:PHE:HD2	1:A:330:THR:HA	1.74	0.53
1:A:137:ILE:CD1	1:A:410:PRO:HD3	2.35	0.53
1:A:59:ALA:HB1	1:A:63:LYS:HE3	1.91	0.53
2:B:224:ILE:O	2:B:224:ILE:HG13	2.09	0.53
2:B:72:LYS:HZ1	2:B:89:ARG:HG3	1.74	0.53
5:G:247:TYR:HB2	5:G:275:ILE:HD11	1.91	0.53
5:G:396:GLN:NE2	5:G:399:ARG:HB3	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:23:VAL:CG1	6:H:109:LYS:HZ1	2.18	0.53
6:H:225:PHE:CB	6:H:228:GLN:HG3	2.39	0.53
6:H:394:MET:O	6:H:397:ARG:HB3	2.08	0.53
6:H:418:LYS:HZ2	6:H:469:ALA:HA	1.74	0.53
7:Q:347:CYS:SG	7:Q:363:PHE:HB3	2.48	0.53
8:Z:44:MET:HB3	8:Z:58:LYS:HG2	1.91	0.53
1:A:115:THR:HG23	3:D:58:LYS:CE	2.39	0.53
1:A:351:VAL:CG2	1:A:364:ILE:HG23	2.37	0.53
5:G:282:ILE:HG22	5:G:287:PRO:HG3	1.90	0.53
6:H:48:LEU:CG	6:H:58:ILE:HG12	2.37	0.53
8:Z:175:SER:O	8:Z:179:ILE:HG12	2.09	0.53
3:D:420:LYS:HB2	3:D:516:LEU:HD12	1.90	0.53
3:D:82:LYS:CE	3:D:99:LYS:HZ3	2.22	0.53
7:Q:226:GLU:HG3	7:Q:314:ARG:CG	2.39	0.53
2:B:190:LEU:HD12	2:B:190:LEU:N	2.24	0.53
3:D:24:LYS:HZ2	3:D:539:VAL:HG11	1.73	0.53
4:E:405:ALA:O	4:E:409:ILE:HG13	2.08	0.53
4:E:94:LEU:HD11	4:E:523:MET:CB	2.39	0.53
5:G:107:SER:HA	5:G:110:GLU:OE2	2.08	0.53
5:G:442:GLN:HA	5:G:445:GLU:OE2	2.09	0.53
5:G:71:GLN:HB3	8:Z:8:ASN:HB2	1.91	0.53
6:H:520:ILE:O	7:Q:56:VAL:HA	2.09	0.53
7:Q:113:GLU:HA	7:Q:116:GLU:OE2	2.09	0.53
7:Q:15:LEU:HA	8:Z:71:HIS:CE1	2.44	0.53
2:B:275:MET:HA	2:B:278:LYS:HD2	1.91	0.52
3:D:194:VAL:HA	3:D:197:VAL:CG2	2.38	0.52
5:G:285:LEU:HD22	5:G:339:ARG:HA	1.90	0.52
5:G:184:GLN:OE1	5:G:402:LEU:HD23	2.10	0.52
6:H:73:HIS:HB3	6:H:76:ALA:HB3	1.92	0.52
8:Z:161:HIS:CE1	8:Z:164:LEU:HB3	2.44	0.52
8:Z:180:LYS:HB3	8:Z:186:ILE:HG12	1.92	0.52
8:Z:218:HIS:HB2	8:Z:302:LEU:HB3	1.91	0.52
1:A:213:GLY:O	1:A:374:SER:N	2.42	0.52
2:B:455:GLY:HA3	3:D:135:ILE:CG1	2.39	0.52
4:E:437:ALA:CB	4:E:448:MET:HB2	2.38	0.52
5:G:355:ILE:HB	5:G:360:PHE:CD2	2.44	0.52
6:H:133:VAL:HG12	6:H:137:LYS:HZ2	1.74	0.52
6:H:191:GLN:HB3	6:H:194:MET:SD	2.48	0.52
8:Z:176:ILE:HA	8:Z:179:ILE:HG12	1.91	0.52
8:Z:290:VAL:HA	8:Z:311:ILE:O	2.10	0.52
1:A:458:GLN:O	1:A:459:ASP:C	2.48	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:ASP:OD2	3:D:53:THR:HG21	2.10	0.52
2:B:446:LEU:HB3	2:B:447:PRO:CD	2.40	0.52
4:E:18:ILE:HG13	6:H:73:HIS:CD2	2.44	0.52
6:H:278:LEU:CD2	6:H:302:TYR:HB2	2.40	0.52
6:H:27:SER:O	6:H:31:VAL:HG23	2.10	0.52
8:Z:355:LEU:HD13	8:Z:375:LEU:HD21	1.90	0.52
1:A:133:SER:HA	1:A:136:LEU:HD11	1.91	0.52
1:A:532:LYS:HG2	3:D:65:GLN:HB3	1.91	0.52
2:B:19:GLU:HB3	2:B:24:ALA:HA	1.91	0.52
2:B:520:ILE:HD12	4:E:60:MET:CB	2.37	0.52
5:G:407:LEU:HA	5:G:499:LEU:N	2.25	0.52
5:G:80:MET:HA	5:G:83:ILE:HD12	1.92	0.52
8:Z:230:ILE:O	8:Z:344:LEU:HA	2.09	0.52
5:G:72:VAL:HG22	8:Z:6:THR:O	2.09	0.52
2:B:218:PHE:HA	2:B:372:THR:OG1	2.09	0.52
4:E:237:PRO:HG2	4:E:238:GLN:H	1.75	0.52
6:H:133:VAL:HG12	6:H:137:LYS:HZ1	1.72	0.52
7:Q:221:MET:HA	7:Q:374:THR:HG1	1.72	0.52
8:Z:14:ALA:HB1	8:Z:19:ALA:HB2	1.92	0.52
5:G:71:GLN:H	8:Z:524:ALA:HB1	1.74	0.52
8:Z:48:VAL:HG13	8:Z:53:ASP:O	2.09	0.52
1:A:214:TYR:HA	1:A:374:SER:OG	2.09	0.52
1:A:9:GLY:HA2	1:A:533:LEU:HD22	1.92	0.52
2:B:407:VAL:CG2	2:B:495:GLU:HB2	2.37	0.52
3:D:404:ALA:O	3:D:408:ILE:HG13	2.10	0.52
5:G:396:GLN:HE22	5:G:399:ARG:HD3	1.74	0.52
6:H:17:GLN:O	6:H:20:PRO:HD2	2.10	0.52
6:H:443:GLU:O	6:H:447:ARG:HB2	2.10	0.52
8:Z:333:LEU:HD23	8:Z:339:LEU:HD23	1.90	0.52
8:Z:514:ASN:O	8:Z:518:VAL:HG23	2.10	0.52
8:Z:103:LEU:CD2	8:Z:516:LEU:HD21	2.36	0.52
1:A:6:SER:HA	3:D:87:LEU:HD11	1.91	0.52
1:A:75:LEU:HB3	1:A:94:VAL:HG13	1.90	0.52
2:B:231:ARG:NH2	2:B:348:LEU:HD11	2.23	0.52
3:D:247:ALA:HA	3:D:299:ASN:ND2	2.20	0.52
3:D:237:ALA:HA	3:D:317:LEU:HD11	1.91	0.52
3:D:290:VAL:HG13	3:D:320:LEU:HD23	1.91	0.52
3:D:226:LEU:HD11	3:D:389:VAL:HB	1.91	0.52
4:E:299:LEU:HD12	4:E:320:PRO:O	2.09	0.52
2:B:11:ILE:HA	4:E:85:HIS:HB2	1.92	0.52
6:H:73:HIS:HB3	6:H:76:ALA:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:422:LEU:HA	8:Z:425:TYR:HB3	1.92	0.52
2:B:53:LEU:HD23	3:D:542:ARG:NH2	2.25	0.52
3:D:450:GLU:O	3:D:454:ILE:HG13	2.10	0.52
3:D:36:ILE:HG23	3:D:536:ASP:HA	1.92	0.52
4:E:45:ALA:CB	4:E:114:GLY:HA3	2.40	0.52
5:G:226:HIS:ND1	5:G:227:PRO:HD2	2.25	0.52
5:G:46:MET:CA	8:Z:517:LEU:HB3	2.40	0.52
5:G:62:ASP:OD2	5:G:64:ASN:HB3	2.10	0.52
7:Q:138:LYS:O	7:Q:142:ILE:HG13	2.10	0.52
7:Q:292:VAL:HG21	7:Q:324:LEU:CD2	2.39	0.52
7:Q:93:GLN:HE22	7:Q:97:VAL:HG22	1.74	0.52
8:Z:426:LYS:N	8:Z:427:PRO:CD	2.73	0.52
2:B:144:SER:CB	2:B:474:THR:HG21	2.33	0.52
2:B:79:PRO:CG	2:B:522:LYS:HG3	2.40	0.52
2:B:90:VAL:O	2:B:94:GLU:HG2	2.10	0.52
4:E:204:VAL:HB	4:E:410:ARG:CG	2.33	0.52
5:G:165:ILE:HG21	5:G:390:ASN:HB3	1.92	0.52
6:H:36:VAL:HG23	6:H:95:THR:HG23	1.92	0.52
8:Z:118:ILE:H	8:Z:118:ILE:CD1	2.20	0.52
1:A:356:ILE:HG23	1:A:378:ARG:CZ	2.40	0.52
6:H:118:PRO:O	6:H:121:ILE:HB	2.10	0.52
6:H:133:VAL:HG13	6:H:500:ILE:HG23	1.92	0.52
6:H:78:THR:HA	6:H:81:ASP:OD2	2.09	0.52
7:Q:188:VAL:HG13	7:Q:197:PHE:CZ	2.45	0.52
7:Q:448:ILE:N	7:Q:448:ILE:HD12	2.25	0.52
8:Z:109:TYR:HA	8:Z:112:GLU:CD	2.30	0.52
3:D:431:PRO:HG2	3:D:432:GLU:OE1	2.09	0.51
4:E:161:ASN:HD22	4:E:164:PRO:CB	2.20	0.51
6:H:71:VAL:HB	6:H:77:LYS:HE3	1.90	0.51
7:Q:33:ILE:HG13	7:Q:112:LEU:CB	2.28	0.51
8:Z:462:THR:HA	8:Z:465:LYS:HE2	1.90	0.51
1:A:277:LYS:HA	1:A:277:LYS:NZ	2.24	0.51
1:A:427:ALA:O	1:A:435:GLN:HG3	2.11	0.51
1:A:438:ILE:O	1:A:441:PHE:HB3	2.10	0.51
2:B:194:GLY:CA	2:B:401:VAL:HG21	2.38	0.51
2:B:202:ILE:HG13	2:B:219:LEU:HD23	1.92	0.51
3:D:230:LEU:CD1	3:D:338:PHE:HB3	2.40	0.51
5:G:286:LYS:N	5:G:287:PRO:CD	2.73	0.51
5:G:404:ASP:OD2	5:G:406:GLN:HG2	2.09	0.51
6:H:216:PHE:CE2	6:H:318:ASP:HB3	2.45	0.51
6:H:230:LYS:O	6:H:349:GLU:HA	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:222:LYS:HB2	8:Z:311:ILE:CG1	2.41	0.51
8:Z:225:VAL:HG21	8:Z:290:VAL:HG22	1.92	0.51
5:G:51:LEU:HD13	8:Z:521:ILE:HG23	1.93	0.51
2:B:196:LEU:HD11	2:B:395:CYS:HA	1.93	0.51
2:B:513:VAL:HG13	2:B:516:ARG:HH12	1.74	0.51
3:D:197:VAL:CG1	3:D:387:LYS:HA	2.35	0.51
6:H:238:ALA:CB	6:H:289:VAL:HG22	2.38	0.51
7:Q:523:GLN:HB3	8:Z:45:LYS:HE3	1.92	0.51
8:Z:138:LYS:HD2	8:Z:406:CYS:SG	2.50	0.51
2:B:135:LYS:O	2:B:139:GLN:HG3	2.11	0.51
2:B:509:GLU:HA	2:B:512:GLU:OE1	2.11	0.51
3:D:178:VAL:HB	3:D:403:GLU:CG	2.36	0.51
3:D:300:VAL:HG13	3:D:326:MET:HE1	1.91	0.51
3:D:206:VAL:HG21	3:D:419:VAL:HG21	1.92	0.51
4:E:248:ILE:HG12	4:E:299:LEU:HD23	1.92	0.51
4:E:463:ALA:HB2	4:E:473:THR:HG21	1.92	0.51
5:G:380:SER:O	5:G:384:LEU:HB2	2.11	0.51
8:Z:144:ASP:O	8:Z:148:LEU:HG	2.11	0.51
8:Z:164:LEU:HD13	8:Z:202:THR:HG22	1.91	0.51
8:Z:160:VAL:CG2	8:Z:386:GLN:HG2	2.40	0.51
1:A:222:SER:OG	1:A:225:MET:HG2	2.11	0.51
2:B:239:ILE:HB	2:B:331:ILE:HA	1.93	0.51
2:B:351:GLU:HG3	2:B:360:ILE:HD13	1.92	0.51
3:D:119:LEU:HB3	3:D:140:PHE:HE2	1.75	0.51
4:E:93:GLU:HB2	4:E:523:MET:HE1	1.93	0.51
6:H:150:GLU:O	6:H:151:GLN:HB3	2.11	0.51
6:H:152:ARG:O	6:H:156:GLU:HG3	2.10	0.51
7:Q:296:ARG:HH12	7:Q:315:LEU:HD11	1.75	0.51
5:G:51:LEU:HD13	8:Z:521:ILE:CG2	2.40	0.51
1:A:32:VAL:HB	1:A:91:THR:HG23	1.93	0.51
1:A:487:GLY:CA	1:A:498:ASN:HD21	2.23	0.51
2:B:279:VAL:HG11	2:B:303:LEU:CB	2.41	0.51
3:D:144:LEU:HG	3:D:526:THR:HB	1.92	0.51
3:D:463:VAL:HG23	3:D:464:ILE:N	2.26	0.51
4:E:445:GLN:O	4:E:449:ARG:HG3	2.10	0.51
5:G:476:GLU:O	5:G:476:GLU:HG2	2.10	0.51
5:G:49:MET:HB2	5:G:59:MET:HE2	1.92	0.51
7:Q:230:ASP:CB	7:Q:311:MET:HA	2.38	0.51
7:Q:225:LYS:HD2	7:Q:352:LEU:HD22	1.92	0.51
7:Q:327:THR:OG1	7:Q:372:ILE:HB	2.10	0.51
5:G:391:LEU:O	5:G:395:MET:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:337:ASN:H	7:Q:338:PRO:CD	2.23	0.51
7:Q:425:SER:O	7:Q:429:THR:HG23	2.11	0.51
8:Z:292:ILE:HD13	8:Z:313:LEU:HD13	1.93	0.51
2:B:446:LEU:HB3	2:B:447:PRO:HD3	1.93	0.51
2:B:479:ASP:OD1	2:B:482:GLU:HG2	2.10	0.51
3:D:179:VAL:HG11	3:D:407:SER:HB2	1.93	0.51
3:D:82:LYS:NZ	3:D:99:LYS:NZ	2.58	0.51
4:E:248:ILE:HD12	4:E:337:THR:HG21	1.92	0.51
4:E:133:ILE:HB	4:E:528:LEU:HD11	1.93	0.51
5:G:406:GLN:O	5:G:499:LEU:N	2.35	0.51
6:H:316:GLU:HG2	6:H:320:LYS:HE3	1.93	0.51
6:H:411:ALA:HB2	6:H:487:ASN:ND2	2.25	0.51
8:Z:311:ILE:N	8:Z:311:ILE:HD12	2.26	0.51
1:A:137:ILE:HG21	1:A:499:LYS:HG3	1.92	0.51
2:B:52:LEU:O	2:B:53:LEU:HD12	2.11	0.51
3:D:333:ARG:O	3:D:337:GLU:HG3	2.11	0.51
4:E:123:LEU:HB3	4:E:128:ILE:HD12	1.91	0.51
2:B:516:ARG:HG2	4:E:57:LEU:HA	1.92	0.51
5:G:512:THR:O	5:G:516:LEU:HG	2.11	0.51
6:H:9:LEU:HB3	6:H:13:THR:HB	1.92	0.51
6:H:294:PRO:HG3	6:H:313:ARG:CG	2.41	0.51
6:H:378:ALA:HB3	6:H:381:PHE:HD1	1.76	0.51
7:Q:171:LYS:HB2	7:Q:173:TYR:CD1	2.45	0.51
7:Q:337:ASN:N	7:Q:338:PRO:CD	2.74	0.51
7:Q:520:ARG:O	7:Q:522:ASP:N	2.44	0.51
1:A:164:ASN:HB3	1:A:206:MET:HE1	1.91	0.51
3:D:196:LYS:HB3	3:D:386:GLY:N	2.25	0.51
3:D:417:CYS:HA	3:D:516:LEU:CD1	2.41	0.51
3:D:525:ALA:O	3:D:529:VAL:HG23	2.11	0.51
4:E:443:LEU:CD2	4:E:443:LEU:N	2.74	0.51
7:Q:155:ARG:HH22	7:Q:192:PRO:CG	2.24	0.51
8:Z:209:GLY:HA3	8:Z:364:GLU:HA	1.92	0.51
1:A:105:ASP:O	1:A:108:VAL:HB	2.11	0.50
1:A:167:PHE:HB2	1:A:206:MET:HE1	1.93	0.50
1:A:408:VAL:HG22	1:A:409:VAL:N	2.26	0.50
1:A:401:ARG:NH2	1:A:506:PRO:HG2	2.27	0.50
2:B:186:ALA:HB2	2:B:214:LEU:HD11	1.92	0.50
2:B:330:GLU:HB2	2:B:342:LYS:HD3	1.91	0.50
2:B:35:ILE:HB	2:B:84:LEU:CD1	2.41	0.50
4:E:231:ASP:OD1	4:E:371:MET:HE3	2.11	0.50
4:E:87:ILE:HG23	4:E:88:ALA:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:407:LEU:CB	5:G:498:PRO:HA	2.40	0.50
6:H:92:ASP:CG	6:H:93:GLY:N	2.64	0.50
7:Q:140:HIS:HE2	7:Q:508:ILE:HB	1.76	0.50
7:Q:156:ASP:O	7:Q:160:VAL:HG23	2.11	0.50
7:Q:24:GLY:O	7:Q:27:GLU:HB3	2.11	0.50
7:Q:68:ASP:O	7:Q:72:ILE:HG13	2.10	0.50
2:B:124:GLN:HG2	4:E:55:ASN:HD21	1.73	0.50
2:B:461:LEU:CD2	2:B:478:LEU:HD13	2.42	0.50
2:B:29:PHE:CZ	2:B:515:LEU:HA	2.46	0.50
2:B:89:ARG:HG2	2:B:89:ARG:HH11	1.76	0.50
3:D:194:VAL:O	3:D:198:ILE:HG23	2.10	0.50
3:D:86:VAL:CG1	3:D:91:ALA:HB3	2.42	0.50
6:H:26:ILE:HG23	6:H:105:LEU:CB	2.36	0.50
6:H:215:ALA:CB	6:H:373:ILE:HD11	2.33	0.50
8:Z:412:GLY:HA2	8:Z:415:GLU:CD	2.32	0.50
4:E:416:ASN:O	4:E:417:ARG:HG2	2.12	0.50
5:G:137:LEU:HA	5:G:140:ILE:CD1	2.41	0.50
7:Q:155:ARG:HH22	7:Q:192:PRO:HG2	1.75	0.50
7:Q:20:LYS:HB3	7:Q:525:ILE:HG13	1.93	0.50
8:Z:422:LEU:HB2	8:Z:441:ALA:HB2	1.93	0.50
8:Z:13:VAL:HG13	8:Z:522:MET:HG2	1.94	0.50
8:Z:99:ILE:HG13	8:Z:512:ALA:HB2	1.92	0.50
3:D:98:SER:O	3:D:109:THR:HG23	2.11	0.50
4:E:134:ALA:HB1	4:E:525:ARG:HG3	1.93	0.50
4:E:344:ARG:NH2	4:E:345:PHE:CD2	2.80	0.50
4:E:426:GLU:HB3	4:E:455:LEU:O	2.11	0.50
5:G:462:LEU:O	5:G:466:LEU:HB2	2.12	0.50
7:Q:408:LEU:O	7:Q:408:LEU:HD12	2.10	0.50
8:Z:164:LEU:HG	8:Z:167:VAL:HB	1.93	0.50
8:Z:168:LEU:O	8:Z:172:VAL:HG23	2.12	0.50
8:Z:198:HIS:O	8:Z:199:LYS:HB2	2.11	0.50
8:Z:293:ASN:HD22	8:Z:297:ILE:CD1	2.23	0.50
1:A:322:ALA:O	1:A:369:ALA:HB3	2.12	0.50
1:A:349:GLU:HB3	1:A:366:ASN:CB	2.35	0.50
1:A:498:ASN:HB3	1:A:503:VAL:HB	1.92	0.50
3:D:187:SER:O	3:D:191:VAL:HG23	2.11	0.50
3:D:252:ILE:HD11	3:D:354:PHE:CG	2.45	0.50
4:E:115:ALA:HB1	4:E:457:VAL:HG11	1.94	0.50
6:H:213:GLY:O	6:H:370:CYS:HA	2.12	0.50
7:Q:138:LYS:HD2	7:Q:141:GLU:OE1	2.11	0.50
8:Z:328:CYS:SG	8:Z:366:CYS:SG	3.06	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:VAL:O	1:A:402:VAL:HG23	2.12	0.50
1:A:24:ALA:HB1	1:A:72:ALA:HB2	1.93	0.50
2:B:487:ASP:O	2:B:491:LEU:HG	2.11	0.50
3:D:483:LEU:HD22	3:D:496:ILE:HD11	1.92	0.50
3:D:486:ARG:HG3	3:D:503:ILE:HG12	1.93	0.50
4:E:300:ALA:HB3	4:E:321:ALA:HB2	1.94	0.50
5:G:283:ILE:HG12	5:G:309:ILE:CD1	2.42	0.50
6:H:331:GLN:CG	6:H:341:VAL:HG11	2.41	0.50
6:H:331:GLN:HG2	6:H:341:VAL:HG11	1.94	0.50
8:Z:333:LEU:HB2	8:Z:339:LEU:CD2	2.42	0.50
8:Z:409:PRO:O	8:Z:414:VAL:HG23	2.11	0.50
1:A:277:LYS:NZ	1:A:280:ALA:HB3	2.26	0.50
1:A:447:VAL:HG13	1:A:448:ILE:N	2.27	0.50
2:B:408:TYR:CZ	2:B:489:SER:HB3	2.46	0.50
4:E:318:ASP:O	4:E:319:LEU:HD12	2.12	0.50
4:E:215:VAL:HB	4:E:392:LYS:HZ2	1.77	0.50
4:E:73:ASP:O	4:E:77:ILE:HG13	2.10	0.50
7:Q:215:SER:HA	7:Q:378:ARG:HG2	1.93	0.50
8:Z:142:GLU:HG3	8:Z:144:ASP:H	1.77	0.50
1:A:5:LEU:CD1	1:A:11:ARG:HB2	2.40	0.50
1:A:409:VAL:HB	1:A:410:PRO:HD2	1.94	0.50
1:A:474:ALA:O	1:A:483:LEU:HB2	2.11	0.50
1:A:114:PRO:HB3	1:A:525:LEU:HD22	1.93	0.50
2:B:408:TYR:OH	2:B:489:SER:HB3	2.12	0.50
3:D:249:ILE:O	3:D:359:LEU:HA	2.12	0.50
3:D:487:HIS:HE1	3:D:492:LYS:HA	1.77	0.50
2:B:51:ILE:N	3:D:538:VAL:HG13	2.26	0.50
2:B:11:ILE:HD11	4:E:40:ALA:HB1	1.93	0.50
5:G:203:LYS:HB2	5:G:384:LEU:HD21	1.93	0.50
5:G:230:ARG:NE	5:G:308:ASN:HB3	2.27	0.50
5:G:95:THR:O	5:G:99:ILE:HG12	2.12	0.50
6:H:238:ALA:O	6:H:289:VAL:HA	2.12	0.50
6:H:50:VAL:HG13	6:H:54:GLY:O	2.12	0.50
6:H:63:ALA:H	6:H:94:THR:HG21	1.76	0.50
3:D:421:LYS:CG	3:D:515:LEU:HB3	2.39	0.50
3:D:82:LYS:HZ3	3:D:99:LYS:HZ3	1.60	0.50
4:E:27:ARG:NH2	4:E:534:ARG:NH2	2.59	0.50
7:Q:171:LYS:HB2	7:Q:173:TYR:HE1	1.77	0.50
8:Z:139:VAL:O	8:Z:407:VAL:HG12	2.11	0.50
8:Z:232:THR:O	8:Z:339:LEU:HD21	2.11	0.50
2:B:465:LEU:HD12	2:B:485:ILE:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:477:GLY:HA3	2:B:488:MET:HG2	1.93	0.49
3:D:169:SER:HB2	3:D:418:LEU:HD22	1.94	0.49
3:D:179:VAL:HG12	3:D:404:ALA:HA	1.93	0.49
3:D:515:LEU:HG	3:D:519:VAL:HG23	1.91	0.49
2:B:51:ILE:H	3:D:538:VAL:HG13	1.76	0.49
4:E:251:LEU:O	4:E:302:CYS:HA	2.12	0.49
4:E:385:ILE:O	4:E:387:ILE:HD12	2.12	0.49
5:G:110:GLU:HA	5:G:113:LEU:HD12	1.94	0.49
5:G:171:LEU:O	5:G:175:ILE:HG13	2.12	0.49
5:G:46:MET:HG2	8:Z:517:LEU:CD2	2.42	0.49
7:Q:353:SER:O	7:Q:360:VAL:HG22	2.11	0.49
8:Z:23:ASN:O	8:Z:73:THR:HG21	2.12	0.49
8:Z:415:GLU:OE2	8:Z:447:ILE:HG21	2.11	0.49
8:Z:35:ARG:HD2	8:Z:450:VAL:HG22	1.94	0.49
8:Z:55:LYS:HE2	8:Z:62:VAL:HG11	1.94	0.49
8:Z:62:VAL:O	8:Z:66:GLU:HG2	2.12	0.49
1:A:532:LYS:HZ2	3:D:65:GLN:HB2	1.77	0.49
2:B:505:LEU:O	2:B:509:GLU:HG2	2.12	0.49
3:D:105:ALA:N	3:D:416:ARG:HH22	2.10	0.49
4:E:178:VAL:HG21	4:E:185:MET:HG3	1.93	0.49
4:E:306:PHE:HB3	4:E:323:ARG:HD3	1.94	0.49
4:E:340:ARG:HD2	4:E:352:LYS:HD3	1.94	0.49
5:G:23:GLN:NE2	5:G:113:LEU:HD22	2.27	0.49
7:Q:44:ARG:HE	7:Q:451:ALA:HB2	1.77	0.49
1:A:119:SER:O	1:A:123:LEU:HG	2.12	0.49
1:A:125:CYS:O	1:A:129:VAL:HG23	2.12	0.49
2:B:522:LYS:HE2	2:B:523:ALA:H	1.77	0.49
3:D:122:SER:HB2	3:D:456:ALA:HB1	1.93	0.49
4:E:145:ILE:HG23	4:E:149:ASP:OD1	2.12	0.49
4:E:363:SER:HA	4:E:370:LYS:HA	1.94	0.49
4:E:400:ARG:O	4:E:403:HIS:HB3	2.12	0.49
1:A:31:ILE:CG1	5:G:16:ARG:HH12	2.24	0.49
7:Q:246:PHE:CB	7:Q:297:VAL:HG13	2.42	0.49
7:Q:218:LEU:HD13	7:Q:362:VAL:CG1	2.42	0.49
7:Q:474:GLY:HA3	7:Q:478:VAL:CG2	2.42	0.49
7:Q:92:MET:O	7:Q:96:GLU:HG2	2.12	0.49
8:Z:15:ARG:O	8:Z:18:ALA:HB3	2.12	0.49
8:Z:224:ARG:NH1	8:Z:349:LEU:HD11	2.28	0.49
1:A:474:ALA:HB3	1:A:486:ILE:HG13	1.94	0.49
1:A:82:GLN:NE2	1:A:86:VAL:HG21	2.27	0.49
2:B:218:PHE:CB	2:B:326:VAL:HG11	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:469:ALA:HB1	3:D:474:LEU:HB2	1.93	0.49
3:D:466:SER:OG	3:D:480:VAL:HG21	2.13	0.49
3:D:61:ASP:O	3:D:62:LYS:HD3	2.12	0.49
5:G:325:ARG:HG2	5:G:325:ARG:HH11	1.78	0.49
5:G:401:VAL:HG13	5:G:402:LEU:CD1	2.42	0.49
5:G:65:ALA:O	5:G:69:GLU:HG2	2.13	0.49
6:H:289:VAL:HB	6:H:310:CYS:SG	2.52	0.49
6:H:378:ALA:HB3	6:H:381:PHE:CD1	2.48	0.49
6:H:390:HIS:O	6:H:394:MET:HG2	2.13	0.49
7:Q:49:PRO:CA	7:Q:170:SER:HA	2.42	0.49
1:A:86:VAL:HG13	1:A:512:LYS:HZ1	1.74	0.49
2:B:215:ASP:O	2:B:371:CYS:HB3	2.12	0.49
3:D:132:HIS:HB3	3:D:135:ILE:CD1	2.42	0.49
3:D:24:LYS:HG3	3:D:30:ARG:HH11	1.77	0.49
3:D:317:LEU:HG	3:D:321:ASN:ND2	2.27	0.49
4:E:511:ILE:H	4:E:511:ILE:CD1	2.23	0.49
4:E:94:LEU:HG	4:E:523:MET:HG2	1.95	0.49
5:G:477:THR:O	5:G:489:ASP:HA	2.13	0.49
7:Q:410:PRO:HG3	7:Q:476:LYS:HG2	1.95	0.49
7:Q:417:ILE:HG13	7:Q:467:LEU:HD21	1.95	0.49
8:Z:35:ARG:HG2	8:Z:453:GLN:HE22	1.77	0.49
8:Z:473:SER:HB2	8:Z:477:VAL:CG2	2.43	0.49
2:B:158:ASP:O	2:B:162:ILE:HG12	2.13	0.49
3:D:36:ILE:HG21	3:D:536:ASP:C	2.33	0.49
3:D:89:PRO:HA	3:D:92:ARG:HD2	1.94	0.49
4:E:193:VAL:HG11	4:E:409:ILE:HG22	1.95	0.49
5:G:38:ARG:HG3	5:G:100:ILE:CD1	2.42	0.49
6:H:443:GLU:OE1	6:H:461:LEU:HD11	2.13	0.49
7:Q:218:LEU:HD13	7:Q:362:VAL:HG13	1.94	0.49
7:Q:17:GLU:CB	8:Z:68:GLN:HG2	2.43	0.49
1:A:224:GLY:HA3	1:A:301:VAL:HG13	1.94	0.49
1:A:2:GLU:CB	3:D:90:ALA:HB3	2.43	0.49
2:B:239:ILE:HD12	2:B:329:GLY:O	2.13	0.49
4:E:87:ILE:CD1	4:E:527:ILE:HD13	2.43	0.49
5:G:285:LEU:HD11	5:G:338:LEU:HB3	1.94	0.49
5:G:203:LYS:CD	5:G:384:LEU:HG	2.34	0.49
5:G:424:GLU:HA	5:G:427:LYS:HZ3	1.78	0.49
7:Q:112:LEU:HD22	7:Q:519:LEU:CD2	2.36	0.49
7:Q:292:VAL:HG21	7:Q:324:LEU:HD21	1.95	0.49
8:Z:132:GLN:O	8:Z:136:GLN:HG3	2.11	0.49
8:Z:131:LEU:CD2	8:Z:505:LEU:HD12	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:14:MET:HG3	8:Z:70:GLN:OE1	2.12	0.49
1:A:445:LEU:N	1:A:446:PRO:CD	2.76	0.49
1:A:59:ALA:HB2	1:A:90:THR:HG21	1.93	0.49
2:B:163:ALA:HB3	2:B:180:THR:HG23	1.95	0.49
3:D:431:PRO:HG2	3:D:432:GLU:CD	2.33	0.49
3:D:470:GLU:C	3:D:472:ALA:H	2.16	0.49
4:E:75:ALA:HB2	4:E:106:THR:HG21	1.95	0.49
5:G:352:ILE:HD11	5:G:359:TYR:HB3	1.95	0.49
5:G:523:VAL:HG12	5:G:524:SER:N	2.28	0.49
7:Q:524:ILE:CG2	8:Z:46:MET:N	2.73	0.49
2:B:187:VAL:CG2	2:B:397:LEU:HD13	2.41	0.49
2:B:353:MET:HA	2:B:357:ASP:O	2.13	0.49
3:D:251:LEU:CB	3:D:347:PRO:HA	2.43	0.49
4:E:173:LEU:HD13	4:E:185:MET:HB2	1.94	0.49
4:E:90:LEU:HA	4:E:93:GLU:CD	2.33	0.49
4:E:95:SER:HB2	4:E:106:THR:HG22	1.95	0.49
8:Z:97:LEU:HB3	8:Z:446:ILE:HD13	1.94	0.49
1:A:483:LEU:O	1:A:486:ILE:HG12	2.13	0.49
2:B:487:ASP:HB3	2:B:490:VAL:HB	1.94	0.49
2:B:522:LYS:NZ	3:D:22:ARG:O	2.46	0.49
6:H:154:LEU:HA	6:H:157:LYS:HZ3	1.78	0.49
6:H:226:GLU:HB3	6:H:227:MET:HE2	1.94	0.49
4:E:20:LYS:HZ3	6:H:32:ILE:CG1	2.26	0.49
7:Q:239:ILE:O	7:Q:344:MET:HA	2.12	0.49
7:Q:448:ILE:HD12	7:Q:448:ILE:H	1.78	0.49
7:Q:44:ARG:HE	7:Q:451:ALA:CB	2.25	0.49
7:Q:407:ARG:HB2	7:Q:501:TYR:HB3	1.94	0.49
1:A:506:PRO:HB2	1:A:509:VAL:CG2	2.37	0.48
1:A:57:ASP:O	1:A:61:ILE:HG13	2.12	0.48
2:B:287:ILE:CG2	2:B:343:LEU:HD21	2.43	0.48
2:B:74:ILE:HA	3:D:541:THR:OG1	2.13	0.48
5:G:23:GLN:NE2	5:G:113:LEU:HD13	2.16	0.48
5:G:183:VAL:HG23	5:G:194:ASP:OD2	2.13	0.48
5:G:72:VAL:HA	8:Z:6:THR:O	2.12	0.48
6:H:450:CYS:HA	6:H:479:ILE:CD1	2.43	0.48
7:Q:222:VAL:HG23	7:Q:374:THR:HG21	1.94	0.48
7:Q:316:ASN:OD1	7:Q:320:ASP:HB2	2.13	0.48
8:Z:410:GLY:HA3	8:Z:496:ASP:OD1	2.13	0.48
8:Z:13:VAL:HG13	8:Z:522:MET:CG	2.43	0.48
2:B:198:ALA:HB1	2:B:369:GLU:O	2.13	0.48
2:B:79:PRO:HD3	2:B:522:LYS:CD	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:174:LEU:HB2	3:D:183:SER:OG	2.13	0.48
3:D:226:LEU:HD21	3:D:389:VAL:HG11	1.95	0.48
3:D:395:GLY:O	3:D:401:ILE:HD11	2.12	0.48
4:E:34:LEU:O	4:E:38:ILE:HG13	2.13	0.48
5:G:101:LEU:HG	5:G:447:ILE:HD11	1.95	0.48
5:G:209:ILE:HD13	5:G:387:VAL:HG21	1.94	0.48
7:Q:138:LYS:HG2	7:Q:426:TYR:CD2	2.48	0.48
7:Q:174:GLY:HA2	7:Q:177:VAL:CG1	2.41	0.48
7:Q:246:PHE:HB2	7:Q:297:VAL:HG13	1.94	0.48
1:A:271:THR:HA	1:A:274:ARG:NH2	2.28	0.48
1:A:350:GLU:HB3	1:A:366:ASN:HD22	1.77	0.48
1:A:483:LEU:HD12	1:A:485:TRP:CH2	2.48	0.48
2:B:11:ILE:HA	4:E:85:HIS:N	2.24	0.48
3:D:483:LEU:HD22	3:D:496:ILE:CD1	2.42	0.48
4:E:18:ILE:HG22	4:E:19:ILE:HG13	1.95	0.48
4:E:315:LEU:C	4:E:315:LEU:HD23	2.34	0.48
5:G:79:SER:O	5:G:83:ILE:HG13	2.13	0.48
6:H:199:LYS:O	6:H:199:LYS:HG3	2.13	0.48
6:H:418:LYS:NZ	6:H:469:ALA:HA	2.27	0.48
7:Q:227:THR:HG23	7:Q:302:LEU:HD22	1.94	0.48
7:Q:351:TYR:CE2	7:Q:364:LYS:HE2	2.49	0.48
7:Q:103:PHE:CE1	7:Q:448:ILE:HG12	2.42	0.48
7:Q:486:VAL:O	7:Q:486:VAL:HG13	2.14	0.48
8:Z:161:HIS:C	8:Z:163:GLU:H	2.15	0.48
1:A:35:SER:HA	1:A:41:LEU:H	1.78	0.48
1:A:384:MET:N	1:A:384:MET:SD	2.87	0.48
2:B:46:LYS:O	2:B:453:ASN:HB3	2.14	0.48
4:E:459:PRO:HA	4:E:462:LEU:HG	1.95	0.48
6:H:129:THR:O	6:H:133:VAL:HG23	2.14	0.48
6:H:214:VAL:HG23	6:H:361:PHE:HB2	1.95	0.48
6:H:366:LYS:O	6:H:368:LYS:N	2.46	0.48
6:H:496:ALA:O	6:H:500:ILE:HG13	2.13	0.48
6:H:516:VAL:HG22	7:Q:53:ASN:O	2.13	0.48
6:H:86:GLN:HE21	6:H:90:VAL:CG2	2.26	0.48
7:Q:199:VAL:CG1	7:Q:396:VAL:HG12	2.35	0.48
7:Q:428:GLU:HA	7:Q:435:GLN:NE2	2.12	0.48
7:Q:55:MET:SD	7:Q:63:LEU:HD21	2.53	0.48
1:A:4:PRO:O	1:A:5:LEU:HD23	2.13	0.48
1:A:9:GLY:HA2	1:A:533:LEU:CD2	2.44	0.48
2:B:196:LEU:HD11	2:B:398:ALA:HB2	1.94	0.48
2:B:238:LEU:HD22	2:B:287:ILE:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:287:ILE:HD11	2:B:290:PHE:HB2	1.95	0.48
3:D:31:ASP:HB3	3:D:36:ILE:CB	2.27	0.48
3:D:364:LEU:HD11	3:D:366:GLU:HB3	1.95	0.48
3:D:464:ILE:O	3:D:468:LEU:HG	2.13	0.48
3:D:486:ARG:C	3:D:494:THR:HG21	2.34	0.48
3:D:420:LYS:HD2	3:D:516:LEU:HD11	1.95	0.48
3:D:79:THR:O	3:D:83:GLN:HG3	2.13	0.48
4:E:375:GLU:HG3	4:E:376:GLN:HG2	1.95	0.48
4:E:456:GLU:C	4:E:459:PRO:HD2	2.34	0.48
5:G:352:ILE:HG23	5:G:352:ILE:O	2.14	0.48
5:G:445:GLU:O	5:G:448:PRO:HG2	2.14	0.48
5:G:468:ALA:O	5:G:472:GLN:HG3	2.14	0.48
5:G:105:MET:HE1	5:G:510:VAL:HA	1.95	0.48
6:H:169:SER:HA	6:H:172:LYS:HB3	1.95	0.48
7:Q:188:VAL:O	7:Q:188:VAL:HG12	2.12	0.48
7:Q:239:ILE:CD1	7:Q:328:VAL:HG11	2.42	0.48
7:Q:417:ILE:HG13	7:Q:467:LEU:CD2	2.44	0.48
1:A:286:ILE:N	1:A:286:ILE:HD12	2.29	0.48
1:A:205:GLN:HA	1:A:378:ARG:O	2.14	0.48
2:B:290:PHE:CE2	2:B:292:ASN:HB2	2.48	0.48
2:B:316:ASP:OD2	2:B:318:VAL:HG12	2.14	0.48
2:B:202:ILE:HB	2:B:374:VAL:HA	1.96	0.48
2:B:37:ASP:O	2:B:40:LYS:HB3	2.13	0.48
3:D:26:ALA:O	3:D:27:TYR:HB2	2.14	0.48
3:D:476:PRO:O	3:D:480:VAL:HG23	2.14	0.48
7:Q:391:ALA:HA	7:Q:394:ASP:OD2	2.13	0.48
7:Q:71:THR:O	7:Q:75:GLU:HG2	2.14	0.48
8:Z:459:LEU:HD23	8:Z:459:LEU:C	2.34	0.48
1:A:286:ILE:HB	1:A:307:ALA:HB2	1.95	0.48
2:B:519:ASN:C	2:B:520:ILE:HD13	2.34	0.48
3:D:430:ALA:N	3:D:431:PRO:HD2	2.29	0.48
4:E:297:ALA:HB2	4:E:353:LEU:HD21	1.96	0.48
5:G:350:LEU:HA	5:G:362:PHE:O	2.14	0.48
5:G:473:GLU:HB3	5:G:478:TRP:HE1	1.79	0.48
6:H:191:GLN:HB3	6:H:194:MET:HG3	1.96	0.48
6:H:288:VAL:HA	6:H:309:PHE:O	2.13	0.48
7:Q:453:ALA:HB1	7:Q:458:VAL:HB	1.96	0.48
8:Z:161:HIS:NE2	8:Z:168:LEU:HB2	2.28	0.48
8:Z:40:PRO:HA	8:Z:158:THR:HA	1.95	0.48
5:G:74:HIS:CB	8:Z:5:LYS:HB2	2.33	0.48
1:A:13:THR:O	1:A:16:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:ASN:OD1	1:A:464:VAL:HG21	2.14	0.48
2:B:232:ILE:HG22	2:B:235:ALA:HB2	1.95	0.48
3:D:454:ILE:O	3:D:457:PHE:HB3	2.13	0.48
3:D:535:ILE:HG22	3:D:535:ILE:O	2.13	0.48
4:E:163:GLU:O	4:E:167:GLN:HG3	2.14	0.48
5:G:204:ILE:HD12	5:G:375:LEU:HD13	1.96	0.48
1:A:41:LEU:HA	5:G:518:ARG:HD2	1.96	0.48
7:Q:191:PHE:H	7:Q:192:PRO:HD3	1.79	0.48
1:A:112:ILE:HG23	1:A:433:ARG:CD	2.36	0.48
1:A:93:VAL:HG13	1:A:94:VAL:N	2.28	0.48
2:B:219:LEU:HB3	2:B:372:THR:CG2	2.43	0.48
3:D:190:SER:O	3:D:194:VAL:HG23	2.14	0.48
3:D:370:LEU:HD13	3:D:392:VAL:HG21	1.94	0.48
6:H:134:ASN:HD22	6:H:134:ASN:N	2.12	0.48
6:H:155:LEU:HD22	6:H:396:VAL:HG13	1.96	0.48
7:Q:45:THR:HA	7:Q:455:ASN:OD1	2.13	0.48
8:Z:181:LYS:HE2	8:Z:370:ARG:NH1	2.28	0.48
8:Z:160:VAL:HG21	8:Z:386:GLN:HG2	1.95	0.48
1:A:137:ILE:HD13	1:A:499:LYS:CG	2.43	0.48
6:H:240:LEU:HD13	6:H:334:VAL:HG22	1.95	0.48
7:Q:241:VAL:HG22	7:Q:324:LEU:HD23	1.96	0.48
8:Z:133:PHE:HD1	8:Z:136:GLN:OE1	1.96	0.48
8:Z:38:LEU:HD23	8:Z:450:VAL:HG11	1.95	0.48
8:Z:14:ALA:O	8:Z:520:GLU:HB3	2.14	0.48
8:Z:50:GLY:C	8:Z:52:GLY:H	2.17	0.48
1:A:137:ILE:HG23	1:A:499:LYS:HZ1	1.79	0.47
1:A:330:THR:HG22	1:A:332:ALA:H	1.79	0.47
1:A:398:VAL:HG23	1:A:399:VAL:N	2.29	0.47
2:B:223:LYS:HZ1	2:B:351:GLU:HB2	1.77	0.47
2:B:238:LEU:HB2	2:B:343:LEU:HD23	1.96	0.47
2:B:399:GLN:O	2:B:403:ASP:N	2.47	0.47
3:D:174:LEU:HD13	3:D:183:SER:HA	1.96	0.47
3:D:186:LEU:HD23	3:D:189:MET:HE1	1.95	0.47
3:D:29:ASP:HB2	3:D:540:ASN:CB	2.44	0.47
3:D:46:ALA:HA	3:D:49:ASP:OD2	2.14	0.47
4:E:410:ARG:O	4:E:413:ILE:HG22	2.14	0.47
5:G:515:LEU:O	5:G:519:ILE:HG13	2.14	0.47
7:Q:113:GLU:O	7:Q:117:GLU:HG3	2.14	0.47
7:Q:205:CYS:SG	7:Q:207:ILE:HD11	2.53	0.47
8:Z:181:LYS:CD	8:Z:370:ARG:HH12	2.27	0.47
2:B:156:ARG:HA	2:B:159:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:281:ARG:HA	2:B:284:LYS:HD2	1.95	0.47
3:D:249:ILE:CG2	3:D:345:THR:HG21	2.42	0.47
4:E:312:HIS:O	4:E:315:LEU:HB3	2.14	0.47
5:G:211:ASP:C	5:G:377:ARG:HG3	2.35	0.47
5:G:397:VAL:HA	5:G:400:ASN:ND2	2.26	0.47
6:H:214:VAL:HA	6:H:371:THR:HB	1.95	0.47
7:Q:525:ILE:CG2	7:Q:526:MET:H	2.03	0.47
1:A:413:GLY:HA3	1:A:449:PRO:HB3	1.95	0.47
2:B:123:PRO:O	2:B:126:ILE:HB	2.13	0.47
2:B:228:GLN:NE2	2:B:301:GLU:HG2	2.29	0.47
3:D:421:LYS:HE2	3:D:515:LEU:CD2	2.37	0.47
3:D:433:ILE:CD1	3:D:465:PRO:HG3	2.42	0.47
3:D:88:HIS:CE1	3:D:90:ALA:H	2.31	0.47
4:E:426:GLU:N	4:E:426:GLU:OE1	2.48	0.47
4:E:454:ALA:O	4:E:457:VAL:HG22	2.14	0.47
5:G:82:GLU:O	5:G:86:THR:HG23	2.15	0.47
6:H:117:HIS:O	6:H:121:ILE:HG13	2.14	0.47
6:H:224:GLY:HA3	6:H:228:GLN:OE1	2.14	0.47
7:Q:212:VAL:HA	7:Q:378:ARG:O	2.14	0.47
7:Q:22:PHE:CD1	7:Q:22:PHE:N	2.83	0.47
7:Q:446:GLU:O	7:Q:450:ARG:HB2	2.14	0.47
8:Z:221:MET:HG2	8:Z:306:ALA:HB2	1.97	0.47
1:A:115:THR:HA	1:A:118:ILE:HD12	1.96	0.47
1:A:121:TYR:HB3	1:A:518:THR:CG2	2.43	0.47
1:A:385:CYS:HA	1:A:388:MET:HE3	1.95	0.47
2:B:33:ILE:CG2	2:B:111:ARG:HD3	2.43	0.47
2:B:340:LEU:HD12	2:B:343:LEU:HD12	1.97	0.47
2:B:346:CYS:SG	2:B:349:ILE:HG13	2.54	0.47
3:D:78:ALA:HB2	3:D:109:THR:CG2	2.42	0.47
5:G:137:LEU:HD11	5:G:506:TYR:HE2	1.78	0.47
5:G:200:ARG:O	5:G:373:THR:HA	2.14	0.47
6:H:224:GLY:O	6:H:300:THR:HG23	2.14	0.47
7:Q:222:VAL:HA	7:Q:361:VAL:O	2.14	0.47
1:A:289:THR:OG1	1:A:316:LEU:HD22	2.14	0.47
1:A:369:ALA:C	1:A:371:THR:H	2.18	0.47
2:B:39:VAL:HA	2:B:50:LYS:HZ1	1.79	0.47
2:B:9:VAL:HG13	4:E:36:SER:HB2	1.97	0.47
3:D:24:LYS:HG3	3:D:30:ARG:NH1	2.30	0.47
3:D:251:LEU:HD12	3:D:336:ILE:HD12	1.95	0.47
5:G:286:LYS:N	5:G:287:PRO:HD3	2.30	0.47
5:G:44:LYS:HD3	5:G:455:CYS:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:416:MET:HE3	5:G:466:LEU:HD22	1.97	0.47
7:Q:21:HIS:CD2	7:Q:21:HIS:H	2.31	0.47
6:H:516:VAL:HA	7:Q:53:ASN:O	2.15	0.47
7:Q:13:GLN:CG	8:Z:71:HIS:HA	2.45	0.47
1:A:210:LEU:HD12	1:A:375:VAL:HG22	1.96	0.47
2:B:203:LYS:HB2	2:B:383:LEU:HG	1.95	0.47
2:B:35:ILE:HB	2:B:84:LEU:HD12	1.97	0.47
3:D:256:LEU:CD1	3:D:256:LEU:N	2.76	0.47
3:D:226:LEU:HG	3:D:389:VAL:HB	1.96	0.47
4:E:207:GLU:C	4:E:209:ILE:H	2.16	0.47
5:G:245:LEU:HD12	5:G:296:ILE:HG12	1.95	0.47
5:G:470:HIS:HE1	5:G:476:GLU:HG3	1.80	0.47
6:H:100:LEU:HD21	6:H:445:ILE:CD1	2.45	0.47
6:H:110:PRO:HG2	6:H:111:TYR:CD1	2.49	0.47
6:H:224:GLY:O	6:H:225:PHE:HB2	2.14	0.47
8:Z:104:LYS:O	8:Z:108:LEU:HG	2.14	0.47
1:A:82:GLN:HG2	1:A:90:THR:HA	1.96	0.47
2:B:51:ILE:H	3:D:538:VAL:CG1	2.28	0.47
3:D:239:SER:CB	3:D:321:ASN:HB3	2.37	0.47
4:E:410:ARG:HA	4:E:413:ILE:CG2	2.44	0.47
4:E:85:HIS:CE1	4:E:87:ILE:HG22	2.49	0.47
5:G:152:MET:HG3	5:G:401:VAL:HG11	1.95	0.47
8:Z:351:TYR:HB2	8:Z:353:TYR:CE1	2.50	0.47
1:A:292:ILE:HG13	1:A:309:ARG:HB3	1.97	0.47
3:D:431:PRO:HG2	3:D:432:GLU:OE2	2.15	0.47
3:D:43:ALA:O	3:D:47:VAL:HG23	2.15	0.47
4:E:109:VAL:HG13	4:E:110:VAL:N	2.29	0.47
4:E:165:LEU:HD13	4:E:190:VAL:HG13	1.97	0.47
5:G:416:MET:HG2	5:G:466:LEU:CD2	2.40	0.47
6:H:175:PHE:O	6:H:179:VAL:HG23	2.14	0.47
6:H:239:LEU:HD22	6:H:319:LEU:CD1	2.41	0.47
6:H:36:VAL:O	6:H:95:THR:HG21	2.14	0.47
7:Q:187:CYS:SG	7:Q:217:VAL:HG13	2.54	0.47
7:Q:390:ARG:HA	7:Q:390:ARG:NE	2.30	0.47
1:A:132:ILE:HD12	1:A:511:VAL:HG22	1.97	0.47
1:A:85:GLU:HB3	1:A:512:LYS:NZ	2.30	0.47
2:B:232:ILE:HD12	2:B:288:ASN:O	2.15	0.47
2:B:367:LEU:C	2:B:369:GLU:H	2.18	0.47
4:E:244:GLU:HB3	4:E:245:ASP:H	1.54	0.47
5:G:319:ASP:O	5:G:323:ILE:HG13	2.14	0.47
7:Q:188:VAL:HG11	7:Q:399:PHE:CG	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:204:VAL:HG11	7:Q:389:GLU:HG3	1.97	0.47
1:A:75:LEU:HD13	1:A:94:VAL:HG13	1.96	0.47
2:B:276:LYS:HB2	2:B:299:TYR:HE2	1.80	0.47
3:D:156:ARG:HB3	3:D:424:LEU:CD1	2.44	0.47
3:D:49:ASP:O	3:D:52:ARG:HB3	2.15	0.47
4:E:298:ASN:O	4:E:320:PRO:HD2	2.15	0.47
4:E:428:SER:HB2	4:E:487:PRO:HB3	1.97	0.47
4:E:522:GLN:CD	4:E:522:GLN:N	2.69	0.47
5:G:471:THR:HG22	5:G:471:THR:O	2.14	0.47
6:H:144:LYS:HD3	6:H:154:LEU:HD11	1.97	0.47
6:H:186:LEU:HD12	6:H:186:LEU:H	1.80	0.47
7:Q:409:VAL:N	7:Q:499:ASP:O	2.43	0.47
8:Z:382:HIS:O	8:Z:385:THR:HB	2.15	0.47
2:B:111:ARG:HA	2:B:114:GLU:OE2	2.15	0.47
2:B:209:LEU:HD21	2:B:382:ILE:CG2	2.38	0.47
2:B:281:ARG:NH1	2:B:281:ARG:HG2	2.29	0.47
2:B:288:ASN:N	2:B:288:ASN:ND2	2.62	0.47
3:D:174:LEU:HD13	3:D:186:LEU:HB2	1.97	0.47
4:E:417:ARG:HG3	4:E:417:ARG:HH11	1.79	0.47
4:E:61:MET:CE	4:E:81:MET:HB2	2.45	0.47
5:G:177:LEU:HD23	5:G:177:LEU:C	2.35	0.47
7:Q:188:VAL:HB	7:Q:399:PHE:CE2	2.49	0.47
1:A:12:SER:HB2	1:A:17:ILE:CB	2.32	0.46
1:A:355:ARG:HA	1:A:359:ASP:O	2.15	0.46
1:A:423:LEU:HD13	1:A:441:PHE:CD2	2.50	0.46
1:A:526:ARG:HD2	3:D:59:GLY:O	2.14	0.46
2:B:454:ALA:CB	2:B:480:MET:SD	2.98	0.46
2:B:83:VAL:HA	2:B:86:ASP:OD2	2.14	0.46
3:D:154:MET:HB3	3:D:492:LYS:CD	2.44	0.46
3:D:185:LEU:HD22	3:D:222:ASP:OD1	2.15	0.46
3:D:348:VAL:HG21	3:D:354:PHE:HA	1.97	0.46
3:D:173:SER:CB	3:D:414:VAL:HG21	2.45	0.46
4:E:456:GLU:O	4:E:459:PRO:HD2	2.14	0.46
6:H:233:HIS:CG	6:H:234:ASN:N	2.83	0.46
6:H:66:LEU:HB3	6:H:80:VAL:HG22	1.97	0.46
7:Q:364:LYS:O	7:Q:365:HIS:HB2	2.15	0.46
7:Q:525:ILE:CG2	8:Z:67:MET:HG2	2.46	0.46
6:H:522:ASN:CG	7:Q:77:GLU:HB2	2.35	0.46
1:A:395:ALA:HA	1:A:398:VAL:HG22	1.97	0.46
1:A:474:ALA:O	1:A:485:TRP:NE1	2.48	0.46
2:B:516:ARG:HG2	4:E:58:ASP:N	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:61:LEU:HD21	2:B:63:VAL:HG23	1.97	0.46
2:B:95:VAL:HG23	2:B:96:GLY:N	2.21	0.46
3:D:148:ILE:O	3:D:152:THR:HG23	2.15	0.46
3:D:286:ILE:HG21	3:D:315:LEU:HB2	1.98	0.46
4:E:18:ILE:HG22	4:E:19:ILE:N	2.30	0.46
4:E:521:THR:HB	4:E:522:GLN:NE2	2.30	0.46
4:E:90:LEU:HD23	4:E:93:GLU:OE1	2.15	0.46
5:G:157:ASN:O	5:G:161:THR:HG23	2.14	0.46
5:G:163:LYS:H	5:G:166:SER:HB3	1.79	0.46
5:G:46:MET:HB3	8:Z:517:LEU:O	2.16	0.46
5:G:499:LEU:O	5:G:503:LEU:N	2.45	0.46
6:H:198:LYS:HZ3	6:H:217:LYS:CG	2.25	0.46
6:H:241:ASN:HD22	6:H:241:ASN:HA	1.52	0.46
6:H:228:GLN:OE1	6:H:309:PHE:HA	2.15	0.46
6:H:213:GLY:O	6:H:371:THR:N	2.49	0.46
7:Q:33:ILE:HG21	7:Q:116:GLU:OE2	2.14	0.46
1:A:241:LEU:HG	1:A:331:LEU:CD2	2.44	0.46
2:B:455:GLY:HA3	3:D:135:ILE:HG12	1.97	0.46
4:E:236:HIS:CD2	4:E:237:PRO:HD2	2.50	0.46
4:E:62:VAL:HA	4:E:67:ASP:O	2.16	0.46
5:G:200:ARG:NH1	5:G:202:GLU:HB2	2.31	0.46
5:G:203:LYS:HB2	5:G:384:LEU:CG	2.45	0.46
5:G:433:GLU:O	5:G:436:PRO:HD2	2.15	0.46
4:E:20:LYS:HZ3	6:H:32:ILE:HG12	1.80	0.46
6:H:286:ALA:HB2	6:H:342:LEU:HD21	1.98	0.46
6:H:349:GLU:HG3	6:H:360:PHE:CD2	2.49	0.46
7:Q:20:LYS:HD2	7:Q:525:ILE:HG13	1.97	0.46
8:Z:188:LEU:HD11	8:Z:396:ARG:HD3	1.98	0.46
8:Z:349:LEU:HG	8:Z:351:TYR:HD2	1.80	0.46
7:Q:520:ARG:O	8:Z:43:THR:HB	2.16	0.46
1:A:496:ARG:HG2	1:A:497:ASP:N	2.31	0.46
1:A:90:THR:O	1:A:93:VAL:HG12	2.15	0.46
3:D:236:VAL:HG21	3:D:329:LYS:H	1.80	0.46
1:A:2:GLU:CD	3:D:44:ALA:H	2.16	0.46
4:E:192:ALA:O	4:E:196:VAL:HG22	2.15	0.46
4:E:227:GLY:HA2	4:E:380:SER:OG	2.16	0.46
7:Q:16:LYS:HD2	7:Q:525:ILE:HB	1.96	0.46
7:Q:393:ASP:O	7:Q:396:VAL:HB	2.15	0.46
8:Z:48:VAL:CG2	8:Z:54:ILE:HG12	2.39	0.46
2:B:187:VAL:HG21	2:B:397:LEU:CD1	2.43	0.46
2:B:320:VAL:HA	2:B:323:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:335:ASP:O	3:D:339:ILE:HG13	2.15	0.46
3:D:252:ILE:HD12	3:D:351:VAL:HA	1.98	0.46
4:E:167:GLN:O	4:E:171:THR:HG23	2.15	0.46
4:E:193:VAL:O	4:E:197:ALA:HB2	2.15	0.46
5:G:129:ALA:O	5:G:132:ASP:HB2	2.16	0.46
5:G:49:MET:HB3	8:Z:518:VAL:HG11	1.97	0.46
6:H:163:LEU:O	6:H:166:LYS:HB2	2.15	0.46
6:H:226:GLU:HB3	6:H:227:MET:HE3	1.97	0.46
7:Q:296:ARG:NH1	7:Q:315:LEU:HD11	2.31	0.46
8:Z:179:ILE:HD13	8:Z:191:VAL:HG23	1.97	0.46
8:Z:34:LEU:HD11	8:Z:60:GLY:HA2	1.98	0.46
1:A:370:ARG:C	1:A:372:SER:H	2.18	0.46
2:B:516:ARG:CG	4:E:57:LEU:HA	2.45	0.46
3:D:258:ALA:HB2	3:D:286:ILE:HG13	1.98	0.46
1:A:533:LEU:HD12	3:D:66:ASP:HA	1.96	0.46
4:E:145:ILE:HD12	4:E:514:LYS:HG3	1.96	0.46
6:H:238:ALA:O	6:H:289:VAL:HG13	2.14	0.46
6:H:350:GLU:OE2	6:H:357:ARG:HD2	2.16	0.46
6:H:197:ILE:CG2	6:H:386:GLU:HG3	2.44	0.46
7:Q:466:LYS:O	7:Q:470:VAL:HG23	2.16	0.46
1:A:423:LEU:HD13	1:A:441:PHE:HD2	1.79	0.46
1:A:467:LEU:HB2	1:A:488:LEU:HD21	1.97	0.46
2:B:413:SER:O	2:B:417:MET:HG2	2.16	0.46
3:D:100:ALA:O	3:D:104:GLU:HG3	2.15	0.46
3:D:251:LEU:HB3	3:D:347:PRO:HA	1.97	0.46
3:D:217:LEU:HG	3:D:401:ILE:HD12	1.98	0.46
4:E:131:ILE:HD12	4:E:131:ILE:H	1.81	0.46
4:E:42:LYS:NZ	4:E:46:ASN:HD21	2.13	0.46
4:E:489:LEU:HD23	4:E:490:GLY:N	2.30	0.46
5:G:448:PRO:O	5:G:451:LEU:HB3	2.16	0.46
7:Q:197:PHE:CB	7:Q:403:THR:HG21	2.46	0.46
8:Z:123:PHE:CE1	8:Z:439:ALA:HB3	2.51	0.46
8:Z:475:GLN:HG3	8:Z:475:GLN:O	2.15	0.46
8:Z:34:LEU:HG	8:Z:93:THR:HG23	1.97	0.46
1:A:176:VAL:O	1:A:180:LYS:HB2	2.16	0.46
1:A:220:VAL:O	1:A:225:MET:SD	2.74	0.46
1:A:520:ALA:O	1:A:524:ILE:HG13	2.16	0.46
2:B:231:ARG:HH21	2:B:348:LEU:CD1	2.27	0.46
2:B:36:GLY:O	2:B:104:VAL:HG22	2.15	0.46
2:B:520:ILE:HD12	4:E:60:MET:N	2.30	0.46
3:D:195:MET:SD	3:D:196:LYS:HG3	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:315:LEU:HD23	4:E:315:LEU:O	2.16	0.46
4:E:317:ASN:O	4:E:318:ASP:HB2	2.15	0.46
6:H:223:ALA:O	6:H:311:ALA:HA	2.16	0.46
6:H:315:PRO:HB2	6:H:318:ASP:OD2	2.15	0.46
6:H:122:ILE:HG23	6:H:511:CYS:SG	2.56	0.46
1:A:190:TYR:HB3	1:A:400:LYS:HG3	1.97	0.46
1:A:275:ILE:HG23	1:A:300:PHE:CE1	2.50	0.46
3:D:174:LEU:HD12	3:D:187:SER:OG	2.16	0.46
3:D:24:LYS:CE	3:D:28:GLN:HE22	2.29	0.46
1:A:2:GLU:OE2	3:D:39:SER:O	2.34	0.46
4:E:22:GLN:HG3	4:E:23:ASP:O	2.16	0.46
4:E:325:VAL:HB	4:E:330:ILE:HD11	1.98	0.46
6:H:411:ALA:HB2	6:H:487:ASN:HD21	1.81	0.46
6:H:36:VAL:CG2	6:H:95:THR:HG23	2.46	0.46
7:Q:13:GLN:N	7:Q:13:GLN:NE2	2.63	0.46
7:Q:168:VAL:O	7:Q:173:TYR:CE1	2.69	0.46
7:Q:148:CYS:HB2	7:Q:476:LYS:NZ	2.31	0.46
7:Q:16:LYS:HD2	7:Q:525:ILE:CB	2.45	0.46
8:Z:141:LYS:O	8:Z:142:GLU:HB3	2.16	0.46
8:Z:175:SER:O	8:Z:179:ILE:HG23	2.16	0.46
8:Z:46:MET:CG	8:Z:54:ILE:HG23	2.45	0.46
1:A:132:ILE:C	1:A:134:GLU:H	2.19	0.46
3:D:36:ILE:HD11	3:D:40:ASN:HD21	1.81	0.46
3:D:416:ARG:HH11	3:D:420:LYS:HZ2	1.63	0.46
3:D:472:ALA:HB2	3:D:498:VAL:HB	1.98	0.46
3:D:475:ASN:HB3	3:D:478:SER:HB3	1.97	0.46
3:D:61:ASP:C	3:D:62:LYS:HD3	2.36	0.46
3:D:64:ILE:HG21	3:D:83:GLN:HB3	1.97	0.46
4:E:518:SER:HA	4:E:522:GLN:HE21	1.81	0.46
5:G:84:SER:HB2	5:G:95:THR:CG2	2.45	0.46
6:H:290:LEU:HD11	6:H:361:PHE:CE2	2.51	0.46
6:H:43:ARG:HH21	6:H:480:ASN:HA	1.77	0.46
7:Q:453:ALA:CB	7:Q:463:VAL:HG11	2.46	0.46
8:Z:123:PHE:HD1	8:Z:440:PHE:HB2	1.81	0.46
8:Z:218:HIS:HB3	8:Z:221:MET:CG	2.43	0.46
8:Z:24:ILE:HD13	8:Z:107:ASP:HB2	1.97	0.46
8:Z:217:ARG:HG2	8:Z:302:LEU:HD22	1.98	0.46
2:B:239:ILE:HG22	2:B:331:ILE:HG23	1.98	0.45
3:D:290:VAL:HG11	3:D:319:PHE:C	2.36	0.45
5:G:26:ASN:OD1	5:G:516:LEU:HB3	2.16	0.45
6:H:521:LYS:O	6:H:522:ASN:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:227:THR:HB	7:Q:230:ASP:CG	2.36	0.45
8:Z:161:HIS:C	8:Z:163:GLU:N	2.67	0.45
8:Z:126:ALA:HB2	8:Z:437:VAL:HA	1.97	0.45
2:B:396:VAL:O	2:B:400:THR:HG23	2.16	0.45
3:D:364:LEU:O	3:D:364:LEU:HG	2.17	0.45
4:E:236:HIS:HB3	4:E:239:MET:CG	2.42	0.45
4:E:443:LEU:HD23	4:E:444:GLU:H	1.80	0.45
5:G:136:THR:O	5:G:140:ILE:HD12	2.16	0.45
5:G:296:ILE:HG13	5:G:313:ARG:HB3	1.98	0.45
6:H:300:THR:O	6:H:303:PHE:HB2	2.16	0.45
7:Q:85:MET:O	7:Q:88:MET:HE2	2.16	0.45
7:Q:73:LEU:HD12	7:Q:90:SER:OG	2.15	0.45
7:Q:99:ASP:OD2	7:Q:398:THR:HG22	2.16	0.45
8:Z:135:GLU:HG3	8:Z:138:LYS:HZ2	1.80	0.45
8:Z:123:PHE:HE1	8:Z:439:ALA:HB3	1.80	0.45
1:A:286:ILE:HB	1:A:307:ALA:CB	2.46	0.45
1:A:118:ILE:CG2	1:A:522:ILE:HG23	2.45	0.45
2:B:415:MET:HE1	2:B:466:ARG:HB2	1.97	0.45
3:D:157:PRO:HA	3:D:423:ALA:HA	1.98	0.45
3:D:170:ALA:O	3:D:174:LEU:HG	2.16	0.45
3:D:302:LEU:HD13	3:D:339:ILE:HD13	1.98	0.45
3:D:462:GLU:O	3:D:465:PRO:HG2	2.15	0.45
5:G:165:ILE:CD1	5:G:387:VAL:HG13	2.45	0.45
6:H:190:LEU:CD2	6:H:397:ARG:HB2	2.40	0.45
6:H:445:ILE:N	6:H:446:PRO:HD2	2.30	0.45
6:H:64:THR:O	6:H:68:LEU:HD12	2.15	0.45
8:Z:447:ILE:N	8:Z:448:PRO:HD2	2.31	0.45
7:Q:13:GLN:HG3	8:Z:71:HIS:HA	1.98	0.45
8:Z:99:ILE:O	8:Z:103:LEU:HG	2.17	0.45
2:B:368:GLY:C	2:B:370:ALA:H	2.20	0.45
2:B:219:LEU:HD22	2:B:374:VAL:CG2	2.47	0.45
3:D:216:LYS:CE	3:D:376:LEU:HD11	2.47	0.45
5:G:160:ILE:HG23	5:G:165:ILE:CG2	2.45	0.45
5:G:347:ALA:O	5:G:349:LEU:HB2	2.16	0.45
5:G:85:ARG:HG3	5:G:85:ARG:HH11	1.82	0.45
6:H:366:LYS:HB3	6:H:368:LYS:HE3	1.98	0.45
4:E:529:LYS:HA	6:H:45:MET:SD	2.56	0.45
6:H:92:ASP:CG	6:H:93:GLY:H	2.20	0.45
7:Q:223:PHE:CZ	7:Q:316:ASN:HA	2.51	0.45
7:Q:206:LYS:HD3	7:Q:389:GLU:CD	2.37	0.45
8:Z:333:LEU:HG	8:Z:338:ASP:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:82:THR:HG22	8:Z:86:ASP:OD2	2.16	0.45
1:A:329:SER:OG	1:A:330:THR:N	2.50	0.45
2:B:452:ASP:C	2:B:454:ALA:H	2.19	0.45
2:B:61:LEU:HD23	2:B:61:LEU:O	2.17	0.45
3:D:32:LYS:HZ1	3:D:33:PRO:HD2	1.80	0.45
3:D:446:LEU:HD23	3:D:454:ILE:CD1	2.45	0.45
4:E:188:ILE:HG21	4:E:385:ILE:HG23	1.98	0.45
4:E:511:ILE:HA	4:E:514:LYS:NZ	2.32	0.45
5:G:27:ILE:HG13	5:G:106:LEU:HB3	1.98	0.45
6:H:163:LEU:HB2	6:H:172:LYS:HB2	1.98	0.45
6:H:239:LEU:HD21	6:H:290:LEU:HD12	1.99	0.45
8:Z:172:VAL:HG13	8:Z:395:LEU:HD23	1.99	0.45
1:A:470:PHE:HD2	1:A:495:PRO:HB2	1.81	0.45
1:A:75:LEU:HD13	1:A:94:VAL:CG1	2.47	0.45
2:B:139:GLN:HA	2:B:142:LEU:CD1	2.47	0.45
4:E:306:PHE:HB2	4:E:323:ARG:CB	2.42	0.45
4:E:236:HIS:HD2	4:E:315:LEU:HD12	1.76	0.45
4:E:443:LEU:H	4:E:443:LEU:HD22	1.82	0.45
5:G:107:SER:O	5:G:110:GLU:HG2	2.17	0.45
6:H:37:ARG:HG3	6:H:99:LEU:CD2	2.47	0.45
7:Q:110:ALA:O	7:Q:114:LEU:HD23	2.17	0.45
7:Q:16:LYS:HG3	7:Q:525:ILE:HD13	1.99	0.45
8:Z:127:LYS:HZ2	8:Z:509:THR:HB	1.81	0.45
1:A:129:VAL:O	1:A:132:ILE:HB	2.17	0.45
1:A:297:LEU:O	1:A:301:VAL:HG23	2.16	0.45
1:A:449:PRO:HA	1:A:452:LEU:HD12	1.99	0.45
1:A:487:GLY:HA3	1:A:498:ASN:ND2	2.31	0.45
2:B:11:ILE:HG12	4:E:85:HIS:CB	2.47	0.45
3:D:224:CYS:HA	3:D:392:VAL:O	2.16	0.45
3:D:26:ALA:C	3:D:28:GLN:H	2.20	0.45
3:D:32:LYS:HZ3	3:D:33:PRO:HD2	1.77	0.45
4:E:153:ASP:O	4:E:154:SER:C	2.55	0.45
6:H:289:VAL:O	6:H:310:CYS:HA	2.17	0.45
7:Q:134:ILE:HD12	7:Q:434:GLU:CD	2.37	0.45
8:Z:148:LEU:HD22	8:Z:398:VAL:HG13	1.99	0.45
8:Z:44:MET:HG3	8:Z:56:LEU:HD11	1.99	0.45
2:B:9:VAL:HG13	4:E:36:SER:CB	2.47	0.45
3:D:108:GLY:O	3:D:110:THR:N	2.50	0.45
4:E:254:PRO:HB3	4:E:304:TRP:CB	2.46	0.45
5:G:453:GLN:C	5:G:455:CYS:H	2.20	0.45
5:G:50:LEU:C	5:G:51:LEU:HD12	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:228:GLN:O	6:H:230:LYS:N	2.50	0.45
6:H:276:ASP:O	6:H:280:LYS:HG3	2.17	0.45
6:H:497:MET:CE	6:H:501:ASN:HB2	2.46	0.45
6:H:119:GLN:HG2	7:Q:50:ASN:HD22	1.81	0.45
8:Z:277:LEU:HD22	8:Z:341:PRO:HD3	1.98	0.45
2:B:172:LEU:CD1	2:B:209:LEU:HD13	2.47	0.45
2:B:94:GLU:O	2:B:395:CYS:HB3	2.16	0.45
3:D:119:LEU:HD12	3:D:529:VAL:CG2	2.39	0.45
3:D:31:ASP:CB	3:D:36:ILE:HB	2.29	0.45
3:D:161:SER:N	3:D:422:ARG:NH1	2.65	0.45
3:D:81:LEU:HD13	3:D:95:VAL:HA	1.99	0.45
4:E:224:LEU:HD12	4:E:384:THR:O	2.16	0.45
4:E:42:LYS:HG2	4:E:46:ASN:ND2	2.32	0.45
4:E:446:TYR:CD1	4:E:446:TYR:N	2.85	0.45
5:G:242:ASP:O	5:G:293:GLU:HB3	2.17	0.45
5:G:467:ARG:HG3	5:G:467:ARG:HH11	1.81	0.45
5:G:48:LYS:O	5:G:59:MET:HA	2.17	0.45
6:H:136:ILE:O	6:H:140:ALA:HB2	2.17	0.45
7:Q:445:PHE:HA	7:Q:448:ILE:HD13	1.99	0.45
7:Q:504:LYS:O	7:Q:508:ILE:HD12	2.17	0.45
7:Q:514:ALA:O	7:Q:518:VAL:HG23	2.16	0.45
8:Z:230:ILE:HG13	8:Z:324:LEU:HD11	1.99	0.45
8:Z:352:GLU:HA	8:Z:360:PHE:O	2.17	0.45
7:Q:126:SER:HB3	8:Z:41:LYS:HD3	1.99	0.45
8:Z:114:LEU:CD2	8:Z:432:ARG:HD3	2.44	0.45
1:A:213:GLY:HA3	1:A:365:LYS:CB	2.46	0.45
1:A:232:ALA:O	1:A:347:GLN:HA	2.17	0.45
1:A:211:ILE:N	1:A:374:SER:O	2.50	0.45
1:A:390:ARG:HD2	1:A:390:ARG:HA	1.81	0.45
2:B:280:GLU:O	2:B:284:LYS:HG3	2.17	0.45
3:D:300:VAL:O	3:D:300:VAL:HG12	2.16	0.45
3:D:484:ARG:HH11	3:D:484:ARG:HG3	1.82	0.45
4:E:219:LEU:O	4:E:222:THR:HG23	2.16	0.45
4:E:48:MET:HG2	4:E:110:VAL:HG11	1.97	0.45
5:G:151:THR:HA	5:G:154:ASN:HD22	1.82	0.45
5:G:183:VAL:HG12	5:G:370:LYS:O	2.17	0.45
6:H:179:VAL:O	6:H:183:VAL:HG23	2.17	0.45
6:H:214:VAL:HA	6:H:371:THR:CB	2.47	0.45
6:H:407:ALA:HB1	6:H:487:ASN:HB2	1.99	0.45
7:Q:223:PHE:C	7:Q:224:LYS:HD2	2.36	0.45
7:Q:407:ARG:HD2	7:Q:501:TYR:CD2	2.53	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:521:VAL:CG1	7:Q:524:ILE:HD13	2.46	0.45
8:Z:186:ILE:HB	8:Z:399:LYS:HG3	1.99	0.45
8:Z:304:ALA:O	8:Z:308:GLU:HG2	2.17	0.45
1:A:168:PHE:HZ	1:A:205:GLN:HB2	1.81	0.44
1:A:180:LYS:CD	1:A:190:TYR:HB2	2.47	0.44
1:A:206:MET:HE2	1:A:206:MET:HA	1.99	0.44
2:B:472:GLY:C	2:B:473:LYS:HD2	2.38	0.44
3:D:136:ILE:HG22	3:D:533:LEU:HD13	1.99	0.44
3:D:420:LYS:CD	3:D:516:LEU:HD11	2.46	0.44
3:D:483:LEU:HD22	3:D:496:ILE:HG13	1.99	0.44
3:D:77:GLY:HA2	3:D:80:ILE:HD12	1.99	0.44
4:E:357:GLY:HA3	4:E:376:GLN:HB2	1.98	0.44
5:G:27:ILE:HG22	5:G:28:ASN:N	2.32	0.44
6:H:417:SER:CA	6:H:439:ALA:HB1	2.45	0.44
8:Z:127:LYS:HD2	8:Z:509:THR:CB	2.47	0.44
5:G:72:VAL:HG13	8:Z:5:LYS:O	2.17	0.44
5:G:70:ILE:CG2	8:Z:6:THR:HG22	2.46	0.44
1:A:190:TYR:HD2	1:A:400:LYS:CB	2.23	0.44
1:A:233:LYS:HB3	1:A:345:LEU:HD13	1.98	0.44
1:A:395:ALA:O	1:A:398:VAL:HG22	2.17	0.44
1:A:502:GLY:O	1:A:504:PHE:HD1	2.00	0.44
2:B:102:VAL:HG13	2:B:103:THR:N	2.32	0.44
2:B:385:GLU:OE1	2:B:385:GLU:HA	2.17	0.44
2:B:44:GLY:C	2:B:46:LYS:H	2.20	0.44
2:B:72:LYS:HZ3	2:B:89:ARG:HG3	1.77	0.44
3:D:123:CYS:SG	3:D:533:LEU:HD22	2.57	0.44
3:D:155:SER:OG	3:D:425:ILE:HG23	2.17	0.44
3:D:444:ARG:O	3:D:444:ARG:HG2	2.18	0.44
3:D:88:HIS:HA	3:D:89:PRO:HD3	1.90	0.44
4:E:297:ALA:HB2	4:E:353:LEU:CD2	2.46	0.44
4:E:510:LEU:HG	4:E:514:LYS:HZ1	1.78	0.44
4:E:86:GLN:H	4:E:86:GLN:CD	2.20	0.44
5:G:101:LEU:HD23	5:G:446:VAL:CG2	2.47	0.44
5:G:137:LEU:HB3	5:G:499:LEU:CD1	2.47	0.44
5:G:145:ASP:OD2	5:G:148:ASN:HB2	2.17	0.44
5:G:204:ILE:HD13	5:G:355:ILE:CG2	2.35	0.44
5:G:366:CYS:O	5:G:369:PRO:HD3	2.17	0.44
5:G:458:SER:HB3	5:G:461:ARG:HB3	2.00	0.44
1:A:27:SER:CB	5:G:9:VAL:HG11	2.41	0.44
6:H:135:LYS:HD2	6:H:135:LYS:HA	1.88	0.44
6:H:455:PHE:HB2	6:H:482:GLU:CD	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:204:VAL:HG22	7:Q:375:ILE:HD12	2.00	0.44
1:A:30:ASN:O	1:A:33:LYS:HB3	2.16	0.44
1:A:137:ILE:HB	1:A:408:VAL:O	2.17	0.44
1:A:453:ALA:HB1	1:A:458:GLN:O	2.17	0.44
1:A:5:LEU:HD21	1:A:531:ILE:HD13	1.99	0.44
1:A:82:GLN:NE2	1:A:86:VAL:CG2	2.81	0.44
2:B:455:GLY:CA	3:D:135:ILE:HD11	2.47	0.44
3:D:33:PRO:HA	3:D:536:ASP:OD2	2.17	0.44
3:D:436:ALA:O	3:D:458:ALA:HB1	2.18	0.44
4:E:139:GLN:O	4:E:143:ILE:HG13	2.18	0.44
4:E:20:LYS:HZ2	6:H:31:VAL:CG1	2.31	0.44
4:E:312:HIS:CE1	4:E:316:GLN:HE22	2.35	0.44
4:E:61:MET:HE2	4:E:81:MET:HB2	1.99	0.44
4:E:40:ALA:CB	4:E:87:ILE:HG21	2.47	0.44
5:G:130:LEU:HA	5:G:133:MET:CE	2.46	0.44
5:G:172:ALA:HA	5:G:175:ILE:HD12	2.00	0.44
5:G:424:GLU:HA	5:G:427:LYS:HZ1	1.81	0.44
5:G:466:LEU:HG	5:G:487:LEU:CD1	2.44	0.44
6:H:46:ASP:O	6:H:47:LYS:HD3	2.17	0.44
8:Z:59:ASP:OD2	8:Z:62:VAL:HG23	2.18	0.44
2:B:183:ALA:O	2:B:187:VAL:HG23	2.18	0.44
2:B:326:VAL:CG1	2:B:365:VAL:HG11	2.35	0.44
3:D:439:LEU:HD13	3:D:457:PHE:HD2	1.82	0.44
3:D:532:ILE:O	3:D:535:ILE:HB	2.18	0.44
4:E:405:ALA:O	4:E:408:VAL:HG22	2.18	0.44
4:E:511:ILE:O	4:E:515:GLN:HB3	2.17	0.44
5:G:407:LEU:HA	5:G:499:LEU:H	1.81	0.44
7:Q:32:ASN:OD1	7:Q:82:ALA:HB2	2.17	0.44
7:Q:434:GLU:O	7:Q:438:ILE:HG13	2.17	0.44
8:Z:196:MET:HG2	8:Z:360:PHE:CZ	2.52	0.44
8:Z:186:ILE:HD12	8:Z:399:LYS:O	2.17	0.44
1:A:222:SER:C	1:A:224:GLY:H	2.21	0.44
1:A:230:VAL:HB	1:A:231:ASN:H	1.60	0.44
2:B:141:LEU:O	2:B:145:ALA:HB2	2.18	0.44
2:B:337:HIS:N	2:B:338:PRO:CD	2.81	0.44
3:D:235:LYS:HG2	3:D:367:GLU:CD	2.38	0.44
3:D:217:LEU:HA	3:D:401:ILE:HD11	1.98	0.44
3:D:414:VAL:HG23	3:D:415:ILE:N	2.33	0.44
4:E:410:ARG:CA	4:E:413:ILE:HG22	2.47	0.44
2:B:518:ASP:C	4:E:59:LYS:HZ2	2.21	0.44
5:G:292:THR:HB	5:G:313:ARG:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:430:THR:HA	5:G:434:GLN:NE2	2.31	0.44
5:G:50:LEU:HD11	5:G:66:ILE:HG23	2.00	0.44
6:H:9:LEU:HD13	6:H:13:THR:HG22	2.00	0.44
7:Q:119:LEU:HD21	7:Q:125:VAL:HA	1.99	0.44
7:Q:22:PHE:HB3	7:Q:525:ILE:HD12	2.00	0.44
7:Q:34:GLN:HA	7:Q:37:LYS:HE2	1.99	0.44
7:Q:59:HIS:C	7:Q:61:GLU:H	2.21	0.44
7:Q:80:HIS:CE1	7:Q:82:ALA:HB3	2.52	0.44
8:Z:87:ILE:N	8:Z:87:ILE:CD1	2.81	0.44
2:B:458:SER:O	2:B:462:VAL:HG23	2.17	0.44
3:D:137:SER:HG	3:D:533:LEU:HB2	1.83	0.44
3:D:315:LEU:H	3:D:315:LEU:CD2	2.10	0.44
3:D:229:GLY:HA3	3:D:380:THR:HA	1.99	0.44
3:D:429:GLY:O	3:D:433:ILE:HG12	2.18	0.44
4:E:132:ARG:HG2	4:E:443:LEU:HG	1.99	0.44
4:E:155:VAL:HG21	4:E:412:LEU:HD11	1.98	0.44
4:E:511:ILE:HA	4:E:514:LYS:HZ3	1.82	0.44
5:G:130:LEU:HD21	5:G:507:LYS:HA	2.00	0.44
6:H:366:LYS:HD3	6:H:368:LYS:HZ2	1.77	0.44
6:H:214:VAL:HG12	6:H:371:THR:OG1	2.18	0.44
6:H:391:ASP:HA	6:H:394:MET:CG	2.48	0.44
6:H:497:MET:HE3	6:H:500:ILE:HB	1.99	0.44
1:A:18:ARG:HH12	1:A:108:VAL:HG13	1.83	0.44
1:A:530:LEU:HD11	3:D:63:MET:O	2.17	0.44
1:A:533:LEU:CD1	3:D:66:ASP:HA	2.47	0.44
2:B:189:ARG:NH1	2:B:189:ARG:HB3	2.33	0.44
2:B:196:LEU:HD21	2:B:394:LEU:O	2.18	0.44
2:B:29:PHE:CE1	2:B:515:LEU:HA	2.52	0.44
2:B:397:LEU:O	2:B:401:VAL:HG13	2.17	0.44
2:B:408:TYR:CD1	2:B:494:THR:HG22	2.52	0.44
2:B:521:ILE:O	4:E:62:VAL:HB	2.18	0.44
4:E:164:PRO:O	4:E:167:GLN:HB2	2.18	0.44
2:B:520:ILE:CD1	4:E:60:MET:HB3	2.38	0.44
4:E:83:VAL:HG13	4:E:88:ALA:CB	2.47	0.44
5:G:374:ILE:HD13	5:G:391:LEU:HD21	1.99	0.44
5:G:415:GLU:H	5:G:415:GLU:CD	2.21	0.44
5:G:41:LEU:HD22	5:G:100:ILE:HD12	2.00	0.44
5:G:133:MET:SD	5:G:444:LEU:HD11	2.58	0.44
5:G:462:LEU:HD13	5:G:462:LEU:O	2.18	0.44
5:G:64:ASN:HD21	5:G:68:ARG:HD2	1.83	0.44
6:H:37:ARG:NH2	6:H:444:ILE:HG13	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:27:GLU:O	7:Q:31:ARG:HG3	2.17	0.44
7:Q:297:VAL:HG23	7:Q:314:ARG:HB3	2.00	0.44
7:Q:225:LYS:CD	7:Q:352:LEU:HD13	2.48	0.44
8:Z:356:GLY:O	8:Z:357:GLU:HB2	2.18	0.44
8:Z:204:THR:HG22	8:Z:377:LYS:N	2.32	0.44
8:Z:470:HIS:HA	8:Z:477:VAL:CG2	2.48	0.44
1:A:16:ALA:O	1:A:20:GLN:HG2	2.18	0.44
1:A:408:VAL:HG23	1:A:505:GLU:C	2.37	0.44
1:A:448:ILE:N	1:A:449:PRO:HD2	2.33	0.44
2:B:155:PHE:CD2	2:B:157:GLN:HB3	2.53	0.44
2:B:439:TYR:OH	2:B:504:LEU:HD22	2.17	0.44
3:D:78:ALA:CB	3:D:109:THR:HG21	2.45	0.44
3:D:179:VAL:HB	3:D:186:LEU:CD1	2.47	0.44
3:D:339:ILE:HG23	3:D:343:ILE:HD12	2.00	0.44
3:D:430:ALA:HB1	3:D:492:LYS:O	2.17	0.44
3:D:144:LEU:HD23	3:D:526:THR:OG1	2.17	0.44
5:G:325:ARG:HG2	5:G:325:ARG:NH1	2.32	0.44
5:G:44:LYS:CD	5:G:455:CYS:HA	2.48	0.44
6:H:117:HIS:NE2	7:Q:454:GLU:O	2.51	0.44
7:Q:160:VAL:HG11	7:Q:185:GLN:HG2	1.99	0.44
8:Z:274:ILE:HD11	8:Z:336:LEU:CD2	2.48	0.44
1:A:392:LEU:O	1:A:396:LEU:HG	2.18	0.44
1:A:513:SER:OG	1:A:514:LEU:N	2.51	0.44
2:B:375:LEU:CD1	2:B:387:GLU:HA	2.48	0.44
2:B:398:ALA:O	2:B:401:VAL:HG22	2.18	0.44
3:D:289:LEU:O	3:D:293:ILE:HG13	2.17	0.44
3:D:226:LEU:HA	3:D:390:THR:O	2.17	0.44
3:D:76:ASP:OD2	3:D:78:ALA:HB3	2.18	0.44
4:E:208:LEU:HD22	4:E:381:ARG:O	2.17	0.44
4:E:478:ARG:O	4:E:482:VAL:HG23	2.18	0.44
4:E:102:ILE:HG12	4:E:515:GLN:OE1	2.18	0.44
4:E:25:LYS:CE	4:E:536:PRO:HB3	2.48	0.44
4:E:20:LYS:HZ1	6:H:31:VAL:HB	1.76	0.44
7:Q:234:VAL:HG11	7:Q:289:ASN:CG	2.38	0.44
8:Z:30:LEU:HD21	8:Z:64:LEU:HD22	2.00	0.44
2:B:229:PRO:O	2:B:310:MET:HG3	2.17	0.43
3:D:193:ALA:HB2	3:D:226:LEU:HD11	2.00	0.43
2:B:48:MET:HB3	3:D:534:LYS:O	2.18	0.43
3:D:28:GLN:HG3	3:D:541:THR:CA	2.47	0.43
4:E:225:ILE:HG22	4:E:227:GLY:H	1.83	0.43
4:E:325:VAL:HG12	4:E:330:ILE:HG12	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:143:PRO:HA	5:G:406:GLN:OE1	2.17	0.43
6:H:208:SER:HA	6:H:375:ARG:HH11	1.82	0.43
6:H:521:LYS:O	6:H:522:ASN:HB2	2.18	0.43
8:Z:341:PRO:HA	8:Z:344:LEU:CD1	2.47	0.43
8:Z:470:HIS:ND1	8:Z:477:VAL:HB	2.32	0.43
8:Z:75:SER:O	8:Z:78:ALA:HB3	2.18	0.43
2:B:11:ILE:HD11	4:E:40:ALA:CA	2.48	0.43
2:B:61:LEU:HD23	2:B:61:LEU:C	2.39	0.43
2:B:68:ALA:HB2	2:B:99:THR:HG21	2.01	0.43
5:G:282:ILE:HG12	5:G:338:LEU:HD13	1.98	0.43
5:G:409:PRO:HA	5:G:495:ILE:O	2.17	0.43
5:G:79:SER:HA	5:G:82:GLU:OE1	2.17	0.43
6:H:431:GLN:O	6:H:435:ILE:HG13	2.17	0.43
6:H:72:VAL:HG12	6:H:72:VAL:O	2.18	0.43
6:H:9:LEU:HD23	7:Q:77:GLU:O	2.18	0.43
7:Q:125:VAL:O	7:Q:128:VAL:HB	2.17	0.43
7:Q:454:GLU:C	7:Q:456:SER:H	2.21	0.43
7:Q:460:ALA:HA	7:Q:463:VAL:CG1	2.48	0.43
7:Q:460:ALA:O	7:Q:464:ILE:HG13	2.18	0.43
7:Q:459:LYS:HE2	7:Q:461:ASN:HB2	2.00	0.43
8:Z:118:ILE:HG21	8:Z:432:ARG:CB	2.42	0.43
8:Z:142:GLU:HG3	8:Z:144:ASP:HB2	2.01	0.43
8:Z:168:LEU:HD23	8:Z:172:VAL:HG23	1.99	0.43
8:Z:321:MET:O	8:Z:325:THR:HG23	2.17	0.43
8:Z:331:ILE:HD12	8:Z:343:CYS:SG	2.57	0.43
8:Z:368:ASN:OD1	8:Z:370:ARG:HB2	2.18	0.43
7:Q:527:ALA:HB2	8:Z:66:GLU:O	2.17	0.43
1:A:285:VAL:HA	1:A:306:MET:O	2.18	0.43
2:B:52:LEU:HB2	2:B:62:MET:HB3	2.00	0.43
2:B:66:ASP:O	2:B:70:ILE:HG13	2.18	0.43
3:D:426:ALA:O	3:D:431:PRO:HD3	2.18	0.43
4:E:61:MET:O	4:E:69:THR:HB	2.19	0.43
5:G:233:ILE:N	5:G:233:ILE:HD12	2.33	0.43
6:H:242:VAL:HG22	6:H:243:GLU:N	2.32	0.43
7:Q:140:HIS:HB3	7:Q:505:TYR:HE1	1.83	0.43
7:Q:231:VAL:HG23	7:Q:311:MET:HB2	2.00	0.43
7:Q:140:HIS:CE1	7:Q:509:LYS:HB2	2.53	0.43
8:Z:225:VAL:HG21	8:Z:290:VAL:CG2	2.48	0.43
1:A:137:ILE:N	1:A:408:VAL:O	2.51	0.43
1:A:446:PRO:O	1:A:450:ASN:HB2	2.19	0.43
2:B:232:ILE:HG21	2:B:235:ALA:HB2	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:288:ASN:HD22	2:B:288:ASN:N	2.16	0.43
2:B:83:VAL:O	2:B:87:MET:HG3	2.19	0.43
3:D:241:ILE:HD11	3:D:324:LYS:HB3	2.01	0.43
3:D:32:LYS:C	3:D:36:ILE:HG22	2.38	0.43
4:E:329:GLU:O	4:E:333:ILE:HG13	2.19	0.43
4:E:369:ASP:O	4:E:370:LYS:C	2.56	0.43
5:G:33:ILE:HD13	5:G:80:MET:HB2	2.00	0.43
6:H:176:ALA:O	6:H:180:VAL:HG23	2.18	0.43
7:Q:191:PHE:N	7:Q:192:PRO:HD2	2.33	0.43
7:Q:221:MET:O	7:Q:363:PHE:HD1	2.01	0.43
1:A:145:ARG:O	1:A:146:ASP:C	2.56	0.43
1:A:278:ILE:HG21	1:A:286:ILE:HG12	2.00	0.43
1:A:317:LYS:O	1:A:321:LYS:HG3	2.18	0.43
1:A:39:VAL:HG21	1:A:455:ASN:O	2.19	0.43
1:A:447:VAL:O	1:A:451:THR:HG23	2.18	0.43
2:B:517:VAL:CG2	2:B:520:ILE:HD11	2.48	0.43
2:B:51:ILE:CG2	2:B:61:LEU:HG	2.48	0.43
3:D:192:ASP:HA	3:D:195:MET:CG	2.48	0.43
3:D:217:LEU:CD1	3:D:401:ILE:HD12	2.49	0.43
5:G:396:GLN:HE22	5:G:399:ARG:HH11	1.66	0.43
5:G:49:MET:HG3	5:G:59:MET:CG	2.46	0.43
5:G:72:VAL:CG1	5:G:73:GLN:N	2.82	0.43
6:H:13:THR:HG22	6:H:13:THR:O	2.17	0.43
6:H:415:GLU:HG2	6:H:473:MET:HG3	2.00	0.43
7:Q:336:LEU:N	7:Q:336:LEU:HD12	2.34	0.43
7:Q:414:ALA:HB1	7:Q:476:LYS:O	2.19	0.43
8:Z:154:THR:HA	8:Z:157:ARG:CD	2.48	0.43
8:Z:156:LEU:HD11	8:Z:168:LEU:HD22	2.01	0.43
1:A:357:CYS:O	1:A:358:ASP:HB2	2.18	0.43
3:D:162:ASP:HB3	3:D:165:THR:OG1	2.18	0.43
3:D:540:ASN:HB3	3:D:542:ARG:CD	2.27	0.43
5:G:316:ARG:HB2	5:G:319:ASP:OD2	2.18	0.43
5:G:89:GLU:CD	5:G:389:ARG:HH22	2.21	0.43
5:G:49:MET:CE	5:G:57:ILE:HD13	2.49	0.43
6:H:127:THR:O	6:H:131:LEU:HG	2.19	0.43
6:H:352:GLN:HG2	6:H:357:ARG:CG	2.48	0.43
6:H:51:ASP:C	6:H:53:ARG:H	2.22	0.43
7:Q:246:PHE:HB2	7:Q:297:VAL:HA	2.01	0.43
7:Q:204:VAL:CG1	7:Q:377:LEU:HG	2.49	0.43
8:Z:417:ALA:CA	8:Z:470:HIS:HE2	2.31	0.43
8:Z:445:LEU:O	8:Z:448:PRO:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:497:ASN:HB3	8:Z:499:CYS:SG	2.59	0.43
8:Z:69:ILE:CG2	8:Z:74:ALA:HB3	2.49	0.43
1:A:240:SER:HB3	1:A:290:GLY:HA3	2.01	0.43
2:B:10:ASN:O	4:E:85:HIS:N	2.51	0.43
2:B:127:ILE:HG23	2:B:512:GLU:HB3	2.01	0.43
2:B:131:ARG:HG3	2:B:131:ARG:HH11	1.83	0.43
2:B:461:LEU:HD13	2:B:461:LEU:C	2.39	0.43
2:B:61:LEU:CD2	2:B:63:VAL:HG23	2.49	0.43
3:D:170:ALA:HB3	3:D:187:SER:HB3	2.01	0.43
3:D:294:LYS:CD	3:D:325:ILE:HD11	2.48	0.43
6:H:189:LEU:O	6:H:190:LEU:O	2.37	0.43
6:H:194:MET:O	6:H:369:THR:HA	2.18	0.43
8:Z:378:GLY:CA	8:Z:384:LEU:HD21	2.47	0.43
1:A:104:ALA:O	1:A:108:VAL:HG23	2.19	0.43
1:A:220:VAL:CG1	1:A:225:MET:HG3	2.48	0.43
1:A:17:ILE:HG21	1:A:528:ASP:O	2.18	0.43
1:A:69:HIS:CE1	1:A:71:ALA:HB3	2.54	0.43
2:B:45:PRO:HA	2:B:169:SER:HA	2.01	0.43
2:B:352:VAL:HG23	2:B:354:ILE:HG13	2.00	0.43
4:E:112:LEU:HD21	4:E:517:ILE:HA	2.01	0.43
4:E:205:ASP:OD2	4:E:207:GLU:HB2	2.19	0.43
4:E:20:LYS:NZ	6:H:32:ILE:N	2.67	0.43
4:E:211:VAL:HG13	4:E:387:ILE:HD13	2.00	0.43
4:E:249:ALA:HB2	4:E:297:ALA:CB	2.49	0.43
5:G:93:ASP:CG	5:G:94:GLY:N	2.72	0.43
8:Z:233:CYS:SG	8:Z:336:LEU:HG	2.59	0.43
8:Z:355:LEU:HD22	8:Z:377:LYS:CE	2.49	0.43
5:G:71:GLN:CG	8:Z:8:ASN:HB2	2.49	0.43
1:A:43:LYS:HG2	5:G:520:ASP:CG	2.39	0.43
2:B:326:VAL:O	2:B:365:VAL:HB	2.18	0.43
4:E:225:ILE:HG22	4:E:227:GLY:N	2.33	0.43
5:G:49:MET:HE3	5:G:57:ILE:HD13	2.01	0.43
5:G:66:ILE:O	5:G:70:ILE:HG13	2.19	0.43
6:H:101:ALA:O	6:H:105:LEU:HG	2.18	0.43
6:H:23:VAL:CA	6:H:109:LYS:HZ1	2.30	0.43
6:H:37:ARG:CG	6:H:448:GLN:HG2	2.49	0.43
7:Q:146:LEU:HD22	7:Q:418:GLU:OE1	2.19	0.43
7:Q:165:HIS:HB2	7:Q:181:LYS:HD3	2.00	0.43
7:Q:85:MET:HA	7:Q:88:MET:CE	2.48	0.43
8:Z:235:VAL:HG22	8:Z:236:SER:N	2.34	0.43
1:A:236:CYS:HB3	1:A:316:LEU:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:218:PHE:CD1	2:B:326:VAL:HG21	2.54	0.43
3:D:212:LYS:HD2	3:D:230:LEU:HD11	2.01	0.43
3:D:28:GLN:HG2	3:D:29:ASP:N	2.33	0.43
3:D:33:PRO:O	3:D:536:ASP:OD1	2.36	0.43
4:E:305:GLY:HA2	4:E:324:TRP:CE2	2.54	0.43
4:E:446:TYR:HD1	4:E:446:TYR:N	2.16	0.43
2:B:11:ILE:CA	4:E:85:HIS:HB2	2.48	0.43
5:G:245:LEU:HD12	5:G:296:ILE:CG1	2.49	0.43
5:G:462:LEU:HD11	5:G:480:VAL:HG22	2.00	0.43
5:G:49:MET:CG	5:G:59:MET:HG2	2.46	0.43
5:G:80:MET:HA	5:G:83:ILE:CD1	2.49	0.43
6:H:471:GLY:HA3	6:H:475:TYR:CE1	2.53	0.43
6:H:497:MET:HE2	6:H:501:ASN:HB2	2.00	0.43
6:H:54:GLY:O	6:H:55:LYS:C	2.56	0.43
6:H:520:ILE:HG21	7:Q:76:LEU:HD22	2.00	0.43
8:Z:380:ASN:HA	8:Z:380:ASN:HD22	1.66	0.43
8:Z:407:VAL:HG22	8:Z:495:TRP:CG	2.53	0.43
1:A:20:GLN:HE21	5:G:7:VAL:N	2.17	0.42
1:A:2:GLU:O	1:A:3:GLY:O	2.36	0.42
3:D:131:ILE:HG12	3:D:449:MET:HE2	2.01	0.42
4:E:189:ALA:HA	4:E:406:LEU:HD21	1.99	0.42
5:G:421:ALA:O	5:G:424:GLU:HB3	2.19	0.42
6:H:228:GLN:CB	6:H:229:PRO:HD2	2.49	0.42
7:Q:41:GLN:HA	7:Q:44:ARG:HB2	2.00	0.42
7:Q:89:ALA:HB1	7:Q:104:VAL:HG21	2.00	0.42
8:Z:76:LEU:O	8:Z:80:VAL:HG23	2.19	0.42
8:Z:91:GLY:O	8:Z:92:THR:C	2.57	0.42
1:A:12:SER:OG	1:A:17:ILE:HD13	2.19	0.42
1:A:138:ILE:HG21	1:A:406:LYS:NZ	2.34	0.42
1:A:328:LEU:HD22	1:A:328:LEU:N	2.34	0.42
2:B:131:ARG:HG2	2:B:135:LYS:HE2	2.01	0.42
3:D:115:ILE:O	3:D:119:LEU:HG	2.20	0.42
3:D:132:HIS:CD2	3:D:133:PRO:HD2	2.54	0.42
3:D:170:ALA:HB1	3:D:187:SER:HA	2.00	0.42
3:D:226:LEU:CG	3:D:389:VAL:HB	2.49	0.42
3:D:416:ARG:O	3:D:420:LYS:HG3	2.19	0.42
3:D:515:LEU:HG	3:D:519:VAL:HG21	2.02	0.42
5:G:194:ASP:HB3	5:G:399:ARG:HG3	2.01	0.42
5:G:40:CYS:HA	5:G:45:SER:HB2	2.00	0.42
6:H:16:SER:O	6:H:21:GLN:HB2	2.19	0.42
6:H:448:GLN:HG3	6:H:452:ASN:HD21	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:201:ASN:HB3	7:Q:371:ALA:O	2.19	0.42
7:Q:212:VAL:C	7:Q:214:SER:H	2.22	0.42
7:Q:225:LYS:CA	7:Q:313:VAL:HG22	2.44	0.42
7:Q:358:THR:O	7:Q:358:THR:HG23	2.19	0.42
7:Q:351:TYR:HE2	7:Q:364:LYS:HE2	1.83	0.42
7:Q:408:LEU:CD1	7:Q:498:LEU:HD13	2.49	0.42
8:Z:511:ILE:HA	8:Z:514:ASN:HD22	1.83	0.42
8:Z:8:ASN:CG	8:Z:9:PRO:HD2	2.40	0.42
1:A:137:ILE:HG22	1:A:137:ILE:O	2.19	0.42
1:A:242:GLN:HG3	1:A:291:GLY:O	2.19	0.42
1:A:5:LEU:HD13	1:A:531:ILE:HG21	2.02	0.42
2:B:243:GLY:HA2	2:B:292:ASN:OD1	2.20	0.42
2:B:187:VAL:HG11	2:B:397:LEU:HB3	2.00	0.42
2:B:414:GLU:HB3	2:B:443:LEU:O	2.19	0.42
3:D:378:LYS:HE2	3:D:380:THR:CG2	2.49	0.42
3:D:99:LYS:O	3:D:103:ILE:HG13	2.19	0.42
4:E:62:VAL:HG22	4:E:68:VAL:HA	2.01	0.42
6:H:110:PRO:HG2	6:H:111:TYR:HD1	1.84	0.42
6:H:168:ILE:HD11	6:H:175:PHE:CE1	2.55	0.42
6:H:348:PHE:HE2	6:H:361:PHE:CE2	2.38	0.42
6:H:448:GLN:HE21	6:H:452:ASN:CG	2.21	0.42
7:Q:148:CYS:HB2	7:Q:476:LYS:HZ2	1.83	0.42
7:Q:93:GLN:NE2	7:Q:97:VAL:HG22	2.34	0.42
8:Z:101:GLU:O	8:Z:104:LYS:HB3	2.20	0.42
8:Z:217:ARG:HG2	8:Z:302:LEU:CD2	2.49	0.42
1:A:136:LEU:O	1:A:138:ILE:N	2.52	0.42
1:A:176:VAL:HG22	1:A:190:TYR:CZ	2.55	0.42
1:A:233:LYS:HB3	1:A:345:LEU:HB3	2.00	0.42
2:B:465:LEU:O	2:B:469:HIS:HB2	2.19	0.42
3:D:340:CYS:HB2	3:D:347:PRO:HD3	2.00	0.42
3:D:477:ILE:H	3:D:477:ILE:CD1	2.28	0.42
4:E:115:ALA:CB	4:E:457:VAL:HG11	2.50	0.42
4:E:520:ALA:O	4:E:524:VAL:HG23	2.19	0.42
4:E:532:ASP:O	6:H:47:LYS:HD2	2.19	0.42
4:E:52:LEU:HD12	4:E:53:GLY:H	1.84	0.42
5:G:185:PHE:CZ	5:G:370:LYS:HB3	2.54	0.42
5:G:37:ILE:O	5:G:40:CYS:HB2	2.20	0.42
6:H:294:PRO:HG3	6:H:313:ARG:CD	2.49	0.42
6:H:348:PHE:HE2	6:H:361:PHE:CZ	2.37	0.42
6:H:414:MET:HE3	6:H:464:LEU:HB3	2.00	0.42
7:Q:168:VAL:HA	7:Q:173:TYR:OH	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:524:ILE:HG21	8:Z:46:MET:N	2.24	0.42
8:Z:196:MET:SD	8:Z:197:LYS:N	2.92	0.42
8:Z:415:GLU:N	8:Z:415:GLU:OE1	2.44	0.42
8:Z:35:ARG:HG3	8:Z:450:VAL:CG1	2.49	0.42
5:G:72:VAL:HG22	8:Z:6:THR:CG2	2.47	0.42
2:B:10:ASN:H	4:E:85:HIS:CD2	2.37	0.42
2:B:203:LYS:HA	2:B:383:LEU:HD11	2.00	0.42
2:B:520:ILE:HG22	2:B:521:ILE:N	2.35	0.42
2:B:96:GLY:O	2:B:97:ASP:O	2.37	0.42
3:D:186:LEU:HA	3:D:189:MET:HE3	2.02	0.42
3:D:36:ILE:CD1	3:D:40:ASN:HD21	2.32	0.42
4:E:535:LYS:HA	4:E:536:PRO:HD2	1.93	0.42
5:G:101:LEU:O	5:G:105:MET:HG3	2.19	0.42
5:G:27:ILE:HG23	5:G:106:LEU:CB	2.45	0.42
7:Q:187:CYS:C	7:Q:189:SER:H	2.22	0.42
8:Z:9:PRO:O	8:Z:10:LYS:HB2	2.20	0.42
2:B:181:LYS:O	2:B:185:GLU:HB2	2.20	0.42
2:B:231:ARG:HE	2:B:348:LEU:HD11	1.84	0.42
2:B:418:ALA:O	2:B:440:ALA:HB1	2.20	0.42
2:B:478:LEU:HD12	2:B:479:ASP:H	1.84	0.42
2:B:95:VAL:O	2:B:392:ASP:HB3	2.19	0.42
3:D:217:LEU:CD1	3:D:398:LYS:HG3	2.45	0.42
5:G:356:GLY:O	5:G:357:ASP:HB2	2.19	0.42
5:G:368:ASP:C	5:G:370:LYS:H	2.23	0.42
5:G:49:MET:N	8:Z:518:VAL:HG13	2.34	0.42
6:H:237:ILE:HG21	6:H:328:GLY:HA3	2.01	0.42
6:H:374:LEU:HB3	6:H:382:MET:CE	2.50	0.42
6:H:51:ASP:O	6:H:53:ARG:N	2.47	0.42
1:A:169:ALA:O	1:A:173:VAL:HG23	2.20	0.42
1:A:222:SER:HG	1:A:301:VAL:HG22	1.85	0.42
1:A:311:VAL:HG12	1:A:315:ASP:HB2	2.01	0.42
1:A:326:THR:HB	1:A:344:MET:HB3	2.02	0.42
1:A:450:ASN:O	1:A:454:VAL:HG23	2.19	0.42
2:B:186:ALA:O	2:B:190:LEU:HD13	2.18	0.42
2:B:219:LEU:HD22	2:B:374:VAL:HG21	2.02	0.42
2:B:244:MET:O	2:B:300:PRO:HG2	2.20	0.42
3:D:378:LYS:HE2	3:D:380:THR:HG21	2.02	0.42
4:E:304:TRP:HB3	4:E:305:GLY:H	1.74	0.42
4:E:248:ILE:CD1	4:E:337:THR:HG21	2.50	0.42
4:E:132:ARG:CG	4:E:443:LEU:HG	2.50	0.42
5:G:354:LYS:HA	5:G:359:TYR:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:165:SER:HB3	6:H:480:ASN:CB	2.48	0.42
7:Q:379:GLY:N	7:Q:385:MET:SD	2.93	0.42
8:Z:55:LYS:CE	8:Z:62:VAL:HG11	2.50	0.42
8:Z:91:GLY:O	8:Z:93:THR:N	2.52	0.42
8:Z:97:LEU:N	8:Z:97:LEU:HD12	2.35	0.42
1:A:97:ALA:HA	1:A:100:LEU:HD12	2.01	0.42
1:A:159:LYS:HB2	1:A:161:ILE:HG22	2.01	0.42
1:A:376:ILE:N	1:A:376:ILE:HD13	2.35	0.42
2:B:31:GLY:O	2:B:35:ILE:HG12	2.20	0.42
2:B:75:GLY:N	3:D:541:THR:OG1	2.51	0.42
4:E:234:PHE:HE2	4:E:240:PRO:O	2.03	0.42
4:E:362:ILE:HB	4:E:364:PHE:HE1	1.77	0.42
5:G:144:VAL:HG11	5:G:407:LEU:HD21	2.01	0.42
6:H:103:GLU:OE2	6:H:106:LYS:HD3	2.20	0.42
6:H:313:ARG:CG	6:H:313:ARG:HH11	2.18	0.42
6:H:136:ILE:HG21	6:H:500:ILE:HG13	2.01	0.42
7:Q:156:ASP:OD2	7:Q:158:ASP:HB2	2.20	0.42
7:Q:179:LEU:HG	7:Q:183:ILE:HD11	2.01	0.42
7:Q:25:LEU:HD22	7:Q:26:GLU:OE1	2.20	0.42
7:Q:59:HIS:CD2	7:Q:59:HIS:H	2.38	0.42
8:Z:297:ILE:HG13	8:Z:314:ARG:HB3	2.02	0.42
8:Z:450:VAL:O	8:Z:453:GLN:HB3	2.18	0.42
1:A:115:THR:HG21	3:D:471:ASN:O	2.19	0.42
1:A:483:LEU:HD12	1:A:485:TRP:CZ2	2.55	0.42
2:B:139:GLN:HA	2:B:142:LEU:HD12	2.01	0.42
2:B:171:LEU:HD21	2:B:382:ILE:HG12	2.02	0.42
2:B:373:ILE:HG21	2:B:390:LEU:HD21	2.02	0.42
3:D:41:ILE:HG21	3:D:124:THR:CG2	2.49	0.42
3:D:182:TYR:CD2	3:D:221:ILE:HB	2.54	0.42
4:E:189:ALA:O	4:E:193:VAL:HG23	2.20	0.42
5:G:105:MET:HE2	5:G:105:MET:HB3	1.71	0.42
5:G:23:GLN:HG3	5:G:24:SER:H	1.84	0.42
5:G:296:ILE:CG1	5:G:313:ARG:HB3	2.49	0.42
5:G:285:LEU:HD22	5:G:339:ARG:C	2.39	0.42
5:G:77:ALA:O	5:G:80:MET:HB2	2.20	0.42
5:G:83:ILE:HG23	5:G:508:THR:HG22	2.02	0.42
7:Q:142:ILE:HD13	7:Q:422:GLN:CB	2.50	0.42
7:Q:13:GLN:CD	8:Z:72:PRO:HD2	2.40	0.42
1:A:2:GLU:OE2	3:D:44:ALA:N	2.39	0.42
1:A:136:LEU:HB3	1:A:407:SER:HB3	2.01	0.42
1:A:445:LEU:C	1:A:447:VAL:H	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:507:THR:O	1:A:511:VAL:HG23	2.20	0.42
3:D:37:ARG:NE	3:D:536:ASP:OD2	2.53	0.42
1:A:530:LEU:HD21	3:D:63:MET:HB3	2.02	0.42
4:E:156:LEU:CD2	4:E:161:ASN:HB3	2.47	0.42
5:G:153:LEU:HD13	5:G:177:LEU:HD12	2.02	0.42
6:H:238:ALA:HB2	6:H:286:ALA:CB	2.44	0.42
6:H:460:ILE:CG2	6:H:461:LEU:N	2.82	0.42
7:Q:124:SER:O	7:Q:128:VAL:HG23	2.19	0.42
7:Q:333:LEU:HD21	7:Q:343:GLU:CG	2.49	0.42
7:Q:401:VAL:O	7:Q:405:ASP:N	2.53	0.42
8:Z:131:LEU:HD21	8:Z:505:LEU:HB2	2.02	0.42
8:Z:195:GLU:HB2	8:Z:384:LEU:HD13	2.02	0.42
8:Z:413:ALA:HA	8:Z:477:VAL:O	2.18	0.42
8:Z:446:ILE:HG23	8:Z:447:ILE:N	2.34	0.42
1:A:381:ASN:HB2	1:A:384:MET:SD	2.60	0.41
1:A:73:LYS:O	1:A:76:CYS:HB2	2.19	0.41
3:D:132:HIS:HB3	3:D:135:ILE:HD12	2.02	0.41
3:D:137:SER:HA	3:D:533:LEU:HD12	2.02	0.41
3:D:213:ILE:HD11	3:D:412:LEU:CD1	2.46	0.41
3:D:439:LEU:HB2	3:D:458:ALA:HB2	2.01	0.41
3:D:104:GLU:OE1	3:D:524:LEU:HD11	2.19	0.41
4:E:147:HIS:O	4:E:150:LYS:HB3	2.20	0.41
5:G:285:LEU:HD22	5:G:339:ARG:CA	2.50	0.41
5:G:202:GLU:O	5:G:375:LEU:HA	2.20	0.41
6:H:522:ASN:ND2	7:Q:75:GLU:O	2.52	0.41
7:Q:356:GLY:O	7:Q:357:ASP:CB	2.67	0.41
7:Q:502:LEU:HD12	7:Q:502:LEU:HA	1.87	0.41
8:Z:176:ILE:HD11	8:Z:395:LEU:CB	2.49	0.41
8:Z:177:LEU:O	8:Z:177:LEU:HD23	2.20	0.41
8:Z:228:ALA:HB1	8:Z:290:VAL:HG23	1.99	0.41
8:Z:352:GLU:CG	8:Z:359:LYS:HB3	2.50	0.41
8:Z:134:LEU:CD2	8:Z:414:VAL:HG11	2.50	0.41
8:Z:476:LEU:HD22	8:Z:490:ALA:HB2	2.01	0.41
1:A:176:VAL:HG21	1:A:399:VAL:HG11	2.02	0.41
3:D:123:CYS:SG	3:D:136:ILE:HG21	2.60	0.41
3:D:197:VAL:HG21	3:D:211:ILE:HD11	2.02	0.41
3:D:256:LEU:HD13	3:D:312:LEU:HD12	2.01	0.41
3:D:346:LYS:HD2	3:D:358:MET:SD	2.60	0.41
3:D:371:ASN:ND2	3:D:394:ARG:HD3	2.36	0.41
3:D:432:GLU:N	3:D:432:GLU:CD	2.73	0.41
4:E:343:PRO:HG2	4:E:347:GLU:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:245:LEU:HD12	5:G:296:ILE:HD13	2.02	0.41
7:Q:281:LYS:HA	7:Q:308:TYR:HE2	1.84	0.41
8:Z:331:ILE:HB	8:Z:343:CYS:SG	2.60	0.41
8:Z:352:GLU:HG2	8:Z:359:LYS:HB3	2.02	0.41
8:Z:350:VAL:HG22	8:Z:363:ILE:HG23	2.01	0.41
8:Z:412:GLY:HA2	8:Z:415:GLU:OE1	2.20	0.41
1:A:220:VAL:HG12	1:A:225:MET:HG3	2.02	0.41
1:A:328:LEU:HD21	1:A:344:MET:CB	2.48	0.41
1:A:484:LYS:O	1:A:486:ILE:N	2.46	0.41
1:A:507:THR:HG23	1:A:508:ILE:N	2.36	0.41
2:B:367:LEU:O	2:B:369:GLU:N	2.54	0.41
3:D:232:LEU:HD21	3:D:339:ILE:CD1	2.47	0.41
3:D:343:ILE:HG12	3:D:382:CYS:SG	2.60	0.41
1:A:2:GLU:N	3:D:88:HIS:HB3	2.35	0.41
4:E:129:HIS:HA	4:E:130:PRO:HD3	1.95	0.41
4:E:344:ARG:HG3	4:E:345:PHE:N	2.35	0.41
4:E:417:ARG:NH1	4:E:417:ARG:HG3	2.35	0.41
5:G:289:VAL:HG12	5:G:310:THR:HB	2.02	0.41
5:G:243:SER:OG	5:G:335:PRO:HD3	2.21	0.41
5:G:394:ALA:O	5:G:397:VAL:HG22	2.20	0.41
6:H:198:LYS:HZ3	6:H:217:LYS:HE3	1.85	0.41
7:Q:130:GLU:O	7:Q:134:ILE:HG13	2.18	0.41
7:Q:415:THR:O	7:Q:419:LEU:HG	2.19	0.41
7:Q:423:ILE:O	7:Q:426:TYR:HB3	2.20	0.41
8:Z:70:GLN:O	8:Z:72:PRO:HD3	2.20	0.41
1:A:138:ILE:HG21	1:A:406:LYS:HZ1	1.85	0.41
1:A:420:SER:HA	1:A:442:ALA:HB1	2.01	0.41
2:B:365:VAL:O	2:B:366:ALA:C	2.59	0.41
2:B:97:ASP:C	2:B:99:THR:N	2.73	0.41
3:D:142:LYS:HZ2	3:D:446:LEU:HD21	1.85	0.41
3:D:237:ALA:CA	3:D:317:LEU:HD11	2.49	0.41
3:D:411:ALA:O	3:D:415:ILE:HG13	2.19	0.41
3:D:421:LYS:CE	3:D:515:LEU:HD23	2.42	0.41
4:E:466:SER:HB3	4:E:493:CYS:HG	1.84	0.41
5:G:130:LEU:HD11	5:G:507:LYS:CD	2.43	0.41
5:G:238:ILE:HD13	5:G:323:ILE:CG2	2.40	0.41
5:G:416:MET:HE2	5:G:466:LEU:HD13	2.02	0.41
5:G:71:GLN:H	8:Z:524:ALA:CB	2.32	0.41
6:H:391:ASP:HA	6:H:394:MET:HG3	2.02	0.41
6:H:415:GLU:O	6:H:418:LYS:HB3	2.20	0.41
6:H:37:ARG:HD2	6:H:99:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:353:SER:OG	7:Q:360:VAL:HG23	2.20	0.41
8:Z:374:LEU:CD2	8:Z:391:ILE:HD13	2.47	0.41
8:Z:7:LEU:HD21	8:Z:522:MET:HB3	2.02	0.41
1:A:77:GLU:O	1:A:81:LEU:HG	2.21	0.41
3:D:151:LEU:HD21	3:D:435:LEU:CD1	2.49	0.41
4:E:145:ILE:HD13	4:E:145:ILE:HA	1.94	0.41
4:E:25:LYS:HB3	4:E:26:SER:H	1.68	0.41
4:E:41:ALA:O	4:E:42:LYS:C	2.58	0.41
5:G:149:ARG:CG	5:G:177:LEU:HD11	2.50	0.41
7:Q:191:PHE:CE1	7:Q:197:PHE:HE1	2.38	0.41
7:Q:147:VAL:HG21	7:Q:501:TYR:HB2	2.02	0.41
8:Z:13:VAL:HG22	8:Z:522:MET:CG	2.45	0.41
8:Z:225:VAL:HG22	8:Z:311:ILE:HG12	2.03	0.41
8:Z:73:THR:O	8:Z:76:LEU:HB2	2.19	0.41
1:A:107:LEU:O	1:A:110:GLN:HB2	2.21	0.41
1:A:137:ILE:HG23	1:A:499:LYS:CE	2.49	0.41
1:A:356:ILE:HD12	1:A:361:LEU:HB2	2.02	0.41
1:A:234:ILE:HD11	1:A:364:ILE:HG21	2.03	0.41
2:B:477:GLY:HA3	2:B:488:MET:CG	2.51	0.41
3:D:98:SER:HB2	3:D:109:THR:HG22	2.02	0.41
3:D:118:SER:OG	3:D:460:ALA:HB1	2.20	0.41
3:D:345:THR:HB	3:D:360:GLY:HA3	2.02	0.41
3:D:173:SER:HB2	3:D:414:VAL:HG11	2.02	0.41
4:E:416:ASN:C	4:E:417:ARG:HG2	2.40	0.41
5:G:119:PRO:O	5:G:122:VAL:HB	2.20	0.41
8:Z:426:LYS:HB2	8:Z:434:GLN:HG2	2.02	0.41
1:A:356:ILE:CD1	1:A:361:LEU:HB2	2.50	0.41
1:A:62:LEU:HD12	1:A:79:ALA:CB	2.51	0.41
2:B:297:TYR:HB3	2:B:300:PRO:CD	2.50	0.41
2:B:26:LEU:O	2:B:30:ILE:HG13	2.20	0.41
2:B:521:ILE:HG13	4:E:61:MET:CE	2.51	0.41
3:D:252:ILE:HB	3:D:303:ILE:CD1	2.46	0.41
4:E:459:PRO:HA	4:E:462:LEU:CD1	2.51	0.41
5:G:383:ILE:HG22	5:G:383:ILE:O	2.21	0.41
5:G:440:VAL:O	5:G:443:ALA:HB3	2.20	0.41
5:G:467:ARG:HG3	5:G:467:ARG:NH1	2.36	0.41
5:G:523:VAL:HG12	5:G:524:SER:H	1.85	0.41
6:H:231:LYS:HE3	6:H:347:VAL:HG13	2.03	0.41
1:A:168:PHE:O	1:A:172:VAL:HG23	2.21	0.41
1:A:448:ILE:HB	1:A:449:PRO:HD3	2.03	0.41
1:A:484:LYS:C	1:A:486:ILE:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:508:ILE:HG23	1:A:509:VAL:N	2.36	0.41
2:B:189:ARG:HH11	2:B:189:ARG:HB3	1.86	0.41
2:B:94:GLU:HA	2:B:94:GLU:OE1	2.20	0.41
3:D:186:LEU:HD23	3:D:189:MET:CE	2.51	0.41
4:E:378:LYS:HB2	4:E:378:LYS:HE3	1.90	0.41
4:E:35:LYS:CA	4:E:38:ILE:HD12	2.46	0.41
5:G:168:TRP:CZ3	5:G:210:GLU:HB2	2.56	0.41
5:G:236:PRO:HA	5:G:288:ASP:OD2	2.21	0.41
5:G:399:ARG:NH1	5:G:399:ARG:HG2	2.36	0.41
6:H:346:GLN:HG3	6:H:347:VAL:HG23	2.03	0.41
6:H:464:LEU:HD13	6:H:476:GLY:O	2.21	0.41
6:H:464:LEU:HA	6:H:484:ILE:HG21	2.02	0.41
7:Q:327:THR:HG22	7:Q:366:GLU:OE2	2.20	0.41
1:A:172:VAL:HG12	1:A:399:VAL:HG21	2.01	0.41
1:A:230:VAL:O	1:A:232:ALA:N	2.54	0.41
1:A:403:LEU:HD12	1:A:403:LEU:HA	1.80	0.41
2:B:238:LEU:CD2	2:B:287:ILE:HG21	2.51	0.41
3:D:111:SER:O	3:D:112:VAL:C	2.59	0.41
3:D:371:ASN:HD22	3:D:394:ARG:NE	2.16	0.41
3:D:179:VAL:HG11	3:D:404:ALA:HA	2.00	0.41
3:D:206:VAL:HG23	3:D:419:VAL:HG21	2.00	0.41
3:D:41:ILE:HG23	3:D:120:LEU:CB	2.47	0.41
4:E:95:SER:HB2	4:E:106:THR:CG2	2.50	0.41
4:E:247:LYS:HD2	4:E:296:GLY:O	2.21	0.41
4:E:104:ASP:OD2	4:E:408:VAL:HG12	2.21	0.41
4:E:457:VAL:HG23	4:E:458:ILE:H	1.84	0.41
5:G:117:MET:O	5:G:118:HIS:C	2.59	0.41
5:G:447:ILE:N	5:G:448:PRO:HD2	2.35	0.41
5:G:46:MET:O	5:G:48:LYS:NZ	2.53	0.41
5:G:504:GLN:HA	5:G:504:GLN:HE21	1.86	0.41
6:H:416:LEU:O	6:H:420:LEU:HG	2.21	0.41
6:H:65:ILE:O	6:H:69:LEU:HG	2.21	0.41
7:Q:155:ARG:HA	7:Q:155:ARG:HD3	1.82	0.41
7:Q:97:VAL:HG12	7:Q:401:VAL:HG22	2.03	0.41
7:Q:504:LYS:O	7:Q:507:ALA:HB3	2.21	0.41
7:Q:525:ILE:HG13	7:Q:526:MET:N	2.35	0.41
8:Z:109:TYR:HA	8:Z:112:GLU:OE1	2.20	0.41
8:Z:325:THR:HB	8:Z:330:GLY:O	2.21	0.41
8:Z:520:GLU:C	8:Z:521:ILE:HD12	2.41	0.41
1:A:369:ALA:C	1:A:371:THR:N	2.74	0.41
2:B:209:LEU:HD11	2:B:382:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:249:ILE:HG13	3:D:343:ILE:HG21	2.03	0.41
4:E:252:THR:HG23	4:E:303:GLN:OE1	2.21	0.41
4:E:481:GLN:NE2	4:E:487:PRO:HB3	2.36	0.41
4:E:518:SER:CA	4:E:522:GLN:HE21	2.34	0.41
6:H:435:ILE:O	6:H:438:TYR:HB3	2.20	0.41
6:H:486:ASP:OD1	6:H:488:PHE:HB3	2.21	0.41
7:Q:526:MET:O	7:Q:527:ALA:HB2	2.21	0.41
8:Z:374:LEU:HD22	8:Z:391:ILE:HG21	2.02	0.41
2:B:437:GLU:HG3	2:B:441:LYS:HE3	2.03	0.41
2:B:521:ILE:HG12	4:E:61:MET:SD	2.60	0.41
5:G:208:ILE:HG13	5:G:210:GLU:H	1.86	0.41
6:H:214:VAL:HA	6:H:371:THR:OG1	2.21	0.41
7:Q:126:SER:CB	8:Z:41:LYS:HD3	2.51	0.41
8:Z:422:LEU:HB3	8:Z:437:VAL:CG1	2.51	0.41
1:A:105:ASP:O	1:A:109:LYS:N	2.50	0.40
1:A:354:GLU:HG3	1:A:363:LEU:HD12	2.02	0.40
2:B:414:GLU:OE1	2:B:414:GLU:HA	2.21	0.40
2:B:133:ALA:HB1	2:B:421:VAL:HG11	2.02	0.40
2:B:441:LYS:HA	2:B:444:ARG:HE	1.87	0.40
3:D:237:ALA:CB	3:D:327:VAL:HG12	2.49	0.40
3:D:332:GLU:HB3	3:D:335:ASP:OD2	2.21	0.40
3:D:345:THR:O	3:D:345:THR:HG23	2.21	0.40
3:D:507:LEU:HD12	3:D:512:VAL:HG12	2.03	0.40
4:E:237:PRO:O	4:E:239:MET:N	2.54	0.40
4:E:441:PRO:O	4:E:442:THR:O	2.39	0.40
4:E:527:ILE:H	4:E:527:ILE:HG13	1.53	0.40
6:H:117:HIS:HA	6:H:118:PRO:HD3	1.93	0.40
6:H:168:ILE:HG13	6:H:168:ILE:O	2.21	0.40
7:Q:197:PHE:HB3	7:Q:403:THR:HG21	2.04	0.40
7:Q:475:ASN:O	7:Q:476:LYS:C	2.59	0.40
8:Z:194:MET:HE1	8:Z:360:PHE:HE2	1.85	0.40
8:Z:407:VAL:HG23	8:Z:495:TRP:HB3	2.03	0.40
1:A:136:LEU:HB3	1:A:407:SER:CB	2.51	0.40
1:A:137:ILE:O	1:A:408:VAL:HG12	2.21	0.40
1:A:44:MET:SD	1:A:52:VAL:HG13	2.62	0.40
1:A:460:SER:O	1:A:464:VAL:HG23	2.22	0.40
1:A:533:LEU:H	1:A:533:LEU:HD23	1.86	0.40
2:B:161:ASN:O	2:B:165:THR:HG23	2.21	0.40
2:B:414:GLU:HG3	2:B:446:LEU:HD22	2.03	0.40
2:B:517:VAL:HA	4:E:58:ASP:O	2.21	0.40
3:D:169:SER:CB	3:D:418:LEU:HD22	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:540:ASN:C	3:D:542:ARG:H	2.24	0.40
4:E:142:ARG:NH2	6:H:167:LEU:HD13	2.36	0.40
4:E:248:ILE:CG1	4:E:299:LEU:HD23	2.50	0.40
4:E:363:SER:HB3	4:E:370:LYS:HG3	2.03	0.40
4:E:430:ALA:O	4:E:452:ALA:HB1	2.21	0.40
4:E:524:VAL:HA	4:E:527:ILE:HD12	2.04	0.40
5:G:470:HIS:CE1	5:G:476:GLU:HG3	2.56	0.40
6:H:241:ASN:HB2	6:H:332:THR:HA	2.02	0.40
6:H:420:LEU:HB2	6:H:439:ALA:HB2	2.03	0.40
6:H:71:VAL:HG12	6:H:77:LYS:HG2	2.03	0.40
7:Q:174:GLY:CA	7:Q:177:VAL:HG13	2.48	0.40
7:Q:508:ILE:H	7:Q:508:ILE:HD12	1.86	0.40
5:G:46:MET:CE	8:Z:517:LEU:HA	2.52	0.40
1:A:441:PHE:O	1:A:445:LEU:HG	2.21	0.40
1:A:11:ARG:CB	1:A:531:ILE:HG12	2.51	0.40
2:B:111:ARG:HG3	2:B:114:GLU:OE2	2.21	0.40
2:B:191:LYS:HZ3	2:B:401:VAL:HG12	1.86	0.40
2:B:223:LYS:CE	2:B:360:ILE:HD12	2.51	0.40
3:D:142:LYS:NZ	3:D:446:LEU:HD21	2.37	0.40
3:D:151:LEU:HD21	3:D:435:LEU:CG	2.51	0.40
3:D:254:PHE:HB2	3:D:350:HIS:HA	2.04	0.40
3:D:300:VAL:HG13	3:D:326:MET:SD	2.61	0.40
3:D:416:ARG:NH1	3:D:420:LYS:HZ2	2.18	0.40
3:D:506:ILE:HG23	3:D:511:VAL:HB	2.04	0.40
4:E:215:VAL:HB	4:E:392:LYS:HE3	2.04	0.40
4:E:25:LYS:NZ	4:E:536:PRO:HB3	2.33	0.40
5:G:104:GLU:HG2	5:G:446:VAL:CG1	2.48	0.40
5:G:275:ILE:HD13	5:G:299:LEU:HD12	2.04	0.40
6:H:19:ILE:O	6:H:23:VAL:HG23	2.20	0.40
6:H:323:MET:HA	6:H:328:GLY:O	2.20	0.40
7:Q:448:ILE:N	7:Q:449:PRO:HD2	2.36	0.40
7:Q:491:ASP:OD1	7:Q:493:LEU:HB3	2.22	0.40
8:Z:404:ASP:C	8:Z:406:CYS:H	2.24	0.40
8:Z:91:GLY:O	8:Z:94:SER:N	2.54	0.40
1:A:2:GLU:HB3	3:D:91:ALA:N	2.36	0.40
2:B:172:LEU:HD13	2:B:209:LEU:HD13	2.02	0.40
2:B:465:LEU:HD12	2:B:485:ILE:CD1	2.51	0.40
3:D:32:LYS:HZ3	3:D:32:LYS:HB3	1.86	0.40
4:E:240:PRO:HD2	4:E:320:PRO:HD3	2.04	0.40
4:E:225:ILE:CG2	4:E:375:GLU:HB3	2.52	0.40
5:G:347:ALA:HB3	5:G:365:GLU:CB	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:447:ILE:HB	5:G:448:PRO:HD3	2.04	0.40
6:H:238:ALA:CB	6:H:286:ALA:HB1	2.42	0.40
6:H:398:ARG:HB3	6:H:495:PRO:HG3	2.03	0.40
7:Q:231:VAL:HG22	7:Q:309:ASN:O	2.21	0.40
7:Q:521:VAL:HG12	7:Q:524:ILE:HD13	2.02	0.40
8:Z:142:GLU:C	8:Z:144:ASP:N	2.73	0.40
8:Z:23:ASN:HD22	8:Z:23:ASN:N	2.19	0.40
1:A:385:CYS:O	1:A:389:GLU:HB2	2.22	0.40
2:B:102:VAL:HA	2:B:503:VAL:HG13	2.03	0.40
2:B:242:THR:HA	2:B:294:GLN:NE2	2.36	0.40
3:D:421:LYS:C	3:D:423:ALA:H	2.25	0.40
5:G:165:ILE:HD11	5:G:172:ALA:CB	2.51	0.40
5:G:203:LYS:HB2	5:G:384:LEU:CD1	2.52	0.40
6:H:126:ARG:HH11	6:H:126:ARG:HG3	1.87	0.40
6:H:351:THR:OG1	6:H:360:PHE:HE2	2.05	0.40
6:H:361:PHE:CD1	6:H:361:PHE:N	2.89	0.40
6:H:6:VAL:O	6:H:7:ILE:HB	2.22	0.40
7:Q:160:VAL:CG1	7:Q:185:GLN:HG2	2.50	0.40
7:Q:188:VAL:HG11	7:Q:399:PHE:CD1	2.55	0.40
7:Q:66:THR:HG21	7:Q:71:THR:CG2	2.51	0.40
8:Z:324:LEU:HD12	8:Z:324:LEU:O	2.22	0.40
8:Z:355:LEU:HD11	8:Z:362:PHE:HZ	1.87	0.40
8:Z:407:VAL:HG22	8:Z:495:TRP:HB3	2.03	0.40
8:Z:520:GLU:OE1	8:Z:522:MET:HG3	2.22	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	471/556 (85%)	390 (83%)	63 (13%)	18 (4%)	3 24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	351/556 (63%)	283 (81%)	50 (14%)	18 (5%)	2	19
2	B	473/535 (88%)	398 (84%)	62 (13%)	13 (3%)	5	31
2	b	353/535 (66%)	301 (85%)	42 (12%)	10 (3%)	5	30
3	D	469/542 (86%)	385 (82%)	70 (15%)	14 (3%)	4	28
3	d	351/542 (65%)	300 (86%)	42 (12%)	9 (3%)	5	31
4	E	471/541 (87%)	392 (83%)	60 (13%)	19 (4%)	3	23
4	e	351/541 (65%)	295 (84%)	39 (11%)	17 (5%)	2	21
5	G	471/545 (86%)	396 (84%)	62 (13%)	13 (3%)	5	30
5	g	351/545 (64%)	291 (83%)	51 (14%)	9 (3%)	5	31
6	H	473/543 (87%)	384 (81%)	73 (15%)	16 (3%)	3	26
6	h	353/543 (65%)	289 (82%)	54 (15%)	10 (3%)	5	30
7	Q	473/548 (86%)	406 (86%)	45 (10%)	22 (5%)	2	21
7	q	351/548 (64%)	292 (83%)	48 (14%)	11 (3%)	4	27
8	Z	473/531 (89%)	400 (85%)	57 (12%)	16 (3%)	3	26
8	z	473/531 (89%)	403 (85%)	57 (12%)	13 (3%)	5	31
All	All	6708/8682 (77%)	5605 (84%)	875 (13%)	228 (3%)	3	26

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	GLY
1	A	145	ARG
1	A	146	ASP
1	A	230	VAL
2	B	54	SER
2	B	97	ASP
2	B	193	SER
2	B	519	ASN
3	D	33	PRO
4	E	63	ASP
4	E	244	GLU
4	E	441	PRO
5	G	148	ASN
5	G	333	SER
5	G	519	ILE
6	H	190	LEU
6	H	233	HIS

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Mol	Chain	Res	Type
6	H	237	ILE
7	Q	235	LYS
7	Q	476	LYS
7	Q	497	VAL
7	Q	526	MET
7	Q	527	ALA
8	Z	226	GLU
8	Z	379	PRO
1	a	1004	PRO
1	a	1011	ARG
1	a	1047	ASP
1	a	1533	LEU
2	b	1018	GLU
2	b	1054	SER
2	b	1148	HIS
4	e	1063	ASP
6	h	1018	GLY
6	h	1189	LEU
6	h	1190	LEU
7	q	1015	LEU
7	q	1016	LYS
8	z	1016	ALA
8	z	1050	GLY
8	z	1051	ALA
8	z	1157	ARG
8	z	1522	MET
1	A	48	ASP
1	A	459	ASP
1	A	485	TRP
2	B	429	PRO
2	B	506	SER
4	E	237	PRO
4	E	242	GLN
4	E	248	ILE
4	E	343	PRO
4	E	370	LYS
4	E	390	GLY
4	E	415	ASP
4	E	442	THR
5	G	11	SER
5	G	45	SER
5	G	93	ASP

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Mol	Chain	Res	Type
5	G	349	LEU
5	G	359	TYR
5	G	468	ALA
5	G	523	VAL
5	G	524	SER
6	H	227	MET
6	H	367	ALA
6	H	498	VAL
7	Q	17	GLU
7	Q	334	PRO
7	Q	475	ASN
7	Q	487	PRO
7	Q	521	VAL
8	Z	407	VAL
8	Z	522	MET
1	a	1006	SER
1	a	1158	SER
1	a	1485	TRP
2	b	1046	LYS
2	b	1168	SER
2	b	1508	ALA
2	b	1523	ALA
3	d	1498	VAL
4	e	1104	ASP
4	e	1177	VAL
4	e	1390	GLY
4	e	1442	THR
4	e	1533	ILE
5	g	1008	LEU
5	g	1011	SER
5	g	1162	THR
5	g	1371	ALA
6	h	1372	ILE
6	h	1507	SER
7	q	1188	VAL
7	q	1487	PRO
8	z	1017	GLN
1	A	461	THR
2	B	233	GLU
2	B	333	SER
2	B	508	ALA
3	D	42	SER

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Mol	Chain	Res	Type
3	D	66	ASP
3	D	109	THR
3	D	249	ILE
3	D	541	THR
4	E	154	SER
4	E	238	GLN
4	E	518	SER
6	H	55	LYS
7	Q	60	LEU
7	Q	169	MET
7	Q	405	ASP
7	Q	525	ILE
8	Z	51	ALA
8	Z	510	VAL
1	a	1088	ASP
1	a	1146	ASP
3	d	1541	THR
4	e	1023	ASP
4	e	1441	PRO
4	e	1518	SER
5	g	1148	ASN
6	h	1051	ASP
7	q	1019	ALA
8	z	1335	SER
1	A	88	ASP
1	A	380	ALA
1	A	460	SER
2	B	10	ASN
3	D	162	ASP
3	D	241	ILE
3	D	245	GLU
3	D	424	LEU
4	E	26	SER
6	H	19	ILE
6	H	189	LEU
6	H	432	GLN
7	Q	105	LEU
7	Q	156	ASP
7	Q	191	PHE
8	Z	92	THR
8	Z	430	LYS
1	a	1111	LYS

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Mol	Chain	Res	Type
1	a	1411	GLY
1	a	1531	ILE
2	b	1014	ALA
2	b	1429	PRO
3	d	1066	ASP
3	d	1428	GLY
4	e	1135	ASP
4	e	1161	ASN
4	e	1381	ARG
4	e	1416	ASN
4	e	1536	PRO
5	g	1521	ASP
6	h	1504	THR
6	h	1518	GLU
7	q	1526	MET
8	z	1189	PHE
8	z	1333	LEU
1	A	133	SER
1	A	231	ASN
1	A	322	ALA
1	A	376	ILE
1	A	432	SER
2	B	499	VAL
3	D	112	VAL
3	D	510	LEU
4	E	22	GLN
6	H	7	ILE
6	H	225	PHE
7	Q	147	VAL
7	Q	332	ALA
8	Z	68	GLN
8	Z	142	GLU
8	Z	143	MET
8	Z	157	ARG
8	Z	504	LEU
1	a	1031	ILE
1	a	1203	ARG
1	a	1432	SER
3	d	1206	VAL
3	d	1224	CYS
5	g	1040	CYS
7	q	1191	PHE

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Mol	Chain	Res	Type
7	q	1505	TYR
8	z	1430	LYS
8	z	1471	SER
1	A	137	ILE
3	D	422	ARG
4	E	240	PRO
4	E	477	VAL
5	G	9	VAL
6	H	23	VAL
7	Q	81	PRO
7	Q	188	VAL
7	Q	505	TYR
3	d	1535	ILE
7	q	1025	LEU
7	q	1173	TYR
1	A	9	GLY
4	E	486	ASN
5	G	410	GLY
6	H	516	VAL
1	a	1211	ILE
2	b	1407	VAL
3	d	1130	GLY
7	q	1516	VAL
2	B	368	GLY
6	H	229	PRO
8	Z	500	VAL
4	e	1178	VAL
4	e	1422	GLY
5	g	1514	VAL
6	h	1139	ILE
8	z	1510	VAL
2	B	194	GLY
6	H	522	ASN
8	Z	518	VAL
8	z	1089	GLY
3	D	300	VAL
8	Z	494	ILE
1	a	1086	VAL
1	a	1415	VAL
3	d	1476	PRO
4	e	1486	ASN
5	g	1122	VAL

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Mol	Chain	Res	Type
6	h	1516	VAL

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	395/461 (86%)	368 (93%)	27 (7%)	16 42
1	a	297/461 (64%)	269 (91%)	28 (9%)	8 29
2	B	382/429 (89%)	372 (97%)	10 (3%)	46 67
2	b	281/429 (66%)	263 (94%)	18 (6%)	17 44
3	D	407/454 (90%)	388 (95%)	19 (5%)	26 52
3	d	303/454 (67%)	285 (94%)	18 (6%)	19 46
4	E	400/455 (88%)	371 (93%)	29 (7%)	14 40
4	e	298/455 (66%)	283 (95%)	15 (5%)	24 50
5	G	416/470 (88%)	402 (97%)	14 (3%)	37 60
5	g	307/470 (65%)	288 (94%)	19 (6%)	18 45
6	H	394/445 (88%)	381 (97%)	13 (3%)	38 61
6	h	292/445 (66%)	274 (94%)	18 (6%)	18 45
7	Q	398/452 (88%)	380 (96%)	18 (4%)	27 53
7	q	296/452 (66%)	279 (94%)	17 (6%)	20 47
8	Z	398/440 (90%)	386 (97%)	12 (3%)	41 63
8	z	398/440 (90%)	374 (94%)	24 (6%)	19 46
All	All	5662/7212 (78%)	5363 (95%)	299 (5%)	22 49

All (299) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	12	SER
1	A	39	VAL

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Mol	Chain	Res	Type
1	A	84	LYS
1	A	105	ASP
1	A	116	SER
1	A	147	CYS
1	A	222	SER
1	A	225	MET
1	A	231	ASN
1	A	240	SER
1	A	243	LYS
1	A	277	LYS
1	A	358	ASP
1	A	372	SER
1	A	381	ASN
1	A	382	ASP
1	A	384	MET
1	A	387	GLU
1	A	403	LEU
1	A	430	MET
1	A	523	THR
1	A	529	ASP
1	A	530	LEU
1	A	532	LYS
1	A	533	LEU
1	A	534	HIS
2	B	19	GLU
2	B	99	THR
2	B	221	ASP
2	B	287	ILE
2	B	288	ASN
2	B	292	ASN
2	B	334	THR
2	B	381	GLN
2	B	406	THR
2	B	480	MET
3	D	32	LYS
3	D	33	PRO
3	D	63	MET
3	D	110	THR
3	D	123	CYS
3	D	195	MET
3	D	210	ASP
3	D	217	LEU

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Mol	Chain	Res	Type
3	D	224	CYS
3	D	256	LEU
3	D	315	LEU
3	D	340	CYS
3	D	364	LEU
3	D	371	ASN
3	D	444	ARG
3	D	452	TYR
3	D	516	LEU
3	D	537	ASP
3	D	542	ARG
4	E	28	LEU
4	E	29	MET
4	E	48	MET
4	E	63	ASP
4	E	84	ASP
4	E	86	GLN
4	E	102	ILE
4	E	107	THR
4	E	148	LEU
4	E	160	LYS
4	E	203	ASP
4	E	219	LEU
4	E	244	GLU
4	E	306	PHE
4	E	345	PHE
4	E	351	GLU
4	E	369	ASP
4	E	381	ARG
4	E	384	THR
4	E	388	ARG
4	E	397	GLU
4	E	426	GLU
4	E	443	LEU
4	E	446	TYR
4	E	509	THR
4	E	515	GLN
4	E	527	ILE
4	E	528	LEU
4	E	535	LYS
5	G	10	LEU
5	G	97	SER

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Mol	Chain	Res	Type
5	G	140	ILE
5	G	225	THR
5	G	234	LYS
5	G	235	ASN
5	G	284	GLN
5	G	336	GLU
5	G	341	GLU
5	G	359	TYR
5	G	382	GLU
5	G	427	LYS
5	G	503	LEU
5	G	504	GLN
6	H	8	LEU
6	H	10	LYS
6	H	11	GLU
6	H	16	SER
6	H	21	GLN
6	H	134	ASN
6	H	138	GLU
6	H	198	LYS
6	H	227	MET
6	H	241	ASN
6	H	345	CYS
6	H	403	ASP
6	H	521	LYS
7	Q	13	GLN
7	Q	14	MET
7	Q	15	LEU
7	Q	17	GLU
7	Q	141	GLU
7	Q	173	TYR
7	Q	175	ASN
7	Q	227	THR
7	Q	383	ASN
7	Q	399	PHE
7	Q	406	LYS
7	Q	428	GLU
7	Q	473	GLU
7	Q	509	LYS
7	Q	518	VAL
7	Q	524	ILE
7	Q	526	MET

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Mol	Chain	Res	Type
7	Q	528	LYS
8	Z	196	MET
8	Z	197	LYS
8	Z	217	ARG
8	Z	225	VAL
8	Z	227	ASP
8	Z	370	ARG
8	Z	374	LEU
8	Z	380	ASN
8	Z	507	SER
8	Z	508	CYS
8	Z	519	ASP
8	Z	523	ARG
1	a	1006	SER
1	a	1010	ASP
1	a	1018	ARG
1	a	1035	SER
1	a	1047	ASP
1	a	1049	ILE
1	a	1068	GLU
1	a	1088	ASP
1	a	1110	GLN
1	a	1125	CYS
1	a	1137	ILE
1	a	1138	ILE
1	a	1143	LEU
1	a	1146	ASP
1	a	1158	SER
1	a	1168	PHE
1	a	1172	VAL
1	a	1177	LEU
1	a	1180	LYS
1	a	1181	TYR
1	a	1212	ASN
1	a	1372	SER
1	a	1382	ASP
1	a	1400	LYS
1	a	1403	LEU
1	a	1523	THR
1	a	1526	ARG
1	a	1534	HIS
2	b	1017	ASP

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Mol	Chain	Res	Type
2	b	1049	ASP
2	b	1062	MET
2	b	1172	LEU
2	b	1195	ASN
2	b	1209	LEU
2	b	1376	ARG
2	b	1388	ARG
2	b	1390	LEU
2	b	1396	VAL
2	b	1427	ARG
2	b	1431	LYS
2	b	1470	SER
2	b	1495	GLU
2	b	1506	SER
2	b	1509	GLU
2	b	1521	ILE
2	b	1522	LYS
3	d	1024	LYS
3	d	1084	MET
3	d	1087	LEU
3	d	1153	ASP
3	d	1176	SER
3	d	1215	LYS
3	d	1216	LYS
3	d	1217	LEU
3	d	1387	LYS
3	d	1394	ARG
3	d	1396	SER
3	d	1397	ASN
3	d	1424	LEU
3	d	1478	SER
3	d	1518	SER
3	d	1520	SER
3	d	1531	SER
3	d	1542	ARG
4	e	1022	GLN
4	e	1023	ASP
4	e	1024	ARG
4	e	1025	LYS
4	e	1027	ARG
4	e	1048	MET
4	e	1055	ASN

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Mol	Chain	Res	Type
4	e	1118	GLU
4	e	1195	THR
4	e	1203	ASP
4	e	1383	VAL
4	e	1392	LYS
4	e	1393	MET
4	e	1426	GLU
4	e	1515	GLN
5	g	1012	GLN
5	g	1016	ARG
5	g	1023	GLN
5	g	1051	LEU
5	g	1059	MET
5	g	1064	ASN
5	g	1091	VAL
5	g	1118	HIS
5	g	1140	ILE
5	g	1158	SER
5	g	1162	THR
5	g	1170	SER
5	g	1216	ARG
5	g	1372	CYS
5	g	1397	VAL
5	g	1398	CYS
5	g	1433	GLU
5	g	1503	LEU
5	g	1518	ARG
6	h	1008	LEU
6	h	1016	SER
6	h	1019	ILE
6	h	1021	GLN
6	h	1043	ARG
6	h	1045	MET
6	h	1051	ASP
6	h	1092	ASP
6	h	1126	ARG
6	h	1186	LEU
6	h	1370	CYS
6	h	1381	PHE
6	h	1403	ASP
6	h	1425	ARG
6	h	1450	CYS

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Mol	Chain	Res	Type
6	h	1473	MET
6	h	1497	MET
6	h	1504	THR
7	q	1015	LEU
7	q	1016	LYS
7	q	1085	MET
7	q	1126	SER
7	q	1138	LYS
7	q	1156	ASP
7	q	1166	THR
7	q	1173	TYR
7	q	1205	CYS
7	q	1208	LEU
7	q	1381	THR
7	q	1399	PHE
7	q	1403	THR
7	q	1408	LEU
7	q	1456	SER
7	q	1499	ASP
7	q	1524	ILE
8	z	1007	LEU
8	z	1017	GLN
8	z	1032	ASP
8	z	1043	THR
8	z	1047	LEU
8	z	1093	THR
8	z	1104	LYS
8	z	1121	GLU
8	z	1135	GLU
8	z	1138	LYS
8	z	1146	GLU
8	z	1196	MET
8	z	1201	GLU
8	z	1208	ARG
8	z	1229	TYR
8	z	1238	GLU
8	z	1337	ASP
8	z	1342	ASP
8	z	1351	TYR
8	z	1374	LEU
8	z	1386	GLN
8	z	1460	GLN

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Mol	Chain	Res	Type
8	z	1504	LEU
8	z	1523	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (144) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	103	ASN
1	A	366	ASN
1	A	425	ASN
1	A	435	GLN
1	A	455	ASN
1	A	472	ASN
1	A	498	ASN
2	B	161	ASN
2	B	227	ASN
2	B	288	ASN
2	B	294	GLN
2	B	302	GLN
2	B	337	HIS
2	B	381	GLN
2	B	391	HIS
2	B	453	ASN
2	B	498	GLN
3	D	40	ASN
3	D	83	GLN
3	D	101	GLN
3	D	132	HIS
3	D	292	GLN
3	D	371	ASN
3	D	471	ASN
4	E	22	GLN
4	E	46	ASN
4	E	98	GLN
4	E	129	HIS
4	E	236	HIS
4	E	311	ASN
4	E	317	ASN
4	E	481	GLN
4	E	522	GLN
5	G	23	GLN
5	G	28	ASN

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Mol	Chain	Res	Type
5	G	64	ASN
5	G	73	GLN
5	G	118	HIS
5	G	154	ASN
5	G	221	ASN
5	G	321	ASN
5	G	396	GLN
5	G	400	ASN
5	G	434	GLN
5	G	454	ASN
6	H	17	GLN
6	H	21	GLN
6	H	25	ASN
6	H	73	HIS
6	H	107	GLN
6	H	134	ASN
6	H	171	GLN
6	H	241	ASN
6	H	432	GLN
6	H	448	GLN
6	H	470	GLN
6	H	487	ASN
6	H	501	ASN
7	Q	59	HIS
7	Q	93	GLN
7	Q	198	ASN
7	Q	201	ASN
7	Q	219	HIS
7	Q	346	HIS
7	Q	435	GLN
7	Q	513	ASN
8	Z	23	ASN
8	Z	71	HIS
8	Z	294	GLN
8	Z	380	ASN
8	Z	400	ASN
8	Z	438	GLN
8	Z	453	GLN
8	Z	454	ASN
8	Z	514	ASN
1	a	1021	ASN
1	a	1082	GLN

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Mol	Chain	Res	Type
1	a	1103	ASN
1	a	1110	GLN
1	a	1393	HIS
1	a	1425	ASN
1	a	1498	ASN
1	a	1500	GLN
2	b	1073	ASN
2	b	1091	GLN
2	b	1124	GLN
2	b	1161	ASN
2	b	1195	ASN
2	b	1200	HIS
2	b	1380	GLN
2	b	1502	GLN
3	d	1028	GLN
3	d	1141	GLN
3	d	1168	ASN
3	d	1175	ASN
3	d	1485	ASN
4	e	1055	ASN
4	e	1098	GLN
4	e	1184	GLN
4	e	1391	ASN
4	e	1411	ASN
4	e	1481	GLN
4	e	1522	GLN
5	g	1012	GLN
5	g	1073	GLN
5	g	1154	ASN
5	g	1434	GLN
5	g	1454	ASN
5	g	1470	HIS
5	g	1504	GLN
6	h	1021	GLN
6	h	1073	HIS
6	h	1134	ASN
6	h	1151	GLN
6	h	1191	GLN
6	h	1201	GLN
6	h	1209	GLN
6	h	1402	ASN
6	h	1431	GLN

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Mol	Chain	Res	Type
6	h	1448	GLN
6	h	1452	ASN
6	h	1487	ASN
7	q	1050	ASN
7	q	1093	GLN
7	q	1102	ASN
7	q	1165	HIS
7	q	1185	GLN
7	q	1435	GLN
7	q	1513	ASN
7	q	1523	GLN
8	z	1023	ASN
8	z	1031	GLN
8	z	1070	GLN
8	z	1234	ASN
8	z	1293	ASN
8	z	1368	ASN
8	z	1386	GLN
8	z	1400	ASN
8	z	1434	GLN
8	z	1438	GLN
8	z	1460	GLN
8	z	1497	ASN
8	z	1503	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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, 95^{th} 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	481/556 (86%)	1.61	142 (29%) 0 1	260, 260, 260, 260	0
1	a	359/556 (64%)	2.09	149 (41%) 0 0	282, 282, 282, 282	0
2	B	481/535 (89%)	2.59	229 (47%) 0 0	281, 281, 281, 281	0
2	b	359/535 (67%)	2.17	159 (44%) 0 0	272, 272, 272, 272	0
3	D	481/542 (88%)	1.80	158 (32%) 0 1	289, 289, 289, 289	0
3	d	359/542 (66%)	1.80	133 (37%) 0 1	266, 266, 266, 266	0
4	E	481/541 (88%)	1.25	109 (22%) 0 2	262, 262, 262, 262	0
4	e	359/541 (66%)	2.40	164 (45%) 0 0	283, 283, 283, 283	0
5	G	481/545 (88%)	1.96	185 (38%) 0 1	283, 283, 283, 283	0
5	g	359/545 (65%)	1.17	75 (20%) 1 2	275, 275, 275, 275	0
6	H	481/543 (88%)	1.70	159 (33%) 0 1	272, 272, 272, 272	0
6	h	359/543 (66%)	1.19	86 (23%) 0 2	258, 258, 258, 258	0
7	Q	481/548 (87%)	2.59	233 (48%) 0 0	308, 308, 308, 308	0
7	q	359/548 (65%)	2.02	154 (42%) 0 0	261, 261, 261, 261	0
8	Z	481/531 (90%)	2.52	218 (45%) 0 0	297, 297, 297, 297	0
8	z	481/531 (90%)	2.37	193 (40%) 0 1	276, 276, 276, 276	0
All	All	6842/8682 (78%)	1.97	2546 (37%) 0 1	258, 276, 308, 308	0

All (2546) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	Z	288	GLY	25.1
8	z	1209	GLY	21.7
6	H	224	GLY	18.4
8	z	1288	GLY	16.3
4	e	1226	LYS	15.8

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Mol	Chain	Res	Type	RSRZ
6	H	228	GLN	14.7
8	z	1268	GLU	14.5
8	z	1216	ALA	14.3
2	B	219	LEU	14.3
2	B	215	ASP	14.2
2	B	218	PHE	13.9
3	d	1170	ALA	13.8
7	Q	192	PRO	13.6
8	Z	312	ALA	13.4
7	Q	412	GLY	13.3
1	A	333	ASN	13.0
2	B	200	HIS	12.7
1	A	334	LEU	12.5
8	z	1312	ALA	12.4
2	B	223	LYS	12.2
7	Q	197	PHE	12.2
8	z	1210	LEU	12.1
8	Z	278	LYS	11.9
1	A	190	TYR	11.8
1	A	331	LEU	11.8
8	z	1267	ILE	11.6
7	Q	67	ASN	11.5
7	Q	290	VAL	11.5
2	b	1406	THR	11.5
6	H	229	PRO	11.3
5	G	156	ILE	11.3
7	Q	219	HIS	11.2
7	Q	311	MET	11.2
8	Z	267	ILE	11.2
4	e	1224	LEU	11.2
8	z	1237	LEU	11.1
2	b	1407	VAL	11.1
2	B	220	LEU	11.0
8	Z	216	ALA	10.9
3	D	327	VAL	10.9
3	D	236	VAL	10.9
7	Q	231	VAL	10.9
8	Z	236	SER	10.8
3	D	312	LEU	10.8
8	z	1208	ARG	10.8
2	b	1013	LYS	10.7
7	Q	309	ASN	10.7

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Mol	Chain	Res	Type	RSRZ
8	Z	289	PHE	10.7
8	z	1311	ILE	10.6
4	e	1493	CYS	10.5
7	Q	289	ASN	10.4
2	B	308	GLY	10.4
4	E	235	SER	10.4
1	A	191	PRO	10.3
8	Z	211	VAL	10.3
8	Z	209	GLY	10.3
6	H	10	LYS	10.3
2	B	221	ASP	10.2
5	G	525	GLY	10.2
2	b	1016	ALA	10.2
2	b	1495	GLU	10.1
2	B	214	LEU	10.1
8	z	1289	PHE	10.1
2	b	1494	THR	10.0
8	z	1310	ILE	10.0
8	Z	344	LEU	10.0
2	b	1015	GLY	10.0
2	b	1496	SER	10.0
8	Z	210	LEU	9.9
7	Q	191	PHE	9.9
8	Z	296	GLY	9.9
7	Q	188	VAL	9.9
8	Z	237	LEU	9.8
8	z	1213	ASP	9.8
7	Q	190	ILE	9.8
2	B	16	ALA	9.7
1	a	1370	ARG	9.7
2	B	224	ILE	9.7
7	Q	310	ILE	9.7
7	Q	189	SER	9.6
2	B	360	ILE	9.6
2	B	244	MET	9.6
8	z	1371	SER	9.5
1	a	1160	VAL	9.5
1	A	275	ILE	9.4
8	z	1222	LYS	9.3
1	A	330	THR	9.3
8	Z	192	GLU	9.2
1	A	243	LYS	9.2

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Mol	Chain	Res	Type	RSRZ
4	e	1380	SER	9.2
2	B	296	ILE	9.2
3	D	235	LYS	9.2
7	q	1219	HIS	9.1
2	B	198	ALA	9.1
4	e	1225	ILE	9.1
5	G	310	THR	9.0
8	z	1225	VAL	9.0
8	z	1339	LEU	8.9
3	d	1169	SER	8.9
8	Z	232	THR	8.9
2	B	313	GLU	8.8
8	z	1223	LYS	8.8
3	d	1199	ASP	8.8
2	b	1014	ALA	8.8
3	D	328	VAL	8.8
3	D	329	LYS	8.8
5	G	14	THR	8.7
2	B	309	VAL	8.7
8	z	1313	LEU	8.7
2	B	236	LYS	8.7
8	Z	295	LYS	8.7
1	A	194	SER	8.7
1	a	1397	CYS	8.7
8	z	1373	THR	8.6
3	D	320	LEU	8.6
8	z	1352	GLU	8.6
2	b	1409	GLY	8.6
5	G	230	ARG	8.5
7	Q	297	VAL	8.5
8	z	1271	VAL	8.5
3	D	232	LEU	8.5
7	Q	196	HIS	8.5
2	B	304	PHE	8.5
7	q	1172	GLN	8.5
3	d	1173	SER	8.4
8	z	1192	GLU	8.4
2	b	1410	GLY	8.4
4	e	1508	GLU	8.4
2	B	213	TYR	8.4
6	H	310	CYS	8.4
3	D	237	ALA	8.4

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Mol	Chain	Res	Type	RSRZ
2	B	216	GLU	8.4
6	H	215	ALA	8.4
8	z	1307	LYS	8.3
8	Z	217	ARG	8.3
2	B	15	GLY	8.3
8	z	1372	VAL	8.3
3	D	189	MET	8.3
8	z	1217	ARG	8.3
2	b	1408	TYR	8.3
2	B	342	LYS	8.2
7	q	1499	ASP	8.2
4	e	1382	ALA	8.2
4	E	323	ARG	8.2
2	B	287	ILE	8.2
5	G	15	LYS	8.1
8	Z	313	LEU	8.1
3	D	238	ASN	8.1
7	Q	413	GLY	8.1
8	z	1224	ARG	8.1
2	B	282	ILE	8.1
2	B	311	ALA	8.1
8	Z	221	MET	8.1
2	B	370	ALA	8.1
7	Q	248	GLY	8.1
8	z	1308	GLU	8.1
4	E	95	SER	8.1
8	Z	274	ILE	8.1
7	Q	225	LYS	8.1
1	a	1086	VAL	8.0
1	a	1373	ALA	8.0
6	H	13	THR	8.0
6	H	223	ALA	8.0
5	G	203	LYS	7.9
8	Z	310	ILE	7.9
8	Z	292	ILE	7.9
8	z	1269	ASP	7.9
8	Z	320	ASN	7.9
4	e	1383	VAL	7.9
8	z	1293	ASN	7.9
8	z	1290	VAL	7.9
7	q	1018	GLY	7.9
8	Z	235	VAL	7.9

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Mol	Chain	Res	Type	RSRZ
8	z	1291	VAL	7.8
7	Q	366	GLU	7.8
2	b	1368	GLY	7.8
3	d	1495	GLY	7.8
8	Z	345	GLY	7.8
7	q	1410	PRO	7.8
7	q	1203	ARG	7.8
3	D	311	ALA	7.8
8	z	1336	LEU	7.7
8	z	1226	GLU	7.7
1	a	1394	ASP	7.7
5	G	290	VAL	7.7
3	D	256	LEU	7.7
1	a	1471	HIS	7.7
5	G	219	MET	7.7
1	a	1205	GLN	7.7
2	B	334	THR	7.7
7	Q	232	THR	7.6
2	B	237	ILE	7.6
4	E	285	PHE	7.6
4	e	1223	LYS	7.6
3	D	377	ILE	7.6
2	B	327	THR	7.6
8	z	1212	LEU	7.6
8	z	1363	ILE	7.5
8	Z	311	ILE	7.5
8	z	1361	THR	7.5
4	E	321	ALA	7.5
5	G	282	ILE	7.5
3	d	1221	ILE	7.5
4	E	306	PHE	7.5
4	e	1102	ILE	7.5
7	Q	500	THR	7.5
1	a	1161	ILE	7.5
7	Q	370	GLY	7.5
7	Q	155	ARG	7.5
4	e	1185	MET	7.5
1	A	195	ILE	7.5
8	Z	497	ASN	7.4
6	H	216	PHE	7.4
4	E	322	VAL	7.4
5	G	289	VAL	7.4

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Mol	Chain	Res	Type	RSRZ
2	B	343	LEU	7.4
2	B	362	PHE	7.4
8	z	1228	ALA	7.4
2	B	300	PRO	7.4
7	Q	308	TYR	7.4
1	a	1472	ASN	7.4
8	z	1304	ALA	7.4
1	A	143	LEU	7.4
5	G	160	ILE	7.3
7	Q	187	CYS	7.3
4	e	1405	ALA	7.3
4	e	1022	GLN	7.3
4	e	1409	ILE	7.3
7	Q	193	ASP	7.3
8	Z	223	LYS	7.3
2	b	1148	HIS	7.3
2	B	338	PRO	7.3
7	q	1370	GLY	7.3
8	Z	233	CYS	7.3
2	B	199	ILE	7.3
1	A	335	GLU	7.2
3	D	190	SER	7.2
6	H	309	PHE	7.2
1	a	1162	GLY	7.2
8	z	1227	ASP	7.2
5	G	524	SER	7.2
7	q	1398	THR	7.2
8	Z	271	VAL	7.2
8	Z	293	ASN	7.2
2	B	312	ILE	7.2
4	E	255	PHE	7.2
1	A	271	THR	7.2
4	e	1172	THR	7.2
8	Z	321	MET	7.1
5	G	287	PRO	7.1
3	d	1428	GLY	7.1
7	Q	288	ALA	7.1
8	Z	230	ILE	7.1
7	q	1173	TYR	7.1
1	A	345	LEU	7.1
2	B	345	SER	7.1
6	H	308	MET	7.1

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Mol	Chain	Res	Type	RSRZ
8	z	1338	ASP	7.1
4	e	1509	THR	7.1
2	B	279	VAL	7.1
2	B	239	ILE	7.1
2	B	372	THR	7.1
5	G	311	ALA	7.1
2	B	494	THR	7.1
3	D	231	VAL	7.1
5	g	1199	ALA	7.0
5	G	526	HIS	7.0
6	H	468	HIS	7.0
8	Z	323	ARG	7.0
7	q	1097	VAL	7.0
7	q	1099	ASP	7.0
8	z	1305	LEU	7.0
6	H	12	GLY	6.9
8	Z	191	VAL	6.9
2	b	1149	GLY	6.9
7	Q	99	ASP	6.9
7	Q	239	ILE	6.9
4	e	1173	LEU	6.9
7	Q	235	LYS	6.9
1	A	332	ALA	6.9
2	B	411	GLY	6.9
8	Z	222	LYS	6.9
2	B	228	GLN	6.9
8	Z	291	VAL	6.9
8	z	1211	VAL	6.9
5	g	1201	VAL	6.9
3	D	378	LYS	6.9
7	q	1197	PHE	6.8
3	d	1159	GLU	6.8
8	Z	234	ASN	6.8
8	z	1274	ILE	6.8
7	Q	287	GLY	6.8
5	g	1372	CYS	6.8
3	D	105	ALA	6.8
5	G	224	VAL	6.8
4	e	1491	ILE	6.8
7	Q	348	ASP	6.8
3	d	1107	ASP	6.8
3	d	1228	GLU	6.8

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Mol	Chain	Res	Type	RSRZ
1	a	1145	ARG	6.7
5	G	283	ILE	6.7
7	Q	365	HIS	6.7
7	q	1374	THR	6.7
8	Z	346	HIS	6.7
8	z	1186	ILE	6.7
8	Z	363	ILE	6.7
4	e	1084	ASP	6.7
8	Z	231	LEU	6.7
4	e	1055	ASN	6.7
6	H	244	LEU	6.7
3	d	1174	LEU	6.7
1	A	372	SER	6.7
4	e	1537	GLY	6.7
2	B	290	PHE	6.7
5	g	1200	ARG	6.6
7	q	1217	VAL	6.6
2	B	297	TYR	6.6
4	e	1387	ILE	6.6
5	G	335	PRO	6.6
2	B	230	LYS	6.6
1	a	1413	GLY	6.6
2	b	1493	ILE	6.6
2	b	1369	GLU	6.6
4	e	1190	VAL	6.6
4	e	1404	ASP	6.6
6	H	402	ASN	6.6
1	a	1144	GLY	6.6
4	e	1497	GLY	6.6
4	e	1183	ARG	6.6
8	z	1297	ILE	6.6
2	B	307	ALA	6.5
4	e	1381	ARG	6.5
7	Q	151	ALA	6.5
8	z	1320	ASN	6.5
2	B	335	PHE	6.5
7	q	1373	SER	6.5
3	D	170	ALA	6.5
8	z	1179	ILE	6.5
5	G	239	VAL	6.5
4	e	1166	ILE	6.5
1	A	274	ARG	6.5

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Mol	Chain	Res	Type	RSRZ
4	e	1054	PRO	6.5
7	Q	367	LYS	6.5
2	B	164	GLY	6.5
8	Z	411	ALA	6.5
2	b	1477	GLY	6.5
5	G	13	ASN	6.5
4	E	289	ILE	6.5
4	E	234	PHE	6.5
7	q	1204	VAL	6.5
6	H	225	PHE	6.5
2	B	217	GLY	6.4
7	q	1048	GLY	6.4
2	B	361	HIS	6.4
3	d	1426	ALA	6.4
8	Z	330	GLY	6.4
8	z	1272	LYS	6.4
7	Q	326	LYS	6.4
7	Q	224	LYS	6.4
7	q	1202	ILE	6.4
7	Q	299	ASP	6.4
3	D	426	ALA	6.4
1	A	283	ALA	6.4
7	Q	373	SER	6.3
3	D	233	THR	6.3
4	e	1170	LYS	6.3
2	B	163	ALA	6.3
7	Q	479	GLY	6.3
4	e	1384	THR	6.3
2	B	301	GLU	6.3
2	B	371	CYS	6.3
4	e	1053	GLY	6.3
2	B	373	ILE	6.3
2	B	298	ASN	6.3
4	e	1082	ASP	6.3
8	Z	350	VAL	6.3
2	B	201	VAL	6.3
1	a	1157	SER	6.3
3	D	326	MET	6.3
3	d	1161	SER	6.3
3	d	1177	LYS	6.3
7	Q	202	ILE	6.3
3	D	212	LYS	6.3

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Mol	Chain	Res	Type	RSRZ
7	q	1216	SER	6.3
4	e	1182	HIS	6.2
8	z	1238	GLU	6.2
4	e	1496	LYS	6.2
5	G	157	ASN	6.2
2	b	1411	GLY	6.2
7	Q	204	VAL	6.2
7	Q	347	CYS	6.2
7	q	1500	THR	6.2
5	G	291	ILE	6.2
3	d	1389	VAL	6.2
7	q	1019	ALA	6.2
1	a	1159	LYS	6.2
8	Z	331	ILE	6.2
1	A	214	TYR	6.2
8	z	1236	SER	6.2
8	Z	294	GLN	6.2
8	Z	179	ILE	6.2
2	B	96	GLY	6.2
7	Q	236	ASP	6.2
7	Q	371	ALA	6.2
2	B	303	LEU	6.2
4	e	1095	SER	6.2
7	Q	291	VAL	6.1
6	h	1014	ASP	6.1
4	e	1189	ALA	6.1
2	b	1500	LYS	6.1
3	d	1211	ILE	6.1
8	Z	180	LYS	6.1
1	a	1156	MET	6.1
2	B	341	VAL	6.1
4	e	1385	ILE	6.1
2	B	235	ALA	6.1
4	e	1406	LEU	6.1
6	H	520	ILE	6.1
7	Q	150	SER	6.1
8	z	1301	SER	6.1
1	a	1473	GLU	6.1
7	Q	489	VAL	6.1
3	D	322	LYS	6.1
4	e	1422	GLY	6.1
8	Z	315	ARG	6.1

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Mol	Chain	Res	Type	RSRZ
7	q	1212	VAL	6.1
1	a	1177	LEU	6.1
7	Q	327	THR	6.1
7	Q	372	ILE	6.1
4	E	236	HIS	6.1
2	B	13	LYS	6.1
3	D	365	ALA	6.0
7	q	1412	GLY	6.0
8	Z	268	GLU	6.0
7	Q	363	PHE	6.0
3	D	214	VAL	6.0
5	G	7	VAL	6.0
2	B	14	ALA	6.0
6	H	494	GLU	6.0
7	q	1395	GLY	6.0
8	Z	212	LEU	6.0
1	a	1155	SER	6.0
3	d	1423	ALA	6.0
2	b	1474	THR	6.0
7	Q	364	LYS	6.0
2	b	1146	VAL	6.0
7	Q	403	THR	6.0
7	q	1215	SER	6.0
3	d	1206	VAL	6.0
7	Q	501	TYR	6.0
7	Q	324	LEU	6.0
5	G	8	LEU	6.0
5	G	16	ARG	6.0
2	b	1476	ALA	5.9
2	B	238	LEU	5.9
1	a	1470	PHE	5.9
4	e	1174	GLY	5.9
8	Z	366	CYS	5.9
3	D	325	ILE	5.9
7	Q	414	ALA	5.9
8	z	1364	GLU	5.9
7	Q	201	ASN	5.9
1	a	1174	ASP	5.9
6	H	14	ASP	5.9
8	z	1207	ILE	5.9
1	A	145	ARG	5.9
8	Z	301	SER	5.8

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Mol	Chain	Res	Type	RSRZ
8	Z	361	THR	5.8
2	B	95	VAL	5.8
1	a	1208	SER	5.8
3	d	1386	GLY	5.8
8	z	1316	ALA	5.8
1	A	66	GLU	5.8
5	G	296	ILE	5.8
6	H	214	VAL	5.8
8	z	1089	GLY	5.8
1	a	1212	ASN	5.8
2	B	365	VAL	5.8
4	E	256	GLU	5.8
6	h	1083	ALA	5.8
2	B	310	MET	5.8
8	Z	218	HIS	5.8
4	e	1408	VAL	5.8
8	Z	10	LYS	5.8
5	G	319	ASP	5.8
3	D	85	GLN	5.8
7	Q	227	THR	5.8
5	G	308	ASN	5.8
8	z	1231	LEU	5.8
7	q	1378	ARG	5.8
5	G	58	VAL	5.8
8	z	1522	MET	5.8
4	e	1191	ASN	5.7
4	e	1176	LYS	5.7
3	D	239	SER	5.7
4	e	1025	LYS	5.7
8	Z	328	CYS	5.7
3	D	313	SER	5.7
3	D	321	ASN	5.7
5	G	394	ALA	5.7
7	Q	198	ASN	5.7
2	B	374	VAL	5.7
5	G	244	SER	5.7
4	E	102	ILE	5.7
4	E	22	GLN	5.7
1	A	210	LEU	5.7
1	A	278	ILE	5.7
2	b	1154	LYS	5.7
1	A	212	ASN	5.7

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Mol	Chain	Res	Type	RSRZ
3	D	224	CYS	5.7
3	D	376	LEU	5.7
6	H	311	ALA	5.7
4	e	1178	VAL	5.7
7	Q	307	LYS	5.7
8	Z	277	LEU	5.7
8	z	1524	ALA	5.7
5	G	91	VAL	5.7
3	d	1493	THR	5.7
5	G	355	ILE	5.6
7	q	1414	ALA	5.6
3	D	215	LYS	5.6
4	e	1402	LEU	5.6
2	B	225	GLY	5.6
4	e	1165	LEU	5.6
2	B	278	LYS	5.6
4	e	1169	ALA	5.6
4	e	1209	ILE	5.6
8	Z	225	VAL	5.6
2	b	1466	ARG	5.6
7	q	1150	SER	5.6
2	B	229	PRO	5.6
3	D	318	HIS	5.6
1	a	1401	ARG	5.6
1	a	1488	LEU	5.6
5	g	1216	ARG	5.6
8	Z	314	ARG	5.6
6	H	9	LEU	5.6
7	Q	416	GLU	5.6
8	Z	229	TYR	5.6
2	B	288	ASN	5.5
5	G	390	ASN	5.5
8	Z	371	SER	5.5
8	Z	336	LEU	5.5
8	Z	496	ASP	5.5
7	q	1375	ILE	5.5
6	H	410	GLY	5.5
3	D	366	GLU	5.5
3	d	1213	ILE	5.5
2	B	329	GLY	5.5
2	B	286	GLY	5.5
7	Q	499	ASP	5.5

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Mol	Chain	Res	Type	RSRZ
3	D	185	LEU	5.5
7	Q	411	GLY	5.5
5	G	17	GLU	5.5
8	z	1309	GLY	5.5
8	Z	213	ASP	5.5
7	Q	237	ALA	5.5
8	Z	316	ALA	5.5
8	Z	373	THR	5.5
4	e	1024	ARG	5.4
5	G	218	VAL	5.4
8	z	1323	ARG	5.4
3	D	324	LYS	5.4
7	Q	240	ALA	5.4
3	d	1496	ILE	5.4
4	E	311	ASN	5.4
1	A	281	THR	5.4
8	Z	275	ILE	5.4
2	b	1497	PHE	5.4
3	d	1388	THR	5.4
5	g	1203	LYS	5.4
8	Z	90	ASP	5.4
4	e	1161	ASN	5.4
4	E	98	GLN	5.4
7	Q	480	LEU	5.4
2	B	289	CYS	5.4
8	Z	364	GLU	5.4
1	a	1372	SER	5.4
8	z	1278	LYS	5.4
3	D	173	SER	5.4
1	A	373	ALA	5.4
1	a	1204	SER	5.4
2	b	1199	ILE	5.3
2	B	344	GLY	5.3
4	e	1168	THR	5.3
8	z	1229	TYR	5.3
2	b	1478	LEU	5.3
5	G	384	LEU	5.3
7	Q	220	GLY	5.3
8	Z	347	ALA	5.3
7	q	1049	PRO	5.3
5	G	245	LEU	5.3
2	B	337	HIS	5.3

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Mol	Chain	Res	Type	RSRZ
8	z	1221	MET	5.3
5	G	159	SER	5.3
6	H	519	THR	5.3
8	z	1181	LYS	5.3
4	E	292	ILE	5.3
5	g	1433	GLU	5.3
4	e	1175	SER	5.3
8	z	1230	ILE	5.3
2	B	421	VAL	5.3
2	B	478	LEU	5.3
2	b	1415	MET	5.3
8	Z	334	ASN	5.3
4	e	1056	GLY	5.2
3	D	367	GLU	5.2
7	Q	147	VAL	5.2
2	B	392	ASP	5.2
8	z	1158	THR	5.2
5	G	152	MET	5.2
8	z	1321	MET	5.2
8	z	1350	VAL	5.2
6	H	11	GLU	5.2
8	Z	88	THR	5.2
2	B	92	ASP	5.2
1	A	342	ALA	5.2
2	B	366	ALA	5.2
2	b	1043	LEU	5.2
3	D	298	CYS	5.2
5	G	202	GLU	5.2
2	b	1499	VAL	5.2
3	D	310	ASP	5.2
4	e	1388	ARG	5.2
7	Q	407	ARG	5.2
1	a	1164	ASN	5.2
2	B	280	GLU	5.2
8	Z	332	ALA	5.2
5	G	363	ILE	5.2
8	z	1292	ILE	5.2
7	Q	215	SER	5.2
7	q	1411	GLY	5.2
6	H	401	LYS	5.2
2	B	331	ILE	5.2
5	G	165	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
6	H	465	ARG	5.2
8	z	1088	THR	5.2
4	e	1459	PRO	5.2
5	G	361	THR	5.1
7	Q	368	GLU	5.1
5	G	304	LEU	5.1
5	G	338	LEU	5.1
4	E	254	PRO	5.1
7	q	1196	HIS	5.1
7	Q	55	MET	5.1
2	b	1184	VAL	5.1
6	H	348	PHE	5.1
6	H	476	GLY	5.1
6	h	1407	ALA	5.1
7	Q	180	ALA	5.1
8	Z	238	GLU	5.1
2	b	1165	THR	5.1
6	h	1495	PRO	5.1
2	B	322	ARG	5.1
4	e	1386	PHE	5.1
7	q	1478	VAL	5.1
7	Q	218	LEU	5.1
2	B	17	ASP	5.1
1	A	404	GLU	5.1
8	z	1525	GLY	5.1
3	D	330	ASP	5.1
4	e	1532	ASP	5.1
8	Z	305	LEU	5.1
4	E	288	MET	5.1
6	H	347	VAL	5.1
2	B	170	LYS	5.0
2	b	1405	ARG	5.0
4	E	26	SER	5.0
1	a	1210	LEU	5.0
5	G	221	ASN	5.0
1	a	1163	ILE	5.0
8	Z	148	LEU	5.0
3	D	56	GLY	5.0
2	B	169	SER	5.0
5	G	11	SER	5.0
7	Q	296	ARG	5.0
6	H	230	LYS	5.0

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Mol	Chain	Res	Type	RSRZ
3	D	368	VAL	5.0
7	Q	223	PHE	5.0
3	d	1422	ARG	5.0
2	B	336	ASP	5.0
5	G	59	MET	5.0
2	b	1414	GLU	5.0
5	G	523	VAL	5.0
6	H	409	GLY	5.0
8	z	1039	GLY	5.0
7	Q	47	TYR	5.0
3	d	1171	ALA	5.0
7	Q	476	LYS	5.0
5	G	315	VAL	5.0
7	q	1201	ASN	5.0
7	Q	298	ALA	5.0
7	q	1050	ASN	5.0
3	d	1178	VAL	4.9
4	e	1192	ALA	4.9
5	G	155	ILE	4.9
5	g	1087	GLN	4.9
4	E	104	ASP	4.9
1	a	1047	ASP	4.9
6	h	1091	GLY	4.9
1	A	344	MET	4.9
2	b	1465	LEU	4.9
5	G	312	ILE	4.9
2	B	485	ILE	4.9
8	Z	297	ILE	4.9
5	g	1432	VAL	4.9
7	q	1067	ASN	4.9
2	B	166	THR	4.9
4	E	373	VAL	4.9
2	B	430	GLY	4.9
7	Q	415	THR	4.9
1	a	1391	SER	4.9
7	Q	399	PHE	4.9
2	b	1485	ILE	4.9
4	E	253	CYS	4.9
6	H	369	THR	4.9
8	z	1195	GLU	4.9
1	a	1051	ASP	4.9
6	H	467	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
8	Z	239	TYR	4.9
7	q	1047	TYR	4.9
7	Q	66	THR	4.9
7	q	1476	LYS	4.9
7	q	1164	LEU	4.9
2	b	1166	THR	4.9
2	B	332	ALA	4.9
1	a	1203	ARG	4.9
4	E	307	ASP	4.9
8	Z	187	ASP	4.9
3	D	188	PRO	4.9
7	q	1390	ARG	4.9
1	a	1484	LYS	4.8
2	b	1164	GLY	4.8
3	D	213	ILE	4.8
3	D	336	ILE	4.8
2	B	291	ILE	4.8
6	h	1187	ASP	4.8
5	G	281	ASP	4.8
8	Z	398	VAL	4.8
8	z	1239	TYR	4.8
2	B	319	GLY	4.8
8	Z	394	GLY	4.8
8	Z	11	ALA	4.8
4	E	364	PHE	4.8
4	e	1186	ALA	4.8
2	b	1012	PHE	4.8
2	b	1145	ALA	4.8
1	A	192	VAL	4.8
3	D	206	VAL	4.8
4	e	1531	ASP	4.8
6	H	400	ILE	4.8
7	Q	146	LEU	4.8
7	Q	286	THR	4.8
7	q	1191	PHE	4.8
7	Q	179	LEU	4.8
2	B	196	LEU	4.8
1	a	1374	SER	4.8
7	Q	230	ASP	4.8
3	d	1198	ILE	4.8
8	Z	402	ILE	4.8
1	a	1044	MET	4.8

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Mol	Chain	Res	Type	RSRZ
5	G	309	ILE	4.8
7	q	1498	LEU	4.8
3	d	1212	LYS	4.8
2	B	167	LEU	4.7
5	g	1431	GLY	4.7
1	a	1375	VAL	4.7
8	z	1206	LEU	4.7
2	B	393	ALA	4.7
2	B	429	PRO	4.7
6	H	140	ALA	4.7
2	B	315	ALA	4.7
4	e	1104	ASP	4.7
8	Z	193	ILE	4.7
7	Q	234	VAL	4.7
1	a	1006	SER	4.7
1	a	1398	VAL	4.7
2	b	1010	ASN	4.7
7	q	1184	ALA	4.7
1	a	1393	HIS	4.7
4	E	286	GLU	4.7
3	d	1417	CYS	4.7
8	Z	341	PRO	4.7
1	a	1211	ILE	4.7
3	D	361	SER	4.7
5	g	1202	GLU	4.7
5	G	9	VAL	4.7
7	Q	305	ALA	4.7
7	q	1371	ALA	4.7
3	d	1140	PHE	4.7
6	H	364	CYS	4.7
2	b	1045	PRO	4.7
4	e	1536	PRO	4.7
2	b	1095	VAL	4.7
4	e	1222	THR	4.7
7	Q	206	LYS	4.7
3	d	1226	LEU	4.7
8	Z	300	PHE	4.7
7	q	1167	SER	4.7
7	q	1188	VAL	4.7
8	Z	270	ARG	4.7
1	A	215	ALA	4.7
8	Z	343	CYS	4.7

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Mol	Chain	Res	Type	RSRZ
7	q	1171	LYS	4.7
8	Z	372	VAL	4.7
3	d	1506	ILE	4.7
4	E	72	ASN	4.7
5	G	288	ASP	4.7
7	Q	325	CYS	4.7
7	q	1394	ASP	4.7
8	z	1004	VAL	4.7
7	Q	185	GLN	4.7
3	D	384	SER	4.6
6	h	1212	ALA	4.6
1	a	1416	GLU	4.6
2	B	339	GLU	4.6
4	e	1072	ASN	4.6
1	a	1158	SER	4.6
4	e	1535	LYS	4.6
2	B	88	SER	4.6
2	b	1206	GLY	4.6
2	b	1469	HIS	4.6
2	b	1492	GLY	4.6
3	d	1158	VAL	4.6
3	d	1492	LYS	4.6
8	Z	324	LEU	4.6
8	z	1275	ILE	4.6
8	z	1180	LYS	4.6
4	e	1187	GLU	4.6
5	G	87	GLN	4.6
2	b	1163	ALA	4.6
3	d	1393	VAL	4.6
8	z	1479	VAL	4.6
8	z	1273	LYS	4.6
7	Q	312	LEU	4.6
8	z	1194	MET	4.6
5	G	173	CYS	4.6
5	G	294	LYS	4.6
8	z	1185	PRO	4.6
7	Q	284	ALA	4.6
7	q	1376	VAL	4.6
3	D	364	LEU	4.6
7	Q	503	GLY	4.6
7	Q	79	GLN	4.6
2	B	305	GLY	4.6

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Mol	Chain	Res	Type	RSRZ
4	e	1389	GLY	4.6
7	Q	302	LEU	4.6
4	e	1052	LEU	4.5
6	H	477	VAL	4.5
2	B	48	MET	4.5
1	a	1505	GLU	4.5
4	e	1421	GLY	4.5
5	G	391	LEU	4.5
4	e	1023	ASP	4.5
7	q	1413	GLY	4.5
1	A	144	GLY	4.5
6	H	286	ALA	4.5
6	H	287	LYS	4.5
5	G	12	GLN	4.5
7	Q	461	ASN	4.5
7	Q	149	CYS	4.5
6	H	367	ALA	4.5
5	g	1088	ASP	4.5
3	d	1166	LEU	4.5
6	H	141	VAL	4.5
8	Z	348	GLY	4.5
7	q	1415	THR	4.5
1	A	196	ASN	4.5
2	B	320	VAL	4.5
5	G	247	TYR	4.5
6	H	361	PHE	4.5
8	Z	335	SER	4.5
5	G	383	ILE	4.5
1	A	241	LEU	4.5
5	G	226	HIS	4.5
2	b	1138	ARG	4.5
4	e	1091	MET	4.5
1	a	1192	VAL	4.5
7	q	1377	LEU	4.5
5	G	60	THR	4.5
2	B	160	MET	4.4
6	H	493	TRP	4.4
1	a	1387	GLU	4.4
7	Q	148	CYS	4.4
3	D	303	ILE	4.4
4	E	421	GLY	4.4
3	d	1194	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
2	B	91	GLN	4.4
1	A	328	LEU	4.4
7	Q	478	VAL	4.4
8	Z	169	THR	4.4
1	A	179	ILE	4.4
1	a	1087	GLY	4.4
4	E	491	ILE	4.4
5	G	169	SER	4.4
6	H	405	VAL	4.4
5	g	1398	CYS	4.4
5	G	411	GLY	4.4
7	q	1403	THR	4.4
2	b	1447	PRO	4.4
3	d	1189	MET	4.4
6	H	458	THR	4.4
2	b	1400	THR	4.4
4	e	1193	VAL	4.4
3	D	301	LEU	4.4
1	A	235	ALA	4.4
2	B	240	ALA	4.4
1	A	193	ASN	4.4
7	Q	246	PHE	4.4
2	b	1401	VAL	4.4
2	b	1159	LEU	4.4
6	H	196	GLY	4.4
6	h	1168	ILE	4.4
2	b	1488	MET	4.4
3	D	323	MET	4.4
6	H	86	GLN	4.4
2	B	306	ALA	4.4
7	Q	184	ALA	4.3
8	Z	181	LYS	4.3
8	z	1335	SER	4.3
6	H	406	VAL	4.3
8	z	1367	ASN	4.3
5	G	376	LEU	4.3
5	g	1214	VAL	4.3
7	Q	408	LEU	4.3
4	E	257	PRO	4.3
5	G	88	ASP	4.3
5	G	241	LEU	4.3
6	H	186	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
8	z	1478	GLY	4.3
3	D	230	LEU	4.3
2	B	326	VAL	4.3
6	h	1094	THR	4.3
8	Z	290	VAL	4.3
7	Q	228	GLU	4.3
1	a	1449	PRO	4.3
7	Q	410	PRO	4.3
8	z	1277	LEU	4.3
1	a	1175	ALA	4.3
7	Q	238	LYS	4.3
6	H	350	GLU	4.3
2	b	1017	ASP	4.3
8	z	1314	ARG	4.3
3	D	405	GLU	4.3
7	q	1372	ILE	4.3
5	G	292	THR	4.3
4	e	1533	ILE	4.3
3	d	1167	LEU	4.3
6	H	232	TYR	4.3
7	q	1218	LEU	4.3
4	e	1051	SER	4.3
2	b	1162	ILE	4.3
3	d	1208	LEU	4.3
5	G	362	PHE	4.3
7	q	1187	CYS	4.3
2	B	162	ILE	4.3
1	a	1178	ALA	4.3
5	G	323	ILE	4.3
5	G	356	GLY	4.3
8	Z	395	LEU	4.3
3	D	171	ALA	4.2
4	E	359	VAL	4.2
6	H	198	LYS	4.2
1	A	209	MET	4.2
1	A	280	ALA	4.2
7	Q	217	VAL	4.2
5	G	388	GLU	4.2
1	a	1415	VAL	4.2
5	G	480	VAL	4.2
7	Q	221	MET	4.2
1	a	1434	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
2	B	299	TYR	4.2
6	h	1150	GLU	4.2
8	Z	208	ARG	4.2
8	Z	304	ALA	4.2
8	Z	342	ASP	4.2
1	a	1412	GLY	4.2
7	q	1180	ALA	4.2
4	e	1177	VAL	4.2
3	D	23	GLY	4.2
3	D	242	THR	4.2
8	z	1369	PRO	4.2
2	B	65	ASN	4.2
3	D	169	SER	4.2
5	G	387	VAL	4.2
7	Q	362	VAL	4.2
2	B	364	GLY	4.2
6	h	1092	ASP	4.2
1	A	374	SER	4.2
5	G	10	LEU	4.2
7	q	1471	HIS	4.2
1	A	4	PRO	4.2
2	B	172	LEU	4.2
5	G	316	ARG	4.2
7	q	1185	GLN	4.2
3	D	316	ALA	4.2
2	B	363	SER	4.2
3	D	104	GLU	4.2
8	Z	412	GLY	4.2
3	D	107	ASP	4.2
6	h	1013	THR	4.1
3	d	1193	ALA	4.1
4	e	1160	LYS	4.1
4	e	1083	VAL	4.1
7	Q	212	VAL	4.1
3	d	1227	VAL	4.1
2	B	323	LEU	4.1
3	d	1215	LYS	4.1
8	z	1411	ALA	4.1
7	Q	303	HIS	4.1
3	D	335	ASP	4.1
5	G	295	GLY	4.1
8	Z	39	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
5	G	204	ILE	4.1
7	Q	301	ALA	4.1
5	G	302	HIS	4.1
8	Z	220	ASP	4.1
5	g	1434	GLN	4.1
2	b	1160	MET	4.1
7	Q	164	LEU	4.1
8	Z	170	GLU	4.1
2	b	1183	ALA	4.1
1	A	208	SER	4.1
3	D	339	ILE	4.1
8	Z	352	GLU	4.1
7	q	1409	VAL	4.1
6	H	484	ILE	4.1
8	Z	188	LEU	4.1
8	Z	524	ALA	4.1
7	Q	304	TYR	4.1
1	a	1071	ALA	4.1
1	A	375	VAL	4.1
8	Z	143	MET	4.1
1	a	1495	PRO	4.1
5	g	1506	TYR	4.1
6	H	15	SER	4.1
6	H	285	GLY	4.1
7	q	1397	ASN	4.1
8	Z	355	LEU	4.1
7	q	1024	GLY	4.1
1	A	233	LYS	4.1
5	G	313	ARG	4.1
2	B	165	THR	4.1
3	d	1141	GLN	4.1
4	e	1492	ASP	4.1
7	Q	471	HIS	4.1
1	A	86	VAL	4.1
2	b	1524	ALA	4.1
1	a	1468	ARG	4.1
5	g	1522	ILE	4.1
7	Q	482	ILE	4.1
3	D	186	LEU	4.0
4	e	1181	CYS	4.0
7	Q	203	ARG	4.0
8	z	1270	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
6	H	411	ALA	4.0
6	H	359	ASN	4.0
6	h	1438	TYR	4.0
8	Z	498	TYR	4.0
2	B	474	THR	4.0
5	G	228	ARG	4.0
6	h	1205	LEU	4.0
6	h	1070	ASP	4.0
7	q	1051	GLY	4.0
8	Z	367	ASN	4.0
3	d	1387	LYS	4.0
2	B	523	ALA	4.0
2	b	1047	GLY	4.0
8	z	1412	GLY	4.0
5	g	1371	ALA	4.0
4	e	1217	GLY	4.0
6	H	362	THR	4.0
3	D	211	ILE	4.0
6	h	1521	LYS	4.0
2	B	275	MET	4.0
8	Z	303	ASP	4.0
2	b	1412	CYS	4.0
3	D	187	SER	4.0
2	B	333	SER	4.0
7	Q	143	LEU	4.0
2	B	64	THR	4.0
4	e	1164	PRO	4.0
7	q	1176	GLU	4.0
8	Z	410	GLY	4.0
5	g	1198	TYR	4.0
8	Z	408	VAL	4.0
4	E	490	GLY	4.0
6	H	282	HIS	4.0
5	g	1402	LEU	4.0
4	e	1219	LEU	4.0
6	H	412	ILE	4.0
1	a	1414	ALA	4.0
4	E	360	LYS	4.0
7	Q	229	GLY	4.0
8	Z	176	ILE	4.0
7	q	1423	ILE	4.0
6	h	1494	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
4	e	1208	LEU	4.0
6	H	325	ALA	4.0
3	d	1414	VAL	4.0
7	Q	285	ASP	4.0
3	d	1105	ALA	3.9
4	e	1395	ILE	3.9
1	a	1395	ALA	3.9
4	e	1188	ILE	3.9
3	D	393	VAL	3.9
7	Q	64	PHE	3.9
1	A	364	ILE	3.9
5	G	301	GLN	3.9
4	E	325	VAL	3.9
2	b	1198	ALA	3.9
2	B	283	LEU	3.9
3	D	380	THR	3.9
1	a	1469	ALA	3.9
5	G	381	LYS	3.9
6	H	199	LYS	3.9
2	B	493	ILE	3.9
3	D	343	ILE	3.9
8	Z	190	MET	3.9
8	Z	309	GLY	3.9
1	a	1121	TYR	3.9
3	d	1415	ILE	3.9
8	z	1008	ASN	3.9
2	B	168	SER	3.9
1	A	396	LEU	3.9
3	d	1416	ARG	3.9
8	z	1303	ASP	3.9
8	z	1349	LEU	3.9
7	q	1477	ASN	3.9
8	z	1365	LYS	3.9
8	Z	152	ALA	3.9
2	b	1096	GLY	3.9
3	D	225	GLU	3.9
4	e	1167	GLN	3.9
7	q	1163	LEU	3.9
2	b	1046	LYS	3.9
1	A	296	CYS	3.9
1	A	36	LEU	3.9
2	B	195	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
3	D	379	ILE	3.9
1	A	367	THR	3.9
2	B	346	CYS	3.9
6	H	371	THR	3.9
6	H	403	ASP	3.9
1	a	1419	LEU	3.9
3	D	317	LEU	3.9
7	q	1399	PHE	3.9
4	E	21	ASP	3.9
4	E	420	TYR	3.9
3	D	106	GLY	3.9
5	G	92	GLY	3.9
1	A	207	GLU	3.9
7	q	1017	GLU	3.9
8	z	1374	LEU	3.9
7	Q	56	VAL	3.9
2	B	410	GLY	3.8
8	Z	325	THR	3.8
7	Q	226	GLU	3.8
8	Z	327	ALA	3.8
4	e	1481	GLN	3.8
7	q	1069	ALA	3.8
6	h	1406	VAL	3.8
4	e	1507	ILE	3.8
6	H	197	ILE	3.8
8	Z	393	ASP	3.8
5	G	220	ILE	3.8
3	d	1066	ASP	3.8
1	A	371	THR	3.8
6	H	284	SER	3.8
4	e	1221	ASP	3.8
6	h	1184	MET	3.8
1	A	234	ILE	3.8
8	z	1324	LEU	3.8
7	Q	135	ALA	3.8
5	g	1376	LEU	3.8
3	D	240	GLY	3.8
3	D	387	LYS	3.8
5	G	238	ILE	3.8
6	h	1183	VAL	3.8
7	Q	222	VAL	3.8
7	Q	404	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
3	D	342	THR	3.8
4	e	1162	THR	3.8
3	D	471	ASN	3.8
7	Q	168	VAL	3.8
2	B	439	TYR	3.8
1	a	1005	LEU	3.8
3	d	1195	MET	3.8
2	b	1397	LEU	3.8
4	E	456	GLU	3.8
5	G	336	GLU	3.8
8	Z	478	GLY	3.8
8	z	1232	THR	3.8
5	G	382	GLU	3.8
8	Z	523	ARG	3.8
5	g	1437	TYR	3.8
3	d	1192	ASP	3.8
6	H	195	ILE	3.8
1	A	303	ALA	3.8
8	Z	269	ASP	3.8
4	E	241	LYS	3.8
1	A	47	ASP	3.8
3	D	362	ALA	3.8
7	Q	349	SER	3.8
4	e	1184	GLN	3.8
1	a	1486	ILE	3.7
2	b	1097	ASP	3.7
5	G	42	GLY	3.7
4	e	1057	LEU	3.7
7	q	1391	ALA	3.7
7	Q	233	SER	3.7
8	Z	155	SER	3.7
4	E	240	PRO	3.7
5	G	209	ILE	3.7
7	Q	498	LEU	3.7
8	Z	186	ILE	3.7
2	B	49	ASP	3.7
6	H	495	PRO	3.7
6	H	523	PRO	3.7
5	g	1137	LEU	3.7
7	q	1056	VAL	3.7
8	z	1366	CYS	3.7
8	z	1395	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
1	a	1417	ALA	3.7
1	A	37	GLY	3.7
1	a	1392	LEU	3.7
2	b	1413	SER	3.7
3	d	1197	VAL	3.7
3	d	1391	ILE	3.7
1	a	1207	GLU	3.7
7	q	1206	LYS	3.7
8	z	1347	ALA	3.7
4	e	1218	ARG	3.7
7	q	1420	ALA	3.7
2	b	1214	LEU	3.7
4	e	1048	MET	3.7
5	G	350	LEU	3.7
3	D	370	LEU	3.7
7	q	1211	GLY	3.7
1	A	6	SER	3.7
1	a	1506	PRO	3.7
7	q	1504	LYS	3.7
2	B	277	GLU	3.7
7	q	1416	GLU	3.7
4	e	1194	LEU	3.7
5	G	278	LEU	3.7
2	B	81	ALA	3.7
2	b	1468	ALA	3.7
1	A	315	ASP	3.7
3	D	331	ILE	3.7
6	h	1197	ILE	3.7
1	a	1085	GLU	3.7
5	g	1388	GLU	3.7
6	H	217	LYS	3.7
7	q	1392	VAL	3.7
3	D	226	LEU	3.7
7	Q	245	PRO	3.7
7	q	1149	CYS	3.7
2	b	1156	ARG	3.7
8	z	1159	LYS	3.7
3	d	1504	SER	3.7
8	z	1409	PRO	3.7
1	a	1402	VAL	3.7
2	B	431	LYS	3.7
2	b	1486	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
5	g	1374	ILE	3.7
7	q	1155	ARG	3.7
2	B	197	GLU	3.7
4	E	320	PRO	3.6
5	g	1212	SER	3.6
1	A	300	PHE	3.6
4	e	1419	VAL	3.6
7	q	1183	ILE	3.6
7	q	1389	GLU	3.6
3	d	1424	LEU	3.6
5	G	225	THR	3.6
3	D	299	ASN	3.6
5	G	229	MET	3.6
8	z	1344	LEU	3.6
2	B	12	PHE	3.6
1	A	211	ILE	3.6
8	Z	391	ILE	3.6
4	E	314	LEU	3.6
7	Q	442	ALA	3.6
3	d	1058	LYS	3.6
1	a	1518	THR	3.6
2	B	285	HIS	3.6
3	D	404	ALA	3.6
7	Q	441	PHE	3.6
6	h	1098	THR	3.6
7	Q	328	VAL	3.6
1	a	1467	LEU	3.6
2	b	1185	GLU	3.6
4	e	1171	THR	3.6
1	A	318	ARG	3.6
7	Q	65	VAL	3.6
4	e	1216	GLY	3.6
7	Q	445	PHE	3.6
8	Z	406	CYS	3.6
7	Q	452	LEU	3.6
6	H	90	VAL	3.6
8	Z	276	GLU	3.6
4	E	448	MET	3.6
4	e	1466	SER	3.6
4	e	1478	ARG	3.6
1	A	504	PHE	3.6
5	G	521	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
2	b	1428	THR	3.6
3	d	1390	THR	3.6
7	Q	375	ILE	3.6
7	Q	418	GLU	3.6
7	Q	292	VAL	3.6
7	Q	409	VAL	3.6
3	d	1144	LEU	3.6
3	D	257	SER	3.6
2	B	389	SER	3.6
4	e	1059	LYS	3.6
6	H	346	GLN	3.6
7	Q	59	HIS	3.6
8	z	1084	GLN	3.6
8	Z	172	VAL	3.6
1	a	1191	PRO	3.6
8	z	1190	MET	3.6
2	B	302	GLN	3.6
4	E	324	TRP	3.6
4	E	478	ARG	3.6
4	E	239	MET	3.6
2	b	1498	GLN	3.6
2	b	1161	ASN	3.5
7	Q	423	ILE	3.5
1	a	1400	LYS	3.5
5	G	56	GLY	3.5
2	b	1429	PRO	3.5
1	A	189	ARG	3.5
7	Q	456	SER	3.5
6	h	1090	VAL	3.5
7	Q	173	TYR	3.5
7	q	1527	ALA	3.5
2	B	234	ASN	3.5
4	E	345	PHE	3.5
3	D	194	VAL	3.5
2	B	50	LYS	3.5
1	a	1378	ARG	3.5
4	e	1103	GLY	3.5
4	e	1462	LEU	3.5
8	z	1337	ASP	3.5
5	G	395	MET	3.5
8	Z	409	PRO	3.5
8	z	1041	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	97	ASP	3.5
5	G	280	GLU	3.5
8	z	1362	PHE	3.5
2	b	1463	ALA	3.5
3	D	391	ILE	3.5
5	G	161	THR	3.5
8	Z	8	ASN	3.5
8	z	1175	SER	3.5
1	A	282	GLY	3.5
5	G	352	ILE	3.5
8	Z	89	GLY	3.5
4	E	310	ALA	3.5
1	A	495	PRO	3.5
3	D	191	VAL	3.5
5	G	522	ILE	3.5
4	E	375	GLU	3.5
3	D	193	ALA	3.5
2	B	242	THR	3.5
7	Q	97	VAL	3.5
8	z	1050	GLY	3.5
7	Q	183	ILE	3.5
1	a	1048	ASP	3.5
6	h	1473	MET	3.5
8	Z	156	LEU	3.5
1	a	1050	GLY	3.5
3	d	1210	ASP	3.5
3	d	1179	VAL	3.5
3	d	1191	VAL	3.5
7	Q	205	CYS	3.5
1	a	1190	TYR	3.5
2	B	369	GLU	3.5
8	Z	319	ARG	3.5
8	z	1497	ASN	3.5
2	B	42	THR	3.5
1	A	277	LYS	3.5
7	Q	406	LYS	3.4
5	g	1401	VAL	3.4
6	H	183	VAL	3.4
8	z	1191	VAL	3.4
7	Q	165	HIS	3.4
5	G	50	LEU	3.4
4	e	1049	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
3	d	1168	ASN	3.4
7	q	1147	VAL	3.4
1	A	197	VAL	3.4
1	A	293	ASP	3.4
5	G	41	LEU	3.4
2	B	180	THR	3.4
2	b	1443	LEU	3.4
4	e	1489	LEU	3.4
8	Z	173	VAL	3.4
1	a	1390	ARG	3.4
4	E	71	THR	3.4
7	Q	241	VAL	3.4
7	q	1103	PHE	3.4
6	H	407	ALA	3.4
6	H	457	ALA	3.4
7	q	1526	MET	3.4
8	Z	479	VAL	3.4
8	Z	501	LYS	3.4
7	Q	247	ASP	3.4
7	q	1386	ASP	3.4
6	H	413	GLU	3.4
8	z	1085	ASP	3.4
4	E	59	LYS	3.4
7	q	1146	LEU	3.4
2	B	276	LYS	3.4
3	d	1418	LEU	3.4
7	Q	346	HIS	3.4
3	d	1143	ALA	3.4
2	b	1158	ASP	3.4
5	g	1521	ASP	3.4
3	d	1190	SER	3.4
7	q	1170	SER	3.4
3	D	382	CYS	3.4
1	A	366	ASN	3.4
6	H	446	PRO	3.4
6	H	290	LEU	3.4
2	B	161	ASN	3.4
5	g	1092	GLY	3.4
6	h	1372	ILE	3.4
6	H	357	ARG	3.4
3	D	101	GLN	3.4
5	G	307	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
6	H	91	GLY	3.4
8	z	1040	PRO	3.4
1	A	176	VAL	3.4
3	D	300	VAL	3.4
6	h	1015	SER	3.4
3	D	319	PHE	3.4
6	h	1119	GLN	3.4
2	B	477	GLY	3.4
7	Q	504	LYS	3.4
5	G	380	SER	3.4
2	B	469	HIS	3.4
2	b	1501	ARG	3.4
2	B	330	GLU	3.4
4	E	433	VAL	3.3
6	H	245	GLU	3.4
3	d	1205	SER	3.3
7	q	1448	ILE	3.3
1	A	279	LEU	3.3
2	B	476	ALA	3.3
5	G	37	ILE	3.3
1	A	326	THR	3.3
2	B	314	HIS	3.3
3	d	1514	PRO	3.3
8	z	1070	GLN	3.3
8	z	1523	ARG	3.3
1	a	1428	THR	3.3
2	B	45	PRO	3.3
8	Z	388	LYS	3.3
5	G	314	ARG	3.3
8	Z	444	LEU	3.3
8	z	1193	ILE	3.3
5	G	170	SER	3.3
5	G	298	ASP	3.3
8	z	1370	ARG	3.3
1	a	1007	VAL	3.3
2	B	179	PHE	3.3
1	a	1410	PRO	3.3
2	B	19	GLU	3.3
2	b	1446	LEU	3.3
3	d	1106	GLY	3.3
5	G	57	ILE	3.3
6	H	190	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
3	d	1214	VAL	3.3
8	Z	443	ALA	3.3
1	a	1171	LEU	3.3
2	b	1182	LEU	3.3
3	d	1503	ILE	3.3
4	E	372	LEU	3.3
3	D	416	ARG	3.3
1	a	1143	LEU	3.3
8	z	1495	TRP	3.3
1	A	365	LYS	3.3
6	h	1413	GLU	3.3
7	q	1449	PRO	3.3
4	e	1534	ARG	3.3
8	Z	495	TRP	3.3
2	B	77	ASP	3.3
5	G	158	SER	3.3
3	D	390	THR	3.3
3	d	1425	ILE	3.3
8	Z	224	ARG	3.3
1	A	148	LEU	3.3
2	B	292	ASN	3.3
2	b	1201	VAL	3.3
1	A	343	SER	3.3
1	a	1038	PRO	3.3
2	B	351	GLU	3.3
5	G	179	ALA	3.3
4	e	1027	ARG	3.3
4	e	1444	GLU	3.3
1	a	1504	PHE	3.3
5	G	231	ARG	3.3
6	h	1010	LYS	3.3
4	E	498	THR	3.3
1	A	228	ARG	3.3
4	E	166	ILE	3.3
6	H	303	PHE	3.2
2	B	386	ALA	3.2
6	H	150	GLU	3.2
7	q	1385	MET	3.2
8	Z	362	PHE	3.2
3	D	221	ILE	3.2
2	B	159	LEU	3.2
2	b	1196	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
3	D	57	PRO	3.2
6	h	1442	LEU	3.2
8	Z	302	LEU	3.2
8	Z	396	ARG	3.2
1	A	48	ASP	3.2
7	Q	283	ILE	3.2
6	h	1211	VAL	3.2
8	Z	368	ASN	3.2
3	d	1406	ARG	3.2
8	z	1306	ALA	3.2
2	b	1399	GLN	3.2
7	q	1068	ASP	3.2
8	Z	219	PRO	3.2
6	h	1186	LEU	3.2
2	B	492	GLY	3.2
3	d	1431	PRO	3.2
6	h	1472	GLY	3.2
2	b	1141	LEU	3.2
8	z	1276	GLU	3.2
6	H	358	TYR	3.2
7	Q	167	SER	3.2
5	G	276	GLN	3.2
6	H	473	MET	3.2
8	z	1298	ASP	3.2
6	H	187	ASP	3.2
7	q	1192	PRO	3.2
1	a	1209	MET	3.2
7	q	1159	GLU	3.2
4	e	1407	CYS	3.2
4	e	1058	ASP	3.2
2	b	1187	VAL	3.2
8	z	1331	ILE	3.2
8	Z	525	GLY	3.2
2	b	1431	LYS	3.2
6	h	1180	VAL	3.2
1	A	51	ASP	3.2
1	A	351	VAL	3.2
2	b	1370	ALA	3.2
3	D	258	ALA	3.2
6	H	239	LEU	3.2
8	Z	494	ILE	3.2
1	A	276	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	284	ASN	3.2
5	G	63	GLY	3.2
4	E	18	ILE	3.2
8	Z	226	GLU	3.2
2	B	367	LEU	3.2
5	G	199	ALA	3.2
5	G	506	TYR	3.2
8	Z	9	PRO	3.2
5	G	346	GLY	3.2
1	a	1049	ILE	3.2
8	Z	415	GLU	3.2
8	z	1376	ILE	3.2
8	Z	370	ARG	3.2
5	g	1519	ILE	3.2
4	E	308	ASP	3.2
5	G	172	ALA	3.2
6	H	231	LYS	3.2
3	D	427	GLY	3.1
1	A	91	THR	3.1
6	h	1132	ALA	3.1
5	G	378	GLY	3.1
5	G	386	GLU	3.1
6	h	1369	THR	3.1
8	z	1332	ALA	3.1
4	E	23	ASP	3.1
4	E	103	GLY	3.1
4	e	1215	VAL	3.1
6	h	1195	ILE	3.1
7	Q	98	GLY	3.1
5	G	305	MET	3.1
5	G	379	ALA	3.1
7	q	1408	LEU	3.1
1	A	292	ILE	3.1
2	b	1134	THR	3.1
1	a	1181	TYR	3.1
1	a	1004	PRO	3.1
2	B	184	VAL	3.1
7	q	1168	VAL	3.1
2	b	1211	ASP	3.1
4	e	1180	SER	3.1
4	e	1087	ILE	3.1
1	A	410	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	242	GLN	3.1
7	Q	181	LYS	3.1
2	B	156	ARG	3.1
7	Q	314	ARG	3.1
7	Q	139	ALA	3.1
8	z	1359	LYS	3.1
2	B	44	GLY	3.1
7	Q	276	MET	3.1
2	b	1402	LYS	3.1
5	g	1390	ASN	3.1
7	Q	502	LEU	3.1
3	D	172	THR	3.1
5	G	279	CYS	3.1
5	g	1133	MET	3.1
6	h	1520	ILE	3.1
2	B	316	ASP	3.1
8	Z	298	ASP	3.1
7	Q	103	PHE	3.1
7	Q	300	MET	3.1
1	a	1409	VAL	3.1
2	B	447	PRO	3.1
7	Q	419	LEU	3.1
5	g	1159	SER	3.1
3	d	1067	GLY	3.1
4	E	344	ARG	3.1
6	H	398	ARG	3.1
8	Z	207	ILE	3.1
6	h	1370	CYS	3.1
1	a	1435	GLN	3.1
5	G	176	ALA	3.1
7	Q	323	ARG	3.1
7	q	1388	ILE	3.1
2	b	1018	GLU	3.1
6	H	306	ARG	3.1
8	z	1340	ASN	3.1
1	A	352	VAL	3.1
5	G	53	PRO	3.1
4	E	348	LEU	3.1
6	H	79	LEU	3.1
3	d	1427	GLY	3.1
2	B	202	ILE	3.1
2	b	1475	THR	3.1

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Mol	Chain	Res	Type	RSRZ
4	e	1021	ASP	3.1
8	z	1090	ASP	3.1
3	D	199	ASP	3.0
3	D	302	LEU	3.0
8	z	1296	GLY	3.0
4	E	25	LYS	3.0
1	A	236	CYS	3.0
1	A	325	ALA	3.0
4	e	1037	HIS	3.0
6	H	521	LYS	3.0
6	h	1190	LEU	3.0
7	Q	361	VAL	3.0
4	e	1458	ILE	3.0
8	Z	369	PRO	3.0
1	A	69	HIS	3.0
7	Q	163	LEU	3.0
2	B	394	LEU	3.0
3	D	293	ILE	3.0
4	E	60	MET	3.0
5	G	233	ILE	3.0
5	g	1017	GLU	3.0
7	Q	400	LYS	3.0
1	a	1003	GLY	3.0
4	E	497	GLY	3.0
2	b	1450	ILE	3.0
3	d	1421	LYS	3.0
6	H	353	ILE	3.0
3	d	1172	THR	3.0
1	A	62	LEU	3.0
1	a	1075	LEU	3.0
1	a	1438	ILE	3.0
5	G	393	ASP	3.0
2	B	328	GLY	3.0
8	z	1475	GLN	3.0
5	g	1391	LEU	3.0
1	a	1206	MET	3.0
8	z	1341	PRO	3.0
8	Z	6	THR	3.0
3	D	351	VAL	3.0
7	q	1023	SER	3.0
3	d	1435	LEU	3.0
2	b	1515	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
6	H	368	LYS	3.0
4	e	1071	THR	3.0
1	a	1431	GLY	3.0
3	D	228	GLU	3.0
8	Z	93	THR	3.0
4	e	1026	SER	3.0
6	H	363	GLY	3.0
7	Q	374	THR	3.0
3	d	1196	LYS	3.0
3	d	1515	LEU	3.0
2	b	1467	ALA	3.0
8	Z	397	ALA	3.0
3	d	1175	ASN	3.0
4	E	422	GLY	3.0
5	G	277	GLN	3.0
2	B	368	GLY	3.0
2	B	480	MET	3.0
2	b	1193	SER	3.0
4	E	474	MET	3.0
6	H	158	CYS	3.0
2	b	1212	SER	3.0
7	Q	330	ALA	3.0
1	A	400	LYS	2.9
7	q	1479	GLY	2.9
1	A	329	SER	2.9
5	G	153	LEU	2.9
5	g	1072	VAL	2.9
7	q	1199	VAL	2.9
1	A	203	ARG	2.9
1	A	213	GLY	2.9
2	B	415	MET	2.9
3	D	388	THR	2.9
4	e	1498	THR	2.9
5	G	55	GLY	2.9
5	G	398	CYS	2.9
8	Z	374	LEU	2.9
5	g	1523	VAL	2.9
6	H	89	GLU	2.9
6	H	435	ILE	2.9
8	z	1155	SER	2.9
1	A	409	VAL	2.9
3	D	249	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
4	e	1490	GLY	2.9
3	D	415	ILE	2.9
5	G	240	LEU	2.9
8	z	1014	ALA	2.9
1	A	3	GLY	2.9
8	z	1317	LYS	2.9
1	A	323	SER	2.9
2	B	465	LEU	2.9
6	h	1396	VAL	2.9
7	Q	350	VAL	2.9
4	e	1468	MET	2.9
2	B	390	LEU	2.9
3	d	1439	LEU	2.9
1	A	405	SER	2.9
6	h	1063	ALA	2.9
6	h	1410	GLY	2.9
8	z	1351	TYR	2.9
8	z	1152	ALA	2.9
2	b	1209	LEU	2.9
2	B	76	VAL	2.9
2	B	80	ALA	2.9
2	b	1396	VAL	2.9
3	d	1069	GLY	2.9
7	Q	178	PHE	2.9
1	a	1072	ALA	2.9
6	h	1086	GLN	2.9
5	G	303	TYR	2.9
2	B	387	GLU	2.9
6	h	1012	GLY	2.9
5	G	357	ASP	2.9
6	H	92	ASP	2.9
7	q	1467	LEU	2.9
2	B	318	VAL	2.9
5	G	320	ASN	2.9
7	q	1198	ASN	2.9
2	b	1439	TYR	2.9
3	d	1162	ASP	2.9
6	H	326	CYS	2.9
1	A	505	GLU	2.9
3	D	363	GLU	2.9
3	d	1419	VAL	2.9
7	q	1401	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
3	d	1025	SER	2.9
4	E	319	LEU	2.9
6	h	1125	PHE	2.9
2	b	1009	VAL	2.9
1	A	322	ALA	2.9
4	e	1220	GLU	2.9
6	H	370	CYS	2.9
8	Z	64	LEU	2.9
7	q	1501	TYR	2.9
4	E	204	VAL	2.9
8	Z	306	ALA	2.9
1	A	370	ARG	2.9
6	H	289	VAL	2.9
8	Z	392	ARG	2.9
7	Q	378	ARG	2.9
7	q	1402	LEU	2.9
8	z	1218	HIS	2.9
8	z	1481	LEU	2.9
2	b	1378	ALA	2.9
8	z	1360	PHE	2.9
7	Q	216	SER	2.9
2	B	245	ASP	2.8
4	e	1099	ASP	2.8
1	a	1418	ALA	2.8
3	D	58	LYS	2.8
6	h	1163	LEU	2.8
8	Z	475	GLN	2.8
4	E	318	ASP	2.8
7	q	1445	PHE	2.8
7	Q	339	PRO	2.8
2	B	295	LEU	2.8
7	Q	417	ILE	2.8
3	D	24	LYS	2.8
7	Q	200	ASP	2.8
3	D	355	THR	2.8
3	d	1165	THR	2.8
8	Z	376	ILE	2.8
5	g	1209	ILE	2.8
7	Q	186	ALA	2.8
5	g	1037	ILE	2.8
8	Z	360	PHE	2.8
1	a	1045	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
4	e	1400	ARG	2.8
7	Q	43	THR	2.8
4	e	1390	GLY	2.8
2	b	1011	ILE	2.8
3	d	1494	THR	2.8
3	D	386	GLY	2.8
5	g	1395	MET	2.8
8	Z	329	GLY	2.8
2	B	103	THR	2.8
5	g	1152	MET	2.8
6	H	414	MET	2.8
6	H	415	GLU	2.8
6	h	1386	GLU	2.8
6	H	464	LEU	2.8
1	a	1053	THR	2.8
2	B	18	GLU	2.8
3	D	241	ILE	2.8
7	Q	48	GLY	2.8
4	E	55	ASN	2.8
6	H	425	ARG	2.8
7	Q	497	VAL	2.8
8	Z	322	GLU	2.8
2	b	1063	VAL	2.8
3	d	1186	LEU	2.8
7	Q	145	ASP	2.8
4	E	252	THR	2.8
8	z	1034	LEU	2.8
4	e	1210	LYS	2.8
3	d	1413	CYS	2.8
6	H	235	PRO	2.8
1	A	488	LEU	2.8
4	e	1454	ALA	2.8
8	z	1328	CYS	2.8
7	q	1175	ASN	2.8
2	B	186	ALA	2.8
4	E	169	ALA	2.8
8	z	1302	LEU	2.8
6	H	328	GLY	2.8
1	a	1062	LEU	2.8
2	b	1517	VAL	2.8
5	g	1394	ALA	2.8
6	h	1414	MET	2.8

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Mol	Chain	Res	Type	RSRZ
7	Q	172	GLN	2.8
1	A	175	ALA	2.8
2	b	1025	ARG	2.8
2	b	1444	ARG	2.8
5	G	180	VAL	2.8
1	A	152	ALA	2.8
1	a	1079	ALA	2.8
1	a	1139	ASN	2.8
3	d	1407	SER	2.8
7	q	1055	MET	2.8
6	H	420	LEU	2.8
2	b	1147	ASP	2.7
3	d	1225	GLU	2.7
5	G	61	ASN	2.7
7	Q	446	GLU	2.7
3	d	1224	CYS	2.7
7	q	1393	ASP	2.7
6	H	295	ILE	2.7
3	d	1207	ASP	2.7
6	H	450	CYS	2.7
2	B	43	LEU	2.7
4	E	101	GLU	2.7
8	z	1160	VAL	2.7
2	b	1418	ALA	2.7
4	e	1398	ALA	2.7
5	G	243	SER	2.7
8	z	1038	LEU	2.7
1	A	304	GLY	2.7
8	z	1233	CYS	2.7
5	g	1126	TYR	2.7
7	Q	160	VAL	2.7
7	Q	58	ASN	2.7
3	D	354	PHE	2.7
4	E	251	LEU	2.7
5	G	96	THR	2.7
7	q	1151	ALA	2.7
6	H	355	GLY	2.7
2	b	1504	LEU	2.7
1	A	327	VAL	2.7
6	H	399	ALA	2.7
4	e	1420	TYR	2.7
1	a	1120	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
6	H	312	GLY	2.7
7	q	1090	SER	2.7
8	Z	448	PRO	2.7
4	E	449	ARG	2.7
1	A	67	VAL	2.7
2	B	284	LYS	2.7
3	d	1163	ARG	2.7
5	G	171	LEU	2.7
3	d	1405	GLU	2.7
4	e	1506	VAL	2.7
6	H	321	ARG	2.7
8	z	1377	LYS	2.7
1	a	1490	LEU	2.7
7	q	1193	ASP	2.7
8	Z	63	LEU	2.7
4	E	237	PRO	2.7
1	A	401	ARG	2.7
1	a	1189	ARG	2.7
3	D	484	ARG	2.7
7	q	1046	ALA	2.7
7	q	1419	LEU	2.7
7	Q	329	GLY	2.7
2	b	1398	ALA	2.7
7	q	1480	LEU	2.7
1	A	305	ALA	2.7
1	A	319	ILE	2.7
5	G	385	SER	2.7
2	B	47	GLY	2.7
4	E	515	GLN	2.7
2	B	183	ALA	2.7
7	Q	402	LEU	2.7
8	z	1346	HIS	2.7
3	d	1429	GLY	2.7
4	E	374	ILE	2.7
1	A	354	GLU	2.7
7	Q	77	GLU	2.7
6	h	1475	TYR	2.7
2	b	1167	LEU	2.7
4	e	1050	THR	2.7
5	G	84	SER	2.7
5	G	286	LYS	2.7
8	Z	407	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	506	PRO	2.7
2	b	1168	SER	2.7
2	b	1480	MET	2.7
3	D	392	VAL	2.7
6	H	322	THR	2.7
6	H	421	ARG	2.7
4	E	309	GLU	2.7
5	G	476	GLU	2.7
6	h	1011	GLU	2.7
6	h	1198	LYS	2.7
6	h	1188	ASP	2.6
8	z	1343	CYS	2.7
2	B	464	GLN	2.6
4	E	66	GLY	2.6
4	E	512	GLY	2.6
6	h	1170	GLN	2.6
6	h	1367	ALA	2.6
5	g	1053	PRO	2.6
6	h	1047	LYS	2.6
5	g	1524	SER	2.6
7	Q	483	GLU	2.6
2	b	1523	ALA	2.6
7	Q	242	TYR	2.6
8	Z	228	ALA	2.6
1	a	1388	MET	2.6
4	e	1086	GLN	2.6
8	z	1187	ASP	2.6
4	e	1163	GLU	2.6
8	Z	356	GLY	2.6
3	d	1449	MET	2.6
2	b	1514	ILE	2.6
3	d	1472	ALA	2.6
4	e	1195	THR	2.6
3	d	1410	ASP	2.6
5	g	1026	ASN	2.6
2	B	396	VAL	2.6
1	A	5	LEU	2.6
6	h	1493	TRP	2.6
7	Q	388	ILE	2.6
3	D	84	MET	2.6
5	g	1093	ASP	2.6
8	Z	432	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
3	D	205	SER	2.6
1	a	1088	ASP	2.6
2	b	1207	GLY	2.6
1	A	299	TYR	2.6
1	A	363	LEU	2.6
7	q	1396	VAL	2.6
8	z	1151	VAL	2.6
8	z	1161	HIS	2.6
3	D	109	THR	2.6
3	D	375	LYS	2.6
8	Z	401	ALA	2.6
2	b	1462	VAL	2.6
2	B	397	LEU	2.6
7	q	1205	CYS	2.6
4	E	509	THR	2.6
4	e	1427	ILE	2.6
6	H	430	LYS	2.6
2	B	391	HIS	2.6
5	g	1386	GLU	2.6
6	h	1087	ASP	2.6
8	Z	339	LEU	2.6
6	h	1412	ILE	2.6
1	a	1046	VAL	2.6
4	e	1041	ALA	2.6
5	G	201	VAL	2.6
3	D	102	ASP	2.6
7	q	1482	ILE	2.6
8	Z	147	THR	2.6
3	d	1151	LEU	2.6
7	q	1148	CYS	2.6
8	Z	77	ILE	2.6
2	b	1028	SER	2.6
4	E	144	ALA	2.6
6	h	1519	THR	2.6
1	a	1058	GLY	2.6
2	B	182	LEU	2.6
7	q	1418	GLU	2.6
1	a	1131	TYR	2.6
2	b	1464	GLN	2.6
2	B	9	VAL	2.6
7	Q	481	ASP	2.6
8	z	1013	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
5	g	1436	PRO	2.6
8	z	1333	LEU	2.6
3	D	462	GLU	2.6
8	Z	138	LYS	2.6
2	b	1044	GLY	2.6
2	b	1430	GLY	2.6
2	b	1483	GLY	2.6
4	e	1065	ASP	2.6
7	Q	331	THR	2.6
1	A	378	ARG	2.6
3	d	1507	LEU	2.6
8	z	1322	GLU	2.6
8	Z	151	VAL	2.5
1	A	357	CYS	2.5
2	B	436	MET	2.5
3	D	417	CYS	2.5
4	E	317	ASN	2.5
5	g	1130	LEU	2.5
5	G	214	VAL	2.5
6	H	462	ASN	2.5
8	Z	272	LYS	2.5
1	a	1176	VAL	2.5
6	H	143	VAL	2.5
8	z	1173	VAL	2.5
3	D	243	ARG	2.5
1	a	1441	PHE	2.5
2	b	1172	LEU	2.5
5	G	36	ILE	2.5
6	H	83	ALA	2.5
6	H	281	ILE	2.5
4	e	1179	ASN	2.5
6	H	291	SER	2.5
7	Q	53	ASN	2.5
6	H	419	TYR	2.5
2	b	1394	LEU	2.5
4	E	78	LEU	2.5
4	e	1401	SER	2.5
4	e	1443	LEU	2.5
6	H	42	PRO	2.5
8	z	1188	LEU	2.5
2	b	1049	ASP	2.5
5	g	1387	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
8	Z	84	GLN	2.5
6	H	396	VAL	2.5
7	Q	136	CYS	2.5
8	z	1007	LEU	2.5
3	d	1471	ASN	2.5
3	D	402	GLU	2.5
3	d	1516	LEU	2.5
8	z	1174	ASP	2.5
7	Q	144	PRO	2.5
2	b	1079	PRO	2.5
7	Q	455	ASN	2.5
5	G	293	GLU	2.5
5	g	1369	PRO	2.5
5	g	1373	THR	2.5
6	h	1390	HIS	2.5
3	D	425	ILE	2.5
4	e	1204	VAL	2.5
2	b	1179	PHE	2.5
5	g	1185	PHE	2.5
7	q	1020	LYS	2.5
1	A	402	VAL	2.5
3	D	255	CYS	2.5
5	G	397	VAL	2.5
2	b	1417	MET	2.5
2	B	349	ILE	2.5
8	Z	81	ALA	2.5
1	A	353	GLN	2.5
2	b	1502	GLN	2.5
4	E	341	ILE	2.5
8	Z	500	VAL	2.5
1	a	1194	SER	2.5
3	D	461	MET	2.5
8	z	1140	SER	2.5
4	e	1463	ALA	2.5
7	Q	177	VAL	2.5
7	Q	355	VAL	2.5
2	B	78	ASN	2.5
4	E	160	LYS	2.5
5	G	401	VAL	2.5
7	q	1066	THR	2.5
8	z	1172	VAL	2.5
4	e	1098	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
6	h	1465	ARG	2.5
7	q	1422	GLN	2.5
1	A	90	THR	2.5
5	g	1502	LYS	2.5
6	H	466	ALA	2.5
4	E	250	ILE	2.4
6	H	360	PHE	2.4
8	z	1493	GLY	2.4
4	E	455	LEU	2.4
6	h	1474	TRP	2.4
6	H	438	TYR	2.4
1	a	1380	ALA	2.4
6	H	125	PHE	2.4
7	q	1379	GLY	2.4
3	D	184	SER	2.4
7	Q	526	MET	2.4
7	q	1417	ILE	2.4
8	Z	472	GLU	2.4
7	q	1502	LEU	2.4
1	a	1487	GLY	2.4
2	b	1186	ALA	2.4
2	b	1518	ASP	2.4
3	d	1057	PRO	2.4
5	G	40	CYS	2.4
8	Z	499	CYS	2.4
3	D	371	ASN	2.4
2	b	1205	LEU	2.4
6	H	159	ALA	2.4
8	Z	38	LEU	2.4
8	Z	365	LYS	2.4
5	G	66	ILE	2.4
3	D	223	ASP	2.4
7	Q	68	ASP	2.4
1	A	58	GLY	2.4
1	A	65	LEU	2.4
7	q	1181	LYS	2.4
7	Q	468	TYR	2.4
3	d	1412	LEU	2.4
7	q	1143	LEU	2.4
6	H	73	HIS	2.4
2	B	187	VAL	2.4
3	D	55	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
4	E	172	THR	2.4
4	E	430	ALA	2.4
1	A	321	LYS	2.4
7	q	1503	GLY	2.4
2	b	1520	ILE	2.4
5	G	194	ASP	2.4
7	Q	199	VAL	2.4
1	A	79	ALA	2.4
2	B	350	GLU	2.4
7	Q	313	VAL	2.4
8	Z	7	LEU	2.4
6	H	456	ASP	2.4
2	B	450	ILE	2.4
2	b	1194	GLY	2.4
1	a	1052	VAL	2.4
1	a	1122	ARG	2.4
8	Z	308	GLU	2.4
2	b	1155	PHE	2.4
3	D	216	LYS	2.4
4	e	1107	THR	2.4
4	E	303	GLN	2.4
6	H	206	GLU	2.4
1	A	75	LEU	2.4
1	a	1114	PRO	2.4
6	H	98	THR	2.4
7	Q	525	ILE	2.4
7	q	1064	PHE	2.4
8	Z	171	ALA	2.4
2	b	1376	ARG	2.4
3	d	1072	THR	2.4
3	D	208	LEU	2.4
3	D	227	VAL	2.4
4	e	1111	VAL	2.4
4	e	1423	GLY	2.4
2	B	519	ASN	2.4
3	D	449	MET	2.4
2	B	231	ARG	2.4
3	d	1457	PHE	2.4
4	e	1110	VAL	2.4
8	z	1235	VAL	2.4
8	z	1398	VAL	2.4
1	a	1180	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
5	g	1071	GLN	2.4
7	Q	90	SER	2.4
1	a	1076	CYS	2.4
3	d	1541	THR	2.4
7	q	1450	ARG	2.4
5	g	1147	SER	2.4
2	b	1516	ARG	2.4
3	d	1222	ASP	2.4
4	e	1530	ILE	2.4
5	G	166	SER	2.4
5	G	236	PRO	2.4
6	H	479	ILE	2.4
1	a	1404	GLU	2.4
4	E	537	GLY	2.4
6	h	1062	GLY	2.4
3	D	496	ILE	2.3
4	e	1418	VAL	2.3
6	h	1399	ALA	2.3
5	G	62	ASP	2.3
6	H	226	GLU	2.3
7	q	1054	LYS	2.3
7	q	1086	ILE	2.3
8	z	1058	LYS	2.3
1	A	156	MET	2.3
1	a	1115	THR	2.3
6	H	213	GLY	2.3
1	A	399	VAL	2.3
2	B	130	TRP	2.3
2	b	1421	VAL	2.3
1	a	1423	LEU	2.3
6	h	1069	LEU	2.3
2	B	522	LYS	2.3
8	z	1012	GLU	2.3
3	d	1180	SER	2.3
1	A	356	ILE	2.3
3	D	72	THR	2.3
4	E	48	MET	2.3
5	G	374	ILE	2.3
8	z	1141	LYS	2.3
8	Z	67	MET	2.3
8	z	1069	ILE	2.3
2	b	1403	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
7	Q	78	VAL	2.3
2	b	1180	THR	2.3
2	B	340	LEU	2.3
3	D	140	PHE	2.3
4	E	82	ASP	2.3
8	Z	340	ASN	2.3
4	E	501	MET	2.3
8	Z	387	ILE	2.3
1	a	1377	LEU	2.3
3	D	389	VAL	2.3
4	E	300	ALA	2.3
6	H	240	LEU	2.3
2	B	243	GLY	2.3
6	H	8	LEU	2.3
3	d	1155	SER	2.3
6	h	1499	ARG	2.3
7	Q	337	ASN	2.3
7	q	1073	LEU	2.3
4	e	1426	GLU	2.3
6	H	139	ILE	2.3
6	h	1082	ILE	2.3
8	z	1176	ILE	2.3
2	B	171	LEU	2.3
5	G	322	ARG	2.3
6	H	318	ASP	2.3
1	a	1376	ILE	2.3
4	E	242	GLN	2.3
4	e	1483	LYS	2.3
5	G	162	THR	2.3
6	h	1144	LYS	2.3
6	h	1175	PHE	2.3
7	Q	398	THR	2.3
2	B	194	GLY	2.3
7	Q	377	LEU	2.3
8	Z	168	LEU	2.3
8	z	1353	TYR	2.3
8	z	1396	ARG	2.3
5	G	354	LYS	2.3
8	Z	515	ILE	2.3
1	a	1196	ASN	2.3
4	E	471	ILE	2.3
6	H	227	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	a	1389	GLU	2.3
7	q	1166	THR	2.3
3	d	1187	SER	2.3
1	A	403	LEU	2.3
2	b	1142	LEU	2.3
2	b	1175	HIS	2.3
8	Z	349	LEU	2.3
7	q	1446	GLU	2.3
2	b	1080	ALA	2.3
3	D	66	ASP	2.3
7	q	1382	ASP	2.3
8	z	1358	GLU	2.3
1	a	1124	ALA	2.3
2	B	317	PHE	2.3
3	d	1392	VAL	2.3
3	D	500	LYS	2.3
5	g	1127	ARG	2.3
6	h	1166	LYS	2.3
4	E	67	ASP	2.3
5	G	392	GLN	2.3
6	h	1066	LEU	2.3
7	q	1208	LEU	2.3
7	Q	439	LYS	2.3
4	E	305	GLY	2.3
7	Q	356	GLY	2.3
8	Z	134	LEU	2.3
8	Z	418	MET	2.3
2	B	375	LEU	2.2
2	b	1200	HIS	2.2
6	H	136	ILE	2.2
3	d	1408	ILE	2.2
5	G	227	PRO	2.2
1	a	1117	VAL	2.2
3	D	498	VAL	2.2
3	d	1462	GLU	2.2
1	a	1448	ILE	2.2
2	b	1189	ARG	2.2
7	Q	394	ASP	2.2
4	e	1394	ILE	2.2
1	a	1112	ILE	2.2
2	B	428	THR	2.2
3	d	1104	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
5	G	149	ARG	2.2
5	G	178	ASP	2.2
3	D	381	GLY	2.2
2	B	246	THR	2.2
4	E	406	LEU	2.2
6	h	1009	LEU	2.2
8	Z	159	LYS	2.2
3	D	411	ALA	2.2
5	G	18	SER	2.2
6	H	319	LEU	2.2
6	H	337	LEU	2.2
8	Z	447	ILE	2.2
5	g	1517	LEU	2.2
6	h	1522	ASN	2.2
7	Q	86	ILE	2.2
2	B	495	GLU	2.2
2	b	1050	LYS	2.2
8	Z	47	LEU	2.2
8	z	1330	GLY	2.2
1	a	1422	TYR	2.2
2	b	1019	GLU	2.2
3	D	314	ASP	2.2
3	d	1411	ALA	2.2
7	Q	351	TYR	2.2
3	d	1542	ARG	2.2
6	h	1371	THR	2.2
7	q	1421	LYS	2.2
8	Z	141	LYS	2.2
1	a	1195	ILE	2.2
1	A	499	LYS	2.2
8	Z	317	LYS	2.2
8	Z	445	LEU	2.2
2	b	1377	GLY	2.2
1	A	306	MET	2.2
1	a	1430	MET	2.2
2	B	414	GLU	2.2
2	b	1074	ILE	2.2
4	E	293	LYS	2.2
5	g	1091	VAL	2.2
2	b	1029	PHE	2.2
4	e	1474	MET	2.2
5	g	1070	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
4	e	1464	GLU	2.2
7	Q	472	GLN	2.2
6	H	29	CYS	2.2
5	G	487	LEU	2.2
8	z	1156	LEU	2.2
8	z	1410	GLY	2.2
3	D	179	VAL	2.2
4	e	1403	HIS	2.2
1	a	1426	TYR	2.2
6	h	1084	LYS	2.2
5	G	67	LEU	2.2
4	E	477	VAL	2.2
5	g	1156	ILE	2.2
7	Q	438	ILE	2.2
8	Z	326	LEU	2.2
8	Z	60	GLY	2.2
2	B	99	THR	2.2
5	G	284	GLN	2.2
8	Z	511	ILE	2.2
2	B	87	MET	2.2
8	z	1408	VAL	2.2
2	b	1022	GLU	2.2
5	g	1095	THR	2.2
5	G	481	ASN	2.2
7	q	1444	ALA	2.2
8	Z	34	LEU	2.2
4	e	1094	LEU	2.2
5	G	359	TYR	2.2
8	z	1327	ALA	2.2
5	G	93	ASP	2.1
6	h	1185	MET	2.1
1	a	1063	LYS	2.1
3	d	1505	ASN	2.1
4	e	1465	ASN	2.1
5	G	43	PRO	2.1
5	g	1510	VAL	2.1
2	B	46	LYS	2.1
7	q	1139	ALA	2.1
8	z	1480	ASP	2.1
4	E	506	VAL	2.1
5	G	482	GLY	2.1
3	d	1182	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
4	E	91	MET	2.1
7	Q	107	PHE	2.1
8	Z	520	GLU	2.1
1	a	1437	ALA	2.1
6	h	1446	PRO	2.1
7	q	1094	GLU	2.1
4	E	63	ASP	2.1
7	q	1424	THR	2.1
7	q	1461	ASN	2.1
8	Z	400	ASN	2.1
1	A	376	ILE	2.1
3	d	1401	ILE	2.1
8	z	1178	ALA	2.1
5	g	1194	ASP	2.1
5	g	1393	ASP	2.1
6	h	1133	VAL	2.1
2	b	1419	HIS	2.1
7	Q	420	ALA	2.1
8	Z	178	ALA	2.1
5	g	1397	VAL	2.1
7	q	1209	GLY	2.1
6	H	237	ILE	2.1
1	A	172	VAL	2.1
6	H	469	ALA	2.1
8	z	1030	LEU	2.1
8	Z	307	LYS	2.1
1	a	1128	ALA	2.1
5	g	1476	GLU	2.1
4	e	1467	GLY	2.1
7	Q	295	GLY	2.1
2	B	281	ARG	2.1
2	B	388	ARG	2.1
6	H	184	MET	2.1
6	h	1477	VAL	2.1
2	B	71	LEU	2.1
5	G	151	THR	2.1
8	z	1345	GLY	2.1
8	z	1494	ILE	2.1
1	A	113	HIS	2.1
2	B	419	HIS	2.1
3	d	1028	GLN	2.1
7	q	1400	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
8	z	1393	ASP	2.1
1	a	1502	GLY	2.1
3	d	1131	ILE	2.1
7	q	1057	ILE	2.1
1	a	1517	ALA	2.1
5	g	1076	ALA	2.1
5	g	1098	VAL	2.1
2	b	1101	SER	2.1
6	h	1398	ARG	2.1
1	a	1148	LEU	2.1
1	a	1179	ILE	2.1
2	b	1416	LEU	2.1
5	G	215	LEU	2.1
7	q	1098	GLY	2.1
8	Z	195	GLU	2.1
8	z	1391	ILE	2.1
3	d	1498	VAL	2.1
2	b	1077	ASP	2.1
4	e	1060	MET	2.1
5	g	1444	LEU	2.1
6	h	1523	PRO	2.1
8	z	1348	GLY	2.1
1	A	216	LEU	2.1
3	D	394	ARG	2.1
3	D	315	LEU	2.1
2	B	39	VAL	2.1
3	D	69	GLY	2.1
3	d	1458	ALA	2.1
1	a	1154	THR	2.1
2	B	100	THR	2.1
3	d	1440	THR	2.1
7	Q	244	CYS	2.1
8	Z	204	THR	2.1
8	z	1315	ARG	2.1
4	E	230	VAL	2.1
5	G	242	ASP	2.1
6	H	76	ALA	2.1
7	q	1179	LEU	2.1
8	z	1204	THR	2.1
3	D	304	GLN	2.1
5	g	1141	SER	2.1
6	H	404	SER	2.1

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Mol	Chain	Res	Type	RSRZ
7	Q	401	VAL	2.1
7	Q	159	GLU	2.1
7	Q	467	LEU	2.1
7	Q	488	ALA	2.1
5	G	200	ARG	2.1
6	h	1136	ILE	2.1
3	d	1448	GLY	2.1
6	H	288	VAL	2.1
7	Q	443	GLU	2.1
1	A	297	LEU	2.1
8	z	1448	PRO	2.1
1	A	68	GLU	2.1
6	H	175	PHE	2.1
7	q	1190	ILE	2.1
2	B	422	THR	2.0
3	D	120	LEU	2.0
1	a	1119	SER	2.0
3	d	1176	SER	2.0
6	h	1199	LYS	2.0
8	z	1294	GLN	2.0
3	d	1185	LEU	2.0
4	E	516	GLN	2.0
5	G	48	LYS	2.0
7	Q	69	ALA	2.0
4	e	1101	GLU	2.0
7	q	1475	ASN	2.0
1	A	46	VAL	2.0
1	A	237	LEU	2.0
5	g	1403	LEU	2.0
1	A	128	ALA	2.0
3	d	1454	ILE	2.0
7	Q	322	ARG	2.0
8	Z	273	LYS	2.0
8	z	1334	ASN	2.0
8	Z	404	ASP	2.0
4	e	1456	GLU	2.0
2	B	74	ILE	2.0
2	b	1456	TYR	2.0
3	d	1430	ALA	2.0
4	e	1513	LYS	2.0
5	g	1123	ILE	2.0
6	H	471	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	a	1396	LEU	2.0
1	A	173	VAL	2.0
6	h	1045	MET	2.0
8	z	1466	VAL	2.0
2	B	444	ARG	2.0
2	B	408	TYR	2.0
3	D	514	PRO	2.0
6	H	299	ALA	2.0
3	D	178	VAL	2.0
7	Q	389	GLU	2.0
1	a	1427	ALA	2.0
5	g	1096	THR	2.0
7	q	1102	ASN	2.0
5	G	168	TRP	2.0
6	H	423	TYR	2.0
2	B	227	ASN	2.0
3	D	25	SER	2.0
4	E	77	ILE	2.0
6	h	1123	ARG	2.0
8	z	1168	LEU	2.0
7	q	1441	PHE	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 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.