



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:39 pm BST

PDB ID : 1M3I
Title : Perfringolysin O, new crystal form
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Deposited on : 2002-06-28
Resolution : 2.90 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
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

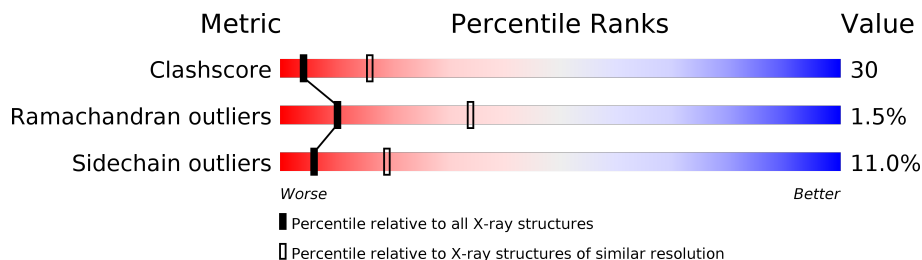
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	471	
1	B	471	
1	C	471	
1	D	471	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14920 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 perfringolysin O.

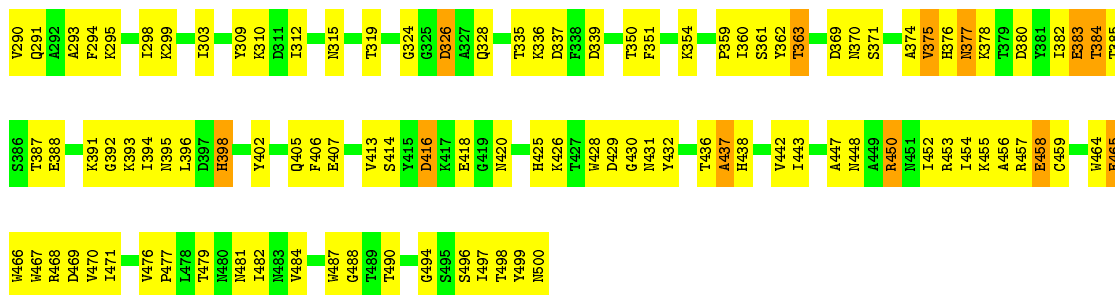
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	465	3657	2304	614	734	5	0	0	0
1	B	465	3657	2304	614	734	5	0	0	0
1	C	465	3657	2304	614	734	5	0	0	0
1	D	465	3657	2304	614	734	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	114	LEU	PHE	see remark 999	UNP P19995
B	114	LEU	PHE	see remark 999	UNP P19995
C	114	LEU	PHE	see remark 999	UNP P19995
D	114	LEU	PHE	see remark 999	UNP P19995

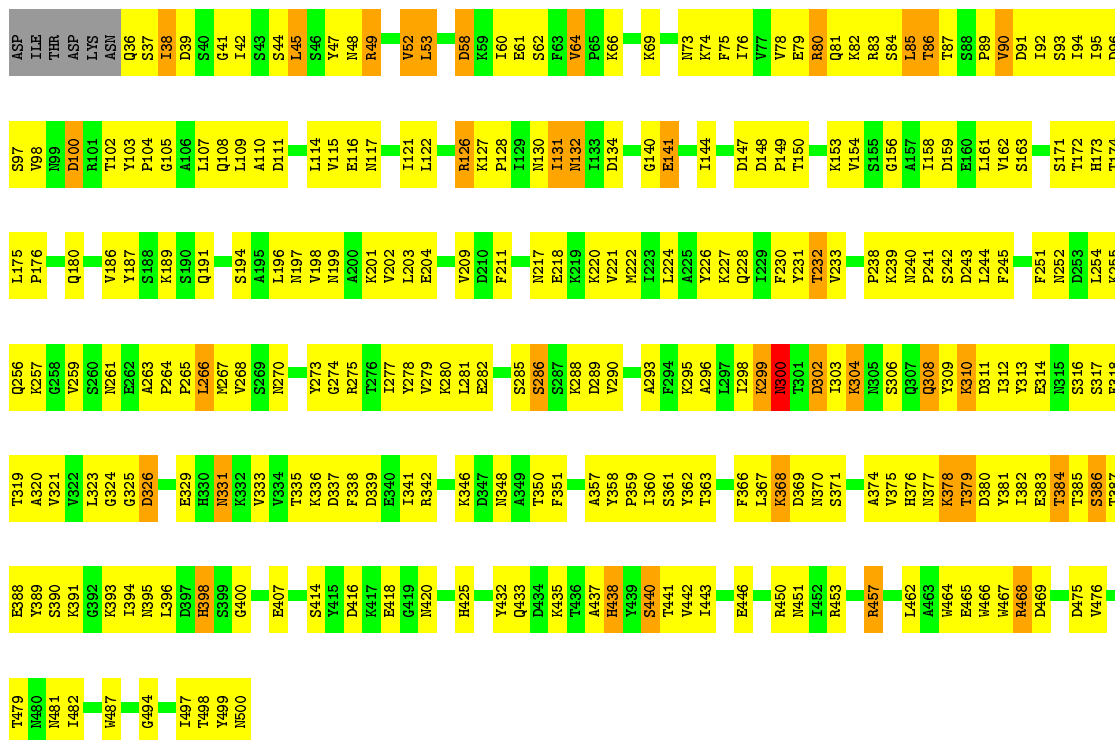
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	70	Total	O	0	0
			70	70		
2	B	88	Total	O	0	0
			88	88		
2	C	58	Total	O	0	0
			58	58		
2	D	76	Total	O	0	0
			76	76		



- Molecule 1: perfringolysin O

Chain C: 41% 49% 8%



N270	F338	E418
Y273	D339	G419
G274	E340	N420
R275	I341	E421
T276	R342	H425
I277	K346	D429
Y278	D347	Q433
V279	N348	D434
E282	F351	K435
T283	S352	T436
S286	T353	A437
S287	A357	R438
K288	Y358	Y439
D289	P359	S440
K295	I360	T441
A296	S361	V442
L297	Y362	I443
I298	T363	P444
K299	F366	I445
L299	L367	E446
N300	K368	A449
T301	D369	R450
D302	D369	N451
I303	N370	I452
K304	S371	R453
N305	V372	R457
S306	A373	W464
Q307	A374	E465
Q308	Y375	W466
Y309	H376	W467
K310	N377	R468
D311	K378	D469
I312	E383	V470
Y313	T384	Y474
E314	I385	D475
N315	S386	V476
S316	K391	F477
S317	G392	L478
F318	K393	T479
T319	I394	N480
A320	N395	N481
V321	L396	I482
V322	L396	W487
L323	D397	G494
D326	H398	S495
A327	S399	S496
Q328	G400	I497
E329	E407	T498
H330	E407	Y499
N331	D411	N500
K332	D411	
Y333	S414	
V334	Y415	
I335	D416	
K336	K417	
D337		

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	130.41Å 130.41Å 129.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.90	Depositor
% Data completeness (in resolution range)	95.2 (20.00-2.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.233 , 0.280	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	14920	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.35	0/3728	0.57	0/5062
1	B	0.36	0/3728	0.56	0/5062
1	C	0.37	0/3728	0.57	1/5062 (0.0%)
1	D	0.35	0/3728	0.56	0/5062
All	All	0.36	0/14912	0.57	1/20248 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	300	ASN	N-CA-C	6.46	128.45	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts i

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3657	0	3611	211	0
1	B	3657	0	3611	174	0
1	C	3657	0	3611	275	0
1	D	3657	0	3611	214	0
2	A	70	0	0	14	0
2	B	88	0	0	6	0
2	C	58	0	0	4	0
2	D	76	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	14920	0	14444	860	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 30.

All (860) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:THR:HG22	1:A:337:ASP:H	1.27	0.99
1:B:335:THR:HG22	1:B:337:ASP:H	1.28	0.98
1:A:87:THR:HG22	1:A:89:PRO:HD3	1.45	0.97
1:C:289:ASP:HB3	1:C:309:TYR:HE1	1.25	0.94
1:A:301:THR:O	1:A:304:LYS:HG3	1.68	0.94
1:C:296:ALA:HB2	1:C:303:ILE:HD13	1.52	0.91
1:C:82:LYS:HA	1:C:382:ILE:HA	1.50	0.91
1:D:457:ARG:HD2	1:D:469:ASP:OD2	1.71	0.90
1:A:109:LEU:HD21	1:A:122:LEU:HD21	1.53	0.89
1:A:104:PRO:HG2	1:A:131:ILE:HD11	1.54	0.88
1:C:481:ASN:HB2	1:C:500:ASN:HB2	1.56	0.88
1:D:481:ASN:HB2	1:D:500:ASN:HB2	1.56	0.87
1:C:457:ARG:HD2	1:C:469:ASP:OD2	1.75	0.87
1:C:90:VAL:HG12	1:C:374:ALA:HB2	1.58	0.86
1:A:481:ASN:HB2	1:A:500:ASN:HB2	1.58	0.85
1:C:66:LYS:HG3	1:C:79:GLU:HG3	1.59	0.85
1:D:457:ARG:HG3	1:D:468:ARG:O	1.78	0.84
1:A:222:MET:HE1	1:A:298:ILE:HD11	1.60	0.84
1:A:75:PHE:HB2	1:A:447:ALA:HB3	1.60	0.83
1:A:131:ILE:HG22	1:A:144:ILE:HG22	1.59	0.83
1:B:481:ASN:HB2	1:B:500:ASN:HB2	1.61	0.82
1:A:464:TRP:HA	1:A:467:TRP:CE3	2.14	0.82
1:B:456:ALA:HB3	1:B:471:ILE:HG22	1.61	0.82
1:B:465:GLU:OE2	1:D:91:ASP:HB2	1.79	0.82
1:C:259:VAL:HG13	1:C:265:PRO:HD3	1.61	0.82
1:D:259:VAL:HG13	1:D:265:PRO:HD3	1.62	0.82
1:B:131:ILE:HG22	1:B:144:ILE:HG22	1.59	0.81
1:A:456:ALA:HB3	1:A:471:ILE:HG22	1.60	0.81
1:D:110:ALA:HB2	1:D:266:LEU:HD21	1.63	0.81
1:A:37:SER:HB3	1:A:40:SER:OG	1.80	0.80
1:A:288:LYS:HB2	2:A:542:HOH:O	1.81	0.80
1:D:429:ASP:HB3	2:D:553:HOH:O	1.81	0.80
1:C:457:ARG:HG3	1:C:468:ARG:O	1.80	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:ALA:HB2	1:C:266:LEU:HD21	1.65	0.79
1:B:73:ASN:HA	1:B:391:LYS:HE2	1.64	0.78
1:B:457:ARG:HD2	1:B:469:ASP:OD2	1.84	0.78
1:D:69:LYS:HG3	1:D:76:ILE:HB	1.65	0.77
1:A:458:GLU:OE2	1:A:490:THR:HG23	1.85	0.77
1:A:75:PHE:CE1	1:A:448:ASN:HB3	2.20	0.77
1:C:289:ASP:HB2	1:C:308:GLN:NE2	2.00	0.76
1:C:275:ARG:HB3	1:C:325:GLY:H	1.50	0.76
1:B:458:GLU:OE2	1:B:490:THR:HG23	1.86	0.76
1:D:335:THR:HG22	1:D:337:ASP:H	1.49	0.76
1:D:61:GLU:HG3	1:D:62:SER:H	1.50	0.75
1:C:39:ASP:OD1	1:C:240:ASN:HB3	1.86	0.75
1:C:44:SER:HA	1:C:368:LYS:HZ2	1.50	0.75
1:C:37:SER:O	1:C:251:PHE:HB2	1.86	0.75
1:D:80:ARG:HG2	1:D:384:THR:HG22	1.69	0.74
1:A:126:ARG:HB2	1:A:244:LEU:O	1.87	0.74
1:D:37:SER:O	1:D:251:PHE:HB2	1.86	0.74
1:C:335:THR:HG22	1:C:337:ASP:H	1.51	0.74
1:C:108:GLN:HG2	1:C:121:ILE:HD13	1.69	0.73
1:D:61:GLU:CG	1:D:62:SER:H	2.01	0.73
1:B:86:THR:OG1	1:B:378:LYS:HG3	1.88	0.73
1:D:88:SER:HA	1:D:375:VAL:O	1.88	0.73
1:A:55:SER:HB3	1:A:115:VAL:HG13	1.69	0.73
1:B:126:ARG:HB2	1:B:244:LEU:O	1.88	0.73
1:C:105:GLY:O	1:C:267:MET:HG3	1.89	0.73
1:C:64:VAL:HB	1:C:80:ARG:NH1	2.03	0.72
1:A:469:ASP:OD2	1:C:180:GLN:HA	1.89	0.72
1:C:36:GLN:O	1:C:251:PHE:HB3	1.89	0.72
1:D:295:LYS:HD2	2:D:539:HOH:O	1.90	0.72
1:D:312:ILE:H	1:D:312:ILE:HD12	1.55	0.71
1:A:252:ASN:O	1:A:256:GLN:HB2	1.90	0.71
1:A:457:ARG:HB2	1:A:464:TRP:CZ3	2.25	0.71
1:C:107:LEU:HD11	1:C:126:ARG:HH21	1.55	0.71
1:C:44:SER:HA	1:C:368:LYS:NZ	2.04	0.71
1:B:464:TRP:HA	1:B:467:TRP:CE3	2.25	0.71
1:A:384:THR:HG22	1:A:385:THR:N	2.06	0.71
1:A:39:ASP:O	1:A:43:SER:HB2	1.90	0.71
1:C:109:LEU:HD21	1:C:122:LEU:HD11	1.72	0.70
1:A:66:LYS:HB2	1:A:66:LYS:NZ	2.05	0.70
1:B:252:ASN:O	1:B:256:GLN:HB2	1.90	0.70
1:D:37:SER:C	1:D:251:PHE:HB2	2.12	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:391:LYS:HE2	1:D:446:GLU:OE1	1.92	0.70
1:C:87:THR:HG22	1:C:89:PRO:HD3	1.73	0.70
1:D:127:LYS:HG3	1:D:245:PHE:O	1.92	0.70
1:B:222:MET:HE3	1:B:298:ILE:HD11	1.72	0.70
1:C:105:GLY:H	1:C:268:VAL:HB	1.56	0.70
1:B:286:SER:HB2	1:B:388:GLU:HB3	1.73	0.69
1:D:322:VAL:HG21	1:D:327:ALA:HB1	1.73	0.69
1:D:94:ILE:HD13	1:D:359:PRO:HB2	1.74	0.69
1:A:342:ARG:HD3	2:A:503:HOH:O	1.92	0.69
1:C:98:VAL:HG21	1:C:329:GLU:OE2	1.92	0.69
1:D:322:VAL:CG2	1:D:331:ASN:HB3	2.23	0.69
1:C:89:PRO:C	1:C:91:ASP:H	1.95	0.69
1:A:84:SER:HB2	1:A:380:ASP:OD2	1.93	0.68
1:C:49:ARG:HD3	2:C:505:HOH:O	1.93	0.68
1:A:131:ILE:CG2	1:A:144:ILE:HG22	2.23	0.68
1:D:60:ILE:HG22	1:D:61:GLU:N	2.08	0.68
1:A:310:LYS:HA	1:A:310:LYS:HE2	1.75	0.68
1:B:131:ILE:CG2	1:B:144:ILE:HG22	2.24	0.68
1:A:48:ASN:O	1:A:52:VAL:HG13	1.94	0.68
1:C:127:LYS:HG3	1:C:245:PHE:O	1.93	0.68
1:C:104:PRO:HD2	1:C:154:VAL:HG11	1.75	0.68
1:C:289:ASP:HB3	1:C:309:TYR:CE1	2.18	0.68
1:A:131:ILE:HG12	1:A:233:VAL:HG12	1.76	0.67
1:C:418:GLU:HB2	1:C:420:ASN:ND2	2.08	0.67
1:A:222:MET:HE1	1:A:298:ILE:CD1	2.23	0.67
1:C:83:ARG:HB2	1:C:381:TYR:CE1	2.29	0.67
1:D:418:GLU:HB2	1:D:420:ASN:ND2	2.09	0.67
1:C:134:ASP:OD1	1:C:232:THR:HG23	1.95	0.67
1:B:90:VAL:O	1:B:363:THR:HG22	1.94	0.67
1:A:462:LEU:HD11	1:C:232:THR:OG1	1.95	0.67
1:A:96:ASP:OD2	1:A:99:ASN:HB2	1.95	0.67
1:C:53:LEU:HD13	1:C:115:VAL:HG22	1.75	0.67
1:B:198:VAL:HG21	1:B:203:LEU:HD21	1.77	0.66
1:D:134:ASP:OD1	1:D:232:THR:HG23	1.96	0.66
1:D:398:HIS:O	1:D:438:HIS:HA	1.96	0.66
1:D:319:THR:HG23	1:D:334:VAL:HG22	1.75	0.66
1:A:55:SER:HB3	1:A:115:VAL:CG1	2.25	0.66
1:A:109:LEU:HD12	2:A:554:HOH:O	1.95	0.66
1:B:295:LYS:HE2	1:B:299:LYS:NZ	2.11	0.66
1:B:90:VAL:HG12	1:B:374:ALA:HB2	1.77	0.66
1:C:335:THR:HG22	1:C:336:LYS:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:GLU:O	1:B:61:GLU:HG2	1.96	0.66
1:D:52:VAL:HB	2:D:568:HOH:O	1.95	0.65
1:C:278:TYR:HE1	1:C:323:LEU:HD22	1.61	0.65
1:D:94:ILE:HG13	1:D:361:SER:HA	1.77	0.65
1:B:131:ILE:HG12	1:B:233:VAL:HG12	1.79	0.65
1:D:335:THR:HG22	1:D:336:LYS:H	1.60	0.65
1:C:80:ARG:HH11	1:C:80:ARG:HG3	1.61	0.65
1:D:61:GLU:HG3	1:D:62:SER:N	2.12	0.65
1:A:346:LYS:HG3	2:A:527:HOH:O	1.97	0.65
1:B:369:ASP:OD2	1:B:371:SER:HB3	1.96	0.65
1:C:398:HIS:O	1:C:438:HIS:HA	1.96	0.65
1:B:222:MET:HE1	1:B:294:PHE:HB3	1.79	0.64
1:D:396:LEU:HB2	1:D:441:THR:HG22	1.80	0.64
1:A:66:LYS:HB2	1:A:66:LYS:HZ3	1.62	0.64
1:B:107:LEU:HD11	1:B:126:ARG:HH21	1.61	0.64
1:C:103:TYR:CD1	1:C:154:VAL:HG21	2.32	0.64
1:D:94:ILE:CD1	1:D:359:PRO:HB2	2.26	0.64
1:A:75:PHE:CD1	1:A:448:ASN:HB3	2.32	0.64
1:B:426:LYS:HD2	2:B:548:HOH:O	1.98	0.64
1:C:199:ASN:HB3	1:C:202:VAL:HG23	1.80	0.64
1:A:198:VAL:HG21	1:A:203:LEU:HD21	1.79	0.64
1:A:398:HIS:O	1:A:438:HIS:HA	1.97	0.64
1:C:308:GLN:NE2	1:C:312:ILE:HD11	2.12	0.64
1:A:395:ASN:HD22	1:A:442:VAL:HG22	1.61	0.64
1:D:148:ASP:HB3	1:D:153:LYS:HE2	1.80	0.64
1:D:335:THR:HG22	1:D:336:LYS:N	2.12	0.64
1:C:64:VAL:HB	1:C:80:ARG:HH12	1.63	0.64
1:A:491:LEU:HD22	1:C:176:PRO:HG2	1.80	0.64
1:C:191:GLN:HA	1:C:379:THR:HG21	1.80	0.64
1:C:61:GLU:HA	1:C:61:GLU:OE1	1.97	0.64
1:A:395:ASN:ND2	1:A:442:VAL:HG22	2.13	0.63
1:B:476:VAL:HG13	1:B:499:TYR:OH	1.98	0.63
1:D:322:VAL:O	1:D:323:LEU:HD23	1.98	0.63
1:B:395:ASN:HD22	1:B:442:VAL:HG22	1.62	0.63
1:C:293:ALA:HB2	1:C:309:TYR:CD1	2.34	0.63
1:D:199:ASN:HB3	1:D:202:VAL:HG23	1.80	0.63
1:B:80:ARG:HD3	1:B:382:ILE:HG21	1.79	0.63
1:A:396:LEU:HD23	1:A:484:VAL:HB	1.81	0.62
1:C:217:ASN:ND2	1:C:384:THR:HB	2.14	0.62
1:C:289:ASP:HB2	1:C:308:GLN:CD	2.19	0.62
1:B:398:HIS:O	1:B:438:HIS:HA	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:THR:OG1	1:A:153:LYS:HB2	1.99	0.62
1:A:369:ASP:OD2	1:A:371:SER:HB3	1.99	0.62
1:A:302:ASP:HA	1:A:304:LYS:HE3	1.80	0.62
1:C:335:THR:HG22	1:C:336:LYS:N	2.14	0.62
1:D:63:PHE:N	1:D:63:PHE:CD2	2.68	0.62
1:C:97:SER:O	1:C:358:TYR:HB3	2.00	0.62
1:A:295:LYS:HE2	1:A:299:LYS:NZ	2.14	0.61
1:A:304:LYS:HD2	1:A:304:LYS:N	2.15	0.61
1:B:395:ASN:ND2	1:B:442:VAL:HG22	2.14	0.61
1:B:173:HIS:HB2	1:B:354:LYS:HG3	1.82	0.61
1:C:296:ALA:HB2	1:C:303:ILE:CD1	2.27	0.61
1:C:227:LYS:HE3	1:C:360:ILE:HG22	1.81	0.61
1:C:191:GLN:HG3	1:C:381:TYR:CD2	2.35	0.61
1:D:116:GLU:O	1:D:117:ASN:HB2	2.00	0.61
1:D:196:LEU:O	1:D:198:VAL:HG13	2.01	0.61
1:B:315:ASN:HB2	2:B:561:HOH:O	2.01	0.61
1:B:326:ASP:OD1	1:B:326:ASP:N	2.33	0.61
1:B:396:LEU:HD23	1:B:484:VAL:HB	1.82	0.61
1:A:335:THR:HG22	1:A:336:LYS:N	2.15	0.61
1:B:222:MET:CE	1:B:298:ILE:HD11	2.31	0.61
1:A:157:ALA:O	1:A:160:GLU:HB2	2.00	0.61
1:A:470:VAL:HG12	1:A:495:SER:HB3	1.83	0.61
1:C:75:PHE:O	1:C:389:TYR:HB2	2.01	0.61
1:A:125:LYS:HE3	2:A:504:HOH:O	1.99	0.60
1:A:335:THR:HG22	1:A:336:LYS:H	1.66	0.60
1:A:254:LEU:HB3	1:A:259:VAL:HG21	1.84	0.60
1:C:148:ASP:HB3	1:C:153:LYS:HE2	1.83	0.60
1:A:173:HIS:HB2	1:A:354:LYS:HG3	1.83	0.60
1:B:324:GLY:HA3	2:B:501:HOH:O	2.01	0.60
1:C:172:THR:HG22	1:C:174:THR:H	1.66	0.60
1:C:196:LEU:O	1:C:198:VAL:HG13	2.01	0.60
1:C:308:GLN:HG3	1:C:309:TYR:N	2.15	0.60
1:C:222:MET:HE1	1:C:298:ILE:HD11	1.83	0.60
1:B:131:ILE:HG22	1:B:144:ILE:CG2	2.30	0.60
1:C:37:SER:C	1:C:251:PHE:HB2	2.23	0.60
1:C:53:LEU:HD22	1:C:115:VAL:HG23	1.84	0.60
1:D:98:VAL:HG21	1:D:329:GLU:HG2	1.83	0.60
1:A:37:SER:C	1:A:251:PHE:HB2	2.23	0.59
1:A:476:VAL:HG13	1:A:499:TYR:OH	2.01	0.59
1:D:172:THR:HG22	1:D:174:THR:H	1.66	0.59
1:C:351:PHE:HE2	2:C:535:HOH:O	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:ARG:HD3	1:C:384:THR:CG2	2.32	0.59
1:C:95:ILE:HG13	1:C:96:ASP:H	1.66	0.59
1:D:78:VAL:HG11	1:D:217:ASN:HD21	1.67	0.59
1:A:119:PRO:HD3	2:A:502:HOH:O	2.03	0.59
1:A:131:ILE:HG22	1:A:144:ILE:CG2	2.31	0.59
1:B:457:ARG:HB2	1:B:464:TRP:CZ3	2.36	0.59
1:A:222:MET:CE	1:A:298:ILE:HD11	2.30	0.59
1:A:328:GLN:CG	1:A:329:GLU:H	2.16	0.59
1:B:150:THR:OG1	1:B:153:LYS:HB2	2.03	0.59
1:B:487:TRP:CH2	1:B:496:SER:HB3	2.36	0.59
1:C:81:GLN:C	1:C:382:ILE:HG13	2.23	0.59
1:A:487:TRP:CH2	1:A:496:SER:HB3	2.38	0.59
1:A:45:LEU:O	1:A:368:LYS:NZ	2.32	0.59
1:A:418:GLU:HB2	1:A:420:ASN:ND2	2.17	0.59
1:A:128:PRO:HB3	1:A:147:ASP:HA	1.85	0.58
1:A:384:THR:CG2	1:A:385:THR:N	2.66	0.58
1:B:335:THR:HG22	1:B:336:LYS:N	2.18	0.58
1:C:47:TYR:CD1	1:C:52:VAL:HG11	2.38	0.58
1:C:82:LYS:HD2	1:C:380:ASP:HB3	1.84	0.58
1:D:337:ASP:OD1	1:D:339:ASP:HB2	2.04	0.58
1:C:45:LEU:H	1:C:368:LYS:HZ2	1.50	0.58
1:D:140:GLY:O	1:D:141:GLU:HG3	2.03	0.58
1:A:101:ARG:HG2	2:A:546:HOH:O	2.03	0.58
1:A:391:LYS:HB3	1:A:445:LEU:O	2.04	0.58
1:B:157:ALA:O	1:B:160:GLU:HB2	2.04	0.58
1:C:186:VAL:HG23	1:C:221:VAL:O	2.04	0.58
1:A:75:PHE:HB2	1:A:447:ALA:CB	2.33	0.58
1:B:108:GLN:HE21	1:B:121:ILE:CD1	2.16	0.58
1:C:116:GLU:O	1:C:117:ASN:HB2	2.03	0.58
1:D:416:ASP:OD2	1:D:420:ASN:HB2	2.04	0.58
1:D:453:ARG:NH2	2:D:515:HOH:O	2.35	0.58
1:B:477:PRO:O	1:B:479:THR:HG23	2.04	0.58
1:C:286:SER:OG	1:C:386:SER:HB3	2.04	0.58
1:D:275:ARG:HA	1:D:360:ILE:HD11	1.85	0.58
1:A:41:GLY:HA3	1:A:251:PHE:CD1	2.39	0.57
1:B:254:LEU:HB3	1:B:259:VAL:HG21	1.86	0.57
1:C:158:ILE:O	1:C:162:VAL:HG23	2.03	0.57
1:D:147:ASP:O	1:D:149:PRO:HD3	2.04	0.57
1:D:109:LEU:HD22	1:D:263:ALA:O	2.03	0.57
1:D:61:GLU:CG	1:D:62:SER:N	2.66	0.57
1:A:464:TRP:HA	1:A:467:TRP:CZ3	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:MET:HE3	1:B:298:ILE:CD1	2.34	0.57
1:C:140:GLY:O	1:C:141:GLU:HG3	2.04	0.57
1:D:275:ARG:NH1	1:D:326:ASP:HB2	2.19	0.57
1:A:60:ILE:HG13	1:A:61:GLU:N	2.20	0.57
1:B:418:GLU:HB2	1:B:420:ASN:ND2	2.19	0.57
1:C:279:VAL:HA	1:C:319:THR:O	2.03	0.57
1:C:337:ASP:OD1	1:C:339:ASP:HB2	2.04	0.57
1:C:498:THR:HG22	1:C:499:TYR:N	2.19	0.57
1:B:295:LYS:HE2	1:B:299:LYS:HZ1	1.68	0.57
1:A:498:THR:HG22	1:A:499:TYR:N	2.19	0.57
1:C:252:ASN:O	1:C:256:GLN:HB2	2.04	0.57
1:C:416:ASP:OD2	1:C:420:ASN:HB2	2.04	0.57
1:A:222:MET:HE2	1:A:294:PHE:HB3	1.87	0.57
1:C:128:PRO:HB3	1:C:147:ASP:HA	1.87	0.57
1:C:175:LEU:HB2	1:C:351:PHE:CZ	2.40	0.57
1:C:89:PRO:HD2	1:C:375:VAL:HG13	1.87	0.57
1:C:91:ASP:O	1:C:92:ILE:HG13	2.05	0.57
1:B:458:GLU:CD	1:B:490:THR:HG23	2.25	0.57
1:D:128:PRO:HB3	1:D:147:ASP:HA	1.87	0.57
1:A:172:THR:HG22	1:A:174:THR:H	1.70	0.57
1:C:147:ASP:O	1:C:149:PRO:HD3	2.04	0.57
1:C:45:LEU:HD23	1:C:261:ASN:OD1	2.05	0.57
1:D:222:MET:HE1	1:D:298:ILE:HD11	1.86	0.57
1:D:230:PHE:HB3	1:D:351:PHE:CE1	2.40	0.57
1:B:454:ILE:HG21	1:B:484:VAL:HG21	1.86	0.56
1:D:127:LYS:N	1:D:244:LEU:O	2.36	0.56
1:C:323:LEU:HD23	1:C:323:LEU:O	2.05	0.56
1:D:158:ILE:O	1:D:162:VAL:HG23	2.05	0.56
1:D:230:PHE:CE2	1:D:274:GLY:HA2	2.40	0.56
1:A:103:TYR:CD1	1:A:154:VAL:HG21	2.40	0.56
1:B:487:TRP:HH2	1:B:496:SER:HB3	1.68	0.56
1:C:396:LEU:HB2	1:C:441:THR:HG22	1.86	0.56
1:A:335:THR:HG22	1:A:337:ASP:N	2.10	0.56
1:B:128:PRO:HB3	1:B:147:ASP:HA	1.88	0.56
1:D:107:LEU:HD11	1:D:126:ARG:HH21	1.70	0.56
1:D:498:THR:HG22	1:D:499:TYR:N	2.19	0.56
1:A:477:PRO:O	1:A:479:THR:HG23	2.05	0.56
1:C:90:VAL:HA	1:C:374:ALA:HA	1.88	0.56
1:D:175:LEU:HB2	1:D:351:PHE:CE2	2.40	0.56
1:B:454:ILE:HD13	1:B:484:VAL:HG21	1.88	0.56
1:C:382:ILE:HG23	1:C:382:ILE:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:ARG:HG3	1:C:80:ARG:NH1	2.20	0.56
1:D:175:LEU:HB2	1:D:351:PHE:CZ	2.40	0.56
1:B:335:THR:HG22	1:B:336:LYS:H	1.70	0.56
1:C:230:PHE:HB3	1:C:351:PHE:CE1	2.41	0.56
1:D:252:ASN:O	1:D:256:GLN:HB2	2.06	0.56
1:A:454:ILE:HG21	1:A:484:VAL:HG21	1.88	0.56
1:C:230:PHE:CE2	1:C:274:GLY:HA2	2.41	0.56
1:A:416:ASP:OD2	1:A:420:ASN:HB2	2.06	0.55
1:A:52:VAL:HG23	1:A:53:LEU:N	2.20	0.55
1:B:263:ALA:HB2	2:B:563:HOH:O	2.06	0.55
1:C:320:ALA:HB3	1:C:333:VAL:HB	1.89	0.55
1:A:92:ILE:HD12	1:A:362:TYR:O	2.06	0.55
1:C:98:VAL:HG12	1:C:358:TYR:CD1	2.41	0.55
1:D:60:ILE:CG2	1:D:61:GLU:N	2.69	0.55
1:B:416:ASP:OD2	1:B:420:ASN:HB2	2.06	0.55
1:C:479:THR:HB	1:C:500:ASN:O	2.07	0.55
1:A:108:GLN:HA	1:A:120:THR:O	2.06	0.55
1:A:322:VAL:H	1:A:331:ASN:ND2	2.03	0.55
1:A:487:TRP:HH2	1:A:496:SER:HB3	1.70	0.55
1:D:321:VAL:HG12	1:D:332:LYS:HA	1.89	0.55
1:C:86:THR:HG23	1:C:378:LYS:HG2	1.88	0.55
1:A:49:ARG:NH2	2:A:517:HOH:O	2.40	0.55
1:B:498:THR:HG22	1:B:499:TYR:N	2.21	0.55
1:C:198:VAL:HG21	1:C:203:LEU:HD21	1.88	0.55
1:A:87:THR:CG2	1:A:89:PRO:HD3	2.29	0.55
1:C:127:LYS:N	1:C:244:LEU:O	2.35	0.55
1:C:39:ASP:OD2	1:C:242:SER:N	2.39	0.55
1:D:186:VAL:HG23	1:D:221:VAL:O	2.06	0.55
1:D:303:ILE:O	1:D:306:SER:HB3	2.07	0.55
1:A:306:SER:HB3	1:A:308:GLN:HG3	1.88	0.54
1:B:204:GLU:O	1:B:208:GLY:HA2	2.07	0.54
1:C:97:SER:O	1:C:359:PRO:HD2	2.06	0.54
1:D:95:ILE:HG13	1:D:117:ASN:HD22	1.72	0.54
1:D:64:VAL:HG12	1:D:417:LYS:O	2.06	0.54
1:D:49:ARG:HB3	1:D:366:PHE:CE1	2.43	0.54
1:A:335:THR:CG2	1:A:337:ASP:H	2.11	0.54
1:C:175:LEU:HB2	1:C:351:PHE:CE2	2.41	0.54
1:D:179:THR:HB	2:D:562:HOH:O	2.06	0.54
1:A:428:TRP:HA	2:A:544:HOH:O	2.07	0.54
1:D:103:TYR:HB2	1:D:104:PRO:HD2	1.89	0.54
1:D:433:GLN:O	1:D:435:LYS:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:69:LYS:O	1:D:76:ILE:N	2.39	0.54
1:A:304:LYS:HD2	1:A:304:LYS:H	1.72	0.54
1:C:308:GLN:HE21	1:C:312:ILE:HD11	1.71	0.54
1:C:73:ASN:HA	1:C:391:LYS:HD2	1.88	0.54
1:D:309:TYR:HA	1:D:312:ILE:HD13	1.89	0.54
1:D:57:GLY:HA3	1:D:378:LYS:O	2.07	0.54
1:B:94:ILE:HD13	1:B:359:PRO:HB2	1.88	0.54
1:C:53:LEU:HG	1:C:114:LEU:HD23	1.88	0.54
1:D:198:VAL:HG21	1:D:203:LEU:HD21	1.88	0.54
1:D:39:ASP:OD2	1:D:39:ASP:N	2.41	0.54
1:A:47:TYR:CD1	1:A:52:VAL:HG11	2.42	0.54
1:C:98:VAL:HG12	1:C:358:TYR:CE1	2.43	0.54
1:A:470:VAL:HG11	1:A:486:ILE:HB	1.89	0.54
1:C:131:ILE:HG22	1:C:144:ILE:HG22	1.90	0.54
1:A:458:GLU:CD	1:A:490:THR:HG23	2.27	0.54
1:B:172:THR:HG22	1:B:174:THR:H	1.73	0.54
1:B:289:ASP:HB3	1:B:309:TYR:HE1	1.72	0.54
1:C:227:LYS:HZ1	1:C:361:SER:CB	2.21	0.54
1:D:105:GLY:N	1:D:268:VAL:O	2.36	0.54
1:D:328:GLN:O	1:D:331:ASN:HB2	2.08	0.54
1:D:109:LEU:HD22	1:D:263:ALA:HB1	1.90	0.54
1:A:110:ALA:HB2	1:A:266:LEU:HD21	1.91	0.53
1:C:89:PRO:C	1:C:91:ASP:N	2.62	0.53
1:A:328:GLN:HG2	1:A:329:GLU:HG2	1.90	0.53
1:D:90:VAL:HG12	1:D:374:ALA:HB2	1.89	0.53
1:A:310:LYS:HE2	1:A:313:TYR:HD1	1.72	0.53
1:D:78:VAL:HG11	1:D:217:ASN:ND2	2.24	0.53
1:C:47:TYR:HB2	1:C:52:VAL:CG1	2.38	0.53
1:C:53:LEU:CD2	1:C:115:VAL:HG23	2.39	0.53
1:C:191:GLN:CA	1:C:379:THR:HG21	2.38	0.53
1:D:109:LEU:HD12	1:D:120:THR:HG21	1.89	0.53
1:D:86:THR:HA	1:D:377:ASN:O	2.07	0.53
1:C:100:ASP:C	1:C:102:THR:H	2.12	0.53
1:C:85:LEU:C	1:C:85:LEU:HD23	2.29	0.53
1:A:396:LEU:HD11	1:A:443:ILE:HD11	1.90	0.53
2:A:541:HOH:O	1:C:462:LEU:HD22	2.08	0.53
1:D:479:THR:HB	1:D:500:ASN:O	2.08	0.53
1:C:83:ARG:N	1:C:381:TYR:O	2.40	0.53
1:A:63:PHE:O	1:A:65:PRO:HD3	2.08	0.53
1:C:110:ALA:HB2	1:C:266:LEU:CD2	2.38	0.53
1:C:217:ASN:HD21	1:C:384:THR:HB	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:TYR:O	1:C:295:LYS:NZ	2.42	0.52
1:D:67:GLU:HG2	1:D:69:LYS:HD3	1.90	0.52
1:B:141:GLU:HB3	1:B:164:LYS:HE2	1.92	0.52
1:D:369:ASP:OD2	1:D:371:SER:HB3	2.09	0.52
1:C:79:GLU:HB2	1:C:385:THR:OG1	2.10	0.52
1:D:304:LYS:O	1:D:313:TYR:HE1	1.91	0.52
1:B:131:ILE:HD12	1:B:154:VAL:HG13	1.92	0.52
1:C:148:ASP:H	1:C:153:LYS:HE2	1.75	0.52
1:C:265:PRO:HB2	1:C:367:LEU:HD12	1.91	0.52
1:C:38:ILE:HD12	1:C:242:SER:HB3	1.91	0.52
1:C:465:GLU:CD	1:C:465:GLU:H	2.12	0.52
1:A:484:VAL:HG22	1:A:497:ILE:HD12	1.92	0.52
1:C:433:GLN:O	1:C:435:LYS:HG2	2.10	0.52
1:B:89:PRO:HD2	1:B:375:VAL:O	2.10	0.52
1:B:396:LEU:HD11	1:B:443:ILE:HD11	1.91	0.52
1:B:59:LYS:N	1:B:59:LYS:HD2	2.24	0.52
1:C:53:LEU:HD22	1:C:115:VAL:CG2	2.40	0.52
1:C:280:LYS:O	1:C:318:PHE:HA	2.10	0.52
1:A:392:GLY:HA3	1:A:479:THR:O	2.10	0.52
1:B:335:THR:HG22	1:B:337:ASP:N	2.11	0.52
1:B:459:CYS:HA	1:B:467:TRP:CE2	2.45	0.52
1:B:60:ILE:HG23	1:B:60:ILE:O	2.09	0.52
1:B:179:THR:HA	1:B:227:LYS:O	2.10	0.52
1:A:350:THR:CG2	1:A:351:PHE:N	2.72	0.52
1:B:392:GLY:HA3	1:B:479:THR:O	2.10	0.52
1:C:53:LEU:HD21	1:C:111:ASP:O	2.10	0.52
1:A:38:ILE:HG12	1:A:254:LEU:HD11	1.90	0.51
1:C:95:ILE:HG23	1:C:117:ASN:HD22	1.75	0.51
1:C:369:ASP:OD2	1:C:371:SER:HB3	2.09	0.51
1:D:131:ILE:HG22	1:D:144:ILE:HG22	1.92	0.51
1:A:457:ARG:HD2	1:A:469:ASP:OD1	2.11	0.51
1:C:310:LYS:NZ	1:C:314:GLU:HG3	2.25	0.51
1:C:61:GLU:HG3	1:C:62:SER:N	2.26	0.51
1:B:107:LEU:CD1	1:B:126:ARG:HH21	2.22	0.51
1:B:464:TRP:HA	1:B:467:TRP:CZ3	2.45	0.51
1:C:302:ASP:OD1	1:C:302:ASP:N	2.42	0.51
1:D:110:ALA:HB2	1:D:266:LEU:CD2	2.36	0.51
1:D:148:ASP:H	1:D:153:LYS:HE2	1.74	0.51
1:D:265:PRO:HB2	1:D:367:LEU:HD12	1.92	0.51
1:D:308:GLN:CA	1:D:308:GLN:HE21	2.24	0.51
1:C:265:PRO:HG2	1:C:367:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:ILE:HD13	1:A:484:VAL:HG21	1.93	0.51
1:B:350:THR:CG2	1:B:351:PHE:N	2.73	0.51
1:D:358:TYR:HB3	1:D:359:PRO:HD2	1.91	0.51
1:D:63:PHE:N	1:D:63:PHE:HD2	2.09	0.51
1:A:452:ILE:HD12	1:A:476:VAL:O	2.11	0.51
1:B:293:ALA:HB2	1:B:309:TYR:CD1	2.46	0.51
1:C:100:ASP:HB3	1:C:102:THR:OG1	2.10	0.51
1:A:222:MET:HE3	1:A:281:LEU:HD13	1.93	0.51
1:A:239:LYS:HG3	1:A:240:ASN:ND2	2.26	0.51
1:A:458:GLU:HG2	1:A:459:CYS:H	1.75	0.51
1:D:148:ASP:CB	1:D:153:LYS:HE2	2.40	0.51
1:B:239:LYS:HG3	1:B:240:ASN:ND2	2.26	0.51
1:B:484:VAL:HG22	1:B:497:ILE:HD12	1.91	0.51
1:D:55:SER:OG	1:D:377:ASN:HA	2.10	0.51
1:A:491:LEU:HD22	1:C:176:PRO:CG	2.40	0.51
1:C:104:PRO:HD2	1:C:154:VAL:CG1	2.40	0.51
1:D:238:PRO:HG3	1:D:244:LEU:HG	1.93	0.51
1:B:458:GLU:O	1:B:467:TRP:HB3	2.11	0.51
1:C:36:GLN:C	1:C:251:PHE:HB3	2.31	0.51
1:C:80:ARG:HD3	1:C:384:THR:HG21	1.93	0.51
1:C:89:PRO:O	1:C:91:ASP:N	2.44	0.51
1:D:144:ILE:HB	1:D:161:LEU:HD21	1.93	0.51
1:A:141:GLU:HB3	1:A:164:LYS:HE2	1.92	0.50
1:A:407:GLU:HG3	1:A:432:TYR:CZ	2.46	0.50
1:A:470:VAL:HG22	1:A:493:PRO:CB	2.41	0.50
1:B:107:LEU:CG	1:B:126:ARG:HH21	2.24	0.50
1:C:275:ARG:HA	1:C:360:ILE:HD11	1.93	0.50
1:C:80:ARG:HG2	1:C:384:THR:HG22	1.93	0.50
1:A:368:LYS:NZ	2:A:551:HOH:O	2.44	0.50
1:B:55:SER:OG	1:B:377:ASN:HB2	2.11	0.50
1:C:41:GLY:O	1:C:45:LEU:HD12	2.11	0.50
1:C:108:GLN:HB2	1:C:266:LEU:HD12	1.93	0.50
1:A:350:THR:HG22	1:A:351:PHE:N	2.25	0.50
1:B:498:THR:HG22	1:B:499:TYR:H	1.76	0.50
1:B:110:ALA:HB2	1:B:266:LEU:HD21	1.94	0.50
1:C:321:VAL:HG23	1:C:321:VAL:O	2.11	0.50
1:C:47:TYR:HB2	1:C:52:VAL:HG11	1.94	0.50
1:D:398:HIS:CE1	1:D:400:GLY:H	2.30	0.50
1:D:230:PHE:HZ	1:D:275:ARG:NH1	2.10	0.50
1:D:270:ASN:O	1:D:362:TYR:HB2	2.12	0.50
1:A:37:SER:O	1:A:251:PHE:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:THR:HG22	1:B:351:PHE:N	2.26	0.50
1:B:452:ILE:HD12	1:B:476:VAL:O	2.12	0.50
1:C:227:LYS:NZ	1:C:361:SER:CB	2.75	0.50
1:C:95:ILE:HG23	1:C:117:ASN:HB3	1.94	0.50
1:D:150:THR:O	1:D:154:VAL:HG23	2.11	0.50
1:D:465:GLU:CD	1:D:465:GLU:H	2.13	0.50
1:A:498:THR:HG22	1:A:499:TYR:H	1.76	0.50
1:B:222:MET:HE2	1:B:281:LEU:HD13	1.94	0.50
1:D:222:MET:HE3	1:D:224:LEU:HD21	1.94	0.50
1:A:131:ILE:HD12	1:A:154:VAL:HG13	1.94	0.50
1:A:85:LEU:HD23	1:A:86:THR:N	2.27	0.50
1:C:238:PRO:HG3	1:C:244:LEU:HG	1.93	0.50
1:C:295:LYS:HE2	1:C:299:LYS:NZ	2.27	0.50
1:D:50:ASN:HA	1:D:376:HIS:NE2	2.26	0.50
1:A:204:GLU:O	1:A:208:GLY:HA2	2.11	0.49
1:D:53:LEU:CD1	1:D:373:ALA:HB1	2.42	0.49
1:D:425:HIS:HE1	1:D:453:ARG:NH2	2.10	0.49
1:A:322:VAL:H	1:A:331:ASN:HD21	1.60	0.49
1:A:394:ILE:HD13	1:A:454:ILE:HD11	1.94	0.49
1:B:309:TYR:O	1:B:312:ILE:N	2.45	0.49
1:D:107:LEU:CD2	1:D:267:MET:HB2	2.42	0.49
1:D:98:VAL:HG11	1:D:329:GLU:CG	2.41	0.49
1:A:66:LYS:NZ	1:A:79:GLU:HG3	2.26	0.49
1:B:407:GLU:HG3	1:B:432:TYR:CZ	2.48	0.49
1:B:464:TRP:O	1:B:466:TRP:N	2.46	0.49
1:C:109:LEU:CD2	1:C:122:LEU:HD11	2.40	0.49
1:C:126:ARG:HG3	1:C:149:PRO:HD2	1.93	0.49
1:A:132:ASN:ND2	1:A:143:SER:OG	2.35	0.49
1:A:291:GLN:O	1:A:295:LYS:HG3	2.13	0.49
1:C:78:VAL:HG12	1:C:386:SER:OG	2.13	0.49
1:D:395:ASN:HD22	1:D:442:VAL:HG22	1.77	0.49
1:A:245:PHE:N	1:A:245:PHE:CD1	2.80	0.49
1:A:328:GLN:CG	1:A:329:GLU:HG2	2.42	0.49
1:A:407:GLU:HG3	1:A:432:TYR:OH	2.12	0.49
1:B:104:PRO:HG2	1:B:131:ILE:HD11	1.94	0.49
1:B:245:PHE:CD1	1:B:245:PHE:N	2.80	0.49
1:D:58:ASP:HB3	2:D:524:HOH:O	2.12	0.49
1:C:377:ASN:ND2	1:C:378:LYS:H	2.10	0.49
1:C:497:ILE:HG23	1:C:497:ILE:O	2.12	0.49
1:D:66:LYS:HG3	1:D:79:GLU:HG2	1.94	0.49
1:A:131:ILE:HG12	1:A:233:VAL:CG1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:ILE:HG13	1:C:39:ASP:H	1.77	0.49
1:D:47:TYR:CE2	1:D:264:PRO:HB3	2.46	0.49
1:B:96:ASP:OD2	1:B:99:ASN:HB2	2.13	0.49
1:C:270:ASN:O	1:C:362:TYR:HB2	2.13	0.49
1:C:300:ASN:ND2	1:C:300:ASN:O	2.39	0.49
1:A:464:TRP:C	1:A:466:TRP:H	2.16	0.49
1:C:255:LYS:HA	1:C:259:VAL:O	2.12	0.49
1:D:96:ASP:OD2	1:D:100:ASP:HB2	2.13	0.49
1:B:468:ARG:HB3	1:D:178:ARG:HA	1.94	0.49
1:C:144:ILE:HB	1:C:161:LEU:HD21	1.95	0.48
1:C:91:ASP:HA	1:C:363:THR:HG22	1.95	0.48
2:B:528:HOH:O	1:C:440:SER:HB3	2.12	0.48
1:D:303:ILE:HG22	1:D:309:TYR:CE2	2.48	0.48
1:D:446:GLU:OE1	1:D:446:GLU:HA	2.12	0.48
1:D:41:GLY:HA3	1:D:251:PHE:CZ	2.49	0.48
1:A:384:THR:CG2	1:A:385:THR:H	2.26	0.48
1:A:470:VAL:HG22	1:A:493:PRO:HB3	1.96	0.48
1:A:76:ILE:HD13	1:A:76:ILE:N	2.27	0.48
1:B:402:TYR:CD1	1:B:458:GLU:HG3	2.48	0.48
1:B:405:GLN:HG3	1:B:459:CYS:SG	2.54	0.48
1:C:288:LYS:HG3	1:C:289:ASP:OD2	2.14	0.48
1:D:265:PRO:HG2	1:D:367:LEU:HD12	1.95	0.48
1:A:82:LYS:HA	1:A:382:ILE:HG12	1.95	0.48
1:C:451:ASN:O	1:C:453:ARG:NH1	2.47	0.48
1:C:150:THR:O	1:C:154:VAL:HG23	2.13	0.48
1:C:105:GLY:N	1:C:268:VAL:O	2.46	0.48
1:D:295:LYS:HE2	1:D:299:LYS:NZ	2.29	0.48
1:A:413:VAL:HG12	1:A:448:ASN:HB2	1.95	0.48
1:B:226:TYR:HB2	1:B:277:ILE:HB	1.96	0.48
1:D:308:GLN:HG3	1:D:309:TYR:N	2.29	0.48
1:D:201:LYS:HE2	1:D:201:LYS:N	2.28	0.48
1:A:226:TYR:HB2	1:A:277:ILE:HB	1.95	0.47
1:B:275:ARG:HA	1:B:360:ILE:HD11	1.96	0.47
1:D:498:THR:CG2	1:D:499:TYR:N	2.77	0.47
1:A:418:GLU:HB2	1:A:420:ASN:HD21	1.79	0.47
1:B:108:GLN:HE21	1:B:121:ILE:HD13	1.79	0.47
1:B:335:THR:CG2	1:B:337:ASP:H	2.12	0.47
1:C:148:ASP:CB	1:C:153:LYS:HE2	2.44	0.47
1:C:217:ASN:ND2	1:C:384:THR:CB	2.77	0.47
1:C:61:GLU:HG3	1:C:62:SER:H	1.80	0.47
1:D:465:GLU:HG2	1:D:466:TRP:CZ3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ARG:HA	1:A:360:ILE:HD11	1.97	0.47
1:D:476:VAL:HG11	1:D:482:ILE:HD13	1.95	0.47
1:C:76:ILE:CD1	1:C:388:GLU:HG3	2.45	0.47
1:C:60:ILE:O	1:C:82:LYS:NZ	2.36	0.47
1:A:222:MET:CE	1:A:224:LEU:HD21	2.45	0.47
1:C:394:ILE:HB	1:C:443:ILE:HB	1.97	0.47
1:B:116:GLU:O	1:B:118:ARG:HG2	2.15	0.47
1:B:54:ALA:HA	1:B:376:HIS:O	2.15	0.47
1:A:491:LEU:CD2	1:C:176:PRO:HG2	2.44	0.47
1:D:283:THR:HB	1:D:316:SER:OG	2.14	0.47
1:A:179:THR:HA	1:A:227:LYS:O	2.15	0.47
1:B:126:ARG:HH11	1:B:126:ARG:HG3	1.80	0.47
1:B:88:SER:N	1:B:89:PRO:HD3	2.30	0.47
1:C:222:MET:HE3	1:C:224:LEU:HD21	1.97	0.47
1:C:98:VAL:HG13	1:C:324:GLY:O	2.15	0.47
1:D:106:ALA:O	1:D:267:MET:HG3	2.15	0.47
1:D:487:TRP:NE1	1:D:494:GLY:HA3	2.29	0.47
1:C:267:MET:HG2	1:C:268:VAL:N	2.30	0.47
1:C:358:TYR:HB3	1:C:359:PRO:HD2	1.96	0.47
1:A:268:VAL:HG13	1:A:362:TYR:CD1	2.50	0.47
1:C:285:SER:HB3	1:C:312:ILE:HG23	1.96	0.47
1:C:375:VAL:HG22	1:C:376:HIS:N	2.30	0.47
1:D:451:ASN:O	1:D:453:ARG:NH1	2.48	0.47
1:C:498:THR:CG2	1:C:499:TYR:N	2.78	0.47
1:C:86:THR:HG23	1:C:378:LYS:CG	2.45	0.47
1:B:295:LYS:NZ	1:D:474:TYR:O	2.48	0.47
1:A:126:ARG:HG3	1:A:126:ARG:HH11	1.80	0.46
1:B:407:GLU:HG3	1:B:432:TYR:OH	2.13	0.46
1:D:224:LEU:HB2	1:D:279:VAL:HB	1.97	0.46
1:D:48:ASN:O	1:D:52:VAL:HG22	2.15	0.46
1:A:109:LEU:HB3	1:A:263:ALA:HB1	1.97	0.46
1:B:94:ILE:HD12	1:B:361:SER:HA	1.97	0.46
1:D:126:ARG:HG3	1:D:149:PRO:HD2	1.96	0.46
1:B:413:VAL:HG12	1:B:448:ASN:HB2	1.98	0.46
1:C:227:LYS:NZ	1:C:361:SER:HB3	2.30	0.46
1:C:425:HIS:HE1	1:C:453:ARG:NH2	2.13	0.46
1:C:95:ILE:CG2	1:C:117:ASN:HB3	2.45	0.46
1:A:116:GLU:O	1:A:118:ARG:HG2	2.16	0.46
1:B:75:PHE:HB2	1:B:447:ALA:HB3	1.96	0.46
1:C:60:ILE:HG13	1:C:61:GLU:N	2.31	0.46
1:B:222:MET:HE3	1:B:224:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:487:TRP:N	1:B:494:GLY:O	2.48	0.46
1:C:108:GLN:HE21	1:C:121:ILE:HD11	1.80	0.46
1:C:446:GLU:HA	1:C:446:GLU:OE1	2.14	0.46
1:C:48:ASN:O	1:C:52:VAL:HG22	2.16	0.46
1:A:101:ARG:HB3	1:A:151:TYR:CG	2.50	0.46
1:C:39:ASP:CG	1:C:242:SER:H	2.18	0.46
1:D:339:ASP:O	1:D:342:ARG:HB2	2.16	0.46
1:D:92:ILE:O	1:D:361:SER:HA	2.16	0.46
1:A:186:VAL:HG13	1:A:192:ILE:HB	1.98	0.46
1:C:187:TYR:CE2	1:C:383:GLU:HG2	2.50	0.46
1:C:94:ILE:HG22	1:C:360:ILE:O	2.15	0.46
1:C:321:VAL:HA	1:C:331:ASN:O	2.16	0.46
1:C:476:VAL:HG11	1:C:482:ILE:HD13	1.96	0.46
1:B:418:GLU:HB2	1:B:420:ASN:HD21	1.80	0.46
1:C:201:LYS:HE2	1:C:201:LYS:N	2.31	0.46
1:D:301:THR:O	1:D:304:LYS:HG3	2.16	0.46
1:D:270:ASN:HB2	1:D:363:THR:OG1	2.15	0.46
1:B:83:ARG:HH22	1:D:421:GLU:CD	2.19	0.46
1:D:64:VAL:O	1:D:80:ARG:HD2	2.16	0.46
1:B:101:ARG:HG2	1:B:101:ARG:NH1	2.31	0.45
1:B:168:LYS:HE2	1:B:169:TYR:OH	2.16	0.45
1:B:222:MET:CE	1:B:224:LEU:HD21	2.46	0.45
1:C:290:VAL:HG22	1:C:312:ILE:HD13	1.98	0.45
1:C:76:ILE:HD13	1:C:388:GLU:HA	1.97	0.45
1:A:306:SER:O	1:A:309:TYR:N	2.49	0.45
1:C:224:LEU:HB2	1:C:279:VAL:HB	1.97	0.45
1:C:220:LYS:O	1:C:282:GLU:HA	2.16	0.45
1:D:288:LYS:HG3	1:D:289:ASP:OD2	2.16	0.45
1:D:60:ILE:CG2	1:D:61:GLU:H	2.29	0.45
1:B:41:GLY:HA3	1:B:251:PHE:CD1	2.52	0.45
1:C:78:VAL:HA	1:C:385:THR:O	2.16	0.45
1:C:398:HIS:CE1	1:C:400:GLY:H	2.34	0.45
1:C:42:ILE:HD12	1:C:241:PRO:CB	2.46	0.45
1:D:38:ILE:O	1:D:42:ILE:HG13	2.17	0.45
1:D:320:ALA:HB2	1:D:341:ILE:HD12	1.98	0.45
1:A:168:LYS:HE2	1:A:169:TYR:OH	2.17	0.45
1:A:96:ASP:O	1:A:100:ASP:N	2.48	0.45
1:C:465:GLU:HG2	1:C:466:TRP:CZ3	2.52	0.45
1:D:148:ASP:H	1:D:153:LYS:CE	2.30	0.45
1:B:458:GLU:OE1	1:B:490:THR:HG23	2.17	0.45
1:C:270:ASN:HB2	1:C:363:THR:OG1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:ASP:O	1:C:100:ASP:N	2.49	0.45
1:A:295:LYS:HE2	1:A:299:LYS:HZ1	1.78	0.45
1:A:38:ILE:HG22	1:A:39:ASP:N	2.32	0.45
1:A:60:ILE:CG1	1:A:61:GLU:N	2.80	0.45
1:B:42:ILE:CD1	1:B:241:PRO:HB3	2.47	0.45
1:B:94:ILE:HD12	1:B:361:SER:CA	2.46	0.45
1:C:395:ASN:HD22	1:C:442:VAL:HG22	1.80	0.45
1:A:406:PHE:HB2	1:A:428:TRP:HZ3	1.80	0.45
1:A:85:LEU:HD21	1:A:87:THR:OG1	2.16	0.45
1:D:320:ALA:HB2	1:D:341:ILE:HG23	1.99	0.45
1:A:108:GLN:O	1:A:266:LEU:HD12	2.17	0.45
1:A:85:LEU:C	1:A:85:LEU:HD23	2.37	0.45
1:B:186:VAL:HG13	1:B:192:ILE:HB	1.98	0.45
1:B:280:LYS:HB3	1:B:319:THR:HB	1.98	0.45
1:B:47:TYR:CD1	1:B:47:TYR:O	2.69	0.45
1:C:227:LYS:HE3	1:C:360:ILE:CG2	2.47	0.45
1:C:47:TYR:HD1	1:C:52:VAL:HG11	1.81	0.45
1:A:110:ALA:HB2	1:A:266:LEU:CD2	2.47	0.45
1:B:384:THR:HG22	1:B:384:THR:O	2.17	0.45
1:C:312:ILE:O	1:C:316:SER:HB2	2.17	0.45
1:D:231:TYR:OH	1:D:357:ALA:HB3	2.17	0.45
1:D:47:TYR:HB2	1:D:52:VAL:HG11	1.99	0.45
1:B:309:TYR:O	1:B:310:LYS:C	2.55	0.44
1:D:91:ASP:OD2	1:D:361:SER:HB2	2.17	0.44
1:A:222:MET:HE3	1:A:224:LEU:HD21	1.99	0.44
1:C:180:GLN:HB2	1:C:227:LYS:HB3	1.97	0.44
1:A:109:LEU:CD2	1:A:122:LEU:HD21	2.37	0.44
1:A:97:SER:HB3	1:A:358:TYR:HB3	1.99	0.44
1:A:94:ILE:CD1	1:A:359:PRO:HB2	2.48	0.44
1:A:416:ASP:OD1	1:A:418:GLU:N	2.51	0.44
1:A:47:TYR:HD1	1:A:52:VAL:HG11	1.82	0.44
1:D:156:GLY:O	1:D:159:ASP:HB2	2.16	0.44
1:D:255:LYS:HA	1:D:259:VAL:O	2.17	0.44
1:A:114:LEU:HD12	2:A:502:HOH:O	2.17	0.44
1:B:335:THR:HG21	1:B:337:ASP:HB3	2.00	0.44
1:B:73:ASN:ND2	1:B:391:LYS:HE3	2.32	0.44
1:B:394:ILE:HD13	1:B:454:ILE:HD11	1.99	0.44
1:C:278:TYR:CE1	1:C:323:LEU:HD22	2.47	0.44
1:C:49:ARG:NH2	1:C:369:ASP:OD2	2.50	0.44
1:C:457:ARG:HG2	1:C:467:TRP:HB2	2.00	0.44
1:A:295:LYS:HE2	1:A:299:LYS:HZ2	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:GLU:HG2	1:A:329:GLU:H	1.45	0.44
1:A:487:TRP:N	1:A:494:GLY:O	2.47	0.44
1:A:69:LYS:HB3	1:A:69:LYS:HE3	1.85	0.44
1:B:406:PHE:HB2	1:B:428:TRP:HZ3	1.83	0.44
1:B:75:PHE:CB	1:B:447:ALA:HB3	2.48	0.44
1:C:339:ASP:O	1:C:342:ARG:HB2	2.17	0.44
1:D:222:MET:CE	1:D:298:ILE:HD11	2.48	0.44
1:D:393:LYS:HD2	2:D:512:HOH:O	2.18	0.44
1:B:268:VAL:HG13	1:B:362:TYR:CD1	2.53	0.44
1:B:83:ARG:NH2	1:D:421:GLU:OE1	2.48	0.44
1:D:425:HIS:CE1	1:D:453:ARG:NH2	2.85	0.44
1:A:234:SER:HB3	1:A:270:ASN:OD1	2.18	0.44
1:A:327:ALA:HA	2:A:543:HOH:O	2.18	0.44
1:A:406:PHE:O	1:A:431:ASN:HA	2.17	0.44
1:A:465:GLU:HG3	1:A:466:TRP:CZ3	2.53	0.44
1:A:58:ASP:OD2	1:A:58:ASP:N	2.50	0.44
1:B:416:ASP:OD1	1:B:418:GLU:N	2.50	0.44
1:B:73:ASN:ND2	1:B:391:LYS:CE	2.80	0.44
1:C:303:ILE:CG1	1:C:304:LYS:N	2.80	0.44
1:A:232:THR:HG21	1:C:466:TRP:CD1	2.53	0.44
1:D:267:MET:HG2	1:D:268:VAL:N	2.32	0.44
1:C:156:GLY:O	1:C:159:ASP:HB2	2.17	0.44
1:C:275:ARG:NH1	1:C:326:ASP:HB2	2.33	0.44
1:C:98:VAL:HG21	1:C:329:GLU:CD	2.36	0.44
1:D:37:SER:O	1:D:38:ILE:C	2.56	0.44
1:D:407:GLU:HB2	1:D:464:TRP:CH2	2.53	0.44
1:A:244:LEU:HA	2:A:550:HOH:O	2.18	0.44
1:A:66:LYS:HZ1	1:A:79:GLU:HG3	1.83	0.44
1:C:231:TYR:OH	1:C:357:ALA:HB3	2.18	0.44
1:C:36:GLN:N	2:C:518:HOH:O	2.50	0.44
1:C:58:ASP:O	1:C:380:ASP:HB2	2.18	0.44
1:D:126:ARG:HB2	1:D:244:LEU:O	2.18	0.44
1:B:303:ILE:HD13	1:B:303:ILE:N	2.33	0.43
1:B:457:ARG:HG3	1:B:468:ARG:O	2.18	0.43
1:A:101:ARG:O	1:A:151:TYR:CD1	2.71	0.43
1:A:425:HIS:CE1	1:A:453:ARG:NH2	2.86	0.43
1:B:49:ARG:O	1:B:52:VAL:HG22	2.17	0.43
1:C:41:GLY:HA3	1:C:251:PHE:CD1	2.54	0.43
1:D:180:GLN:HB2	1:D:227:LYS:HB3	1.99	0.43
1:D:310:LYS:O	1:D:314:GLU:HB2	2.19	0.43
1:D:335:THR:CG2	1:D:336:LYS:H	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:96:ASP:HB2	1:D:100:ASP:HB3	2.00	0.43
1:A:192:ILE:HG23	1:A:193:SER:N	2.34	0.43
1:C:91:ASP:C	1:C:92:ILE:HG13	2.39	0.43
1:D:98:VAL:HG11	1:D:329:GLU:HG3	2.00	0.43
1:D:226:TYR:HB2	1:D:277:ILE:HB	1.99	0.43
1:D:497:ILE:O	1:D:497:ILE:HG23	2.18	0.43
1:A:172:THR:CG2	1:A:174:THR:H	2.31	0.43
1:B:189:LYS:O	1:B:193:SER:HB3	2.19	0.43
1:C:90:VAL:HA	1:C:374:ALA:CB	2.48	0.43
1:D:96:ASP:CB	1:D:100:ASP:CB	2.97	0.43
1:A:238:PRO:HB2	1:A:243:ASP:HB2	2.01	0.43
1:B:101:ARG:HG2	1:B:101:ARG:HH11	1.83	0.43
1:B:131:ILE:HG12	1:B:233:VAL:CG1	2.46	0.43
1:C:148:ASP:H	1:C:153:LYS:CE	2.32	0.43
1:C:187:TYR:CZ	1:C:383:GLU:HG2	2.53	0.43
1:C:66:LYS:HG3	1:C:79:GLU:CG	2.38	0.43
1:C:90:VAL:HA	1:C:374:ALA:CA	2.48	0.43
1:D:263:ALA:N	1:D:264:PRO:HD3	2.34	0.43
1:A:180:GLN:HB2	1:A:227:LYS:HB3	1.99	0.43
1:B:172:THR:CG2	1:B:174:THR:H	2.32	0.43
1:B:94:ILE:HD12	1:B:361:SER:N	2.33	0.43
1:C:108:GLN:HE21	1:C:121:ILE:CD1	2.32	0.43
1:C:265:PRO:HB2	1:C:367:LEU:CD1	2.48	0.43
1:B:275:ARG:NH2	1:B:350:THR:O	2.52	0.43
1:C:122:LEU:HD22	1:C:257:LYS:CB	2.49	0.43
1:C:275:ARG:HH11	1:C:326:ASP:HB2	1.84	0.43
1:C:407:GLU:HB2	1:C:464:TRP:CH2	2.54	0.43
1:B:457:ARG:CZ	1:D:180:GLN:NE2	2.82	0.43
1:B:407:GLU:HB3	1:B:455:LYS:HB3	2.01	0.43
1:B:456:ALA:O	1:B:470:VAL:N	2.47	0.43
1:B:48:ASN:CG	1:B:51:GLU:HG2	2.39	0.43
1:C:263:ALA:N	1:C:264:PRO:HD3	2.34	0.43
1:D:220:LYS:O	1:D:282:GLU:HA	2.19	0.43
1:D:312:ILE:N	1:D:312:ILE:HD12	2.28	0.43
1:D:95:ILE:HG13	1:D:117:ASN:ND2	2.33	0.43
1:A:75:PHE:O	1:A:389:TYR:HB2	2.19	0.43
1:B:406:PHE:O	1:B:431:ASN:HA	2.19	0.43
1:D:109:LEU:HD12	1:D:120:THR:CG2	2.49	0.43
1:B:199:ASN:HB3	1:B:202:VAL:HG23	2.01	0.42
1:B:425:HIS:CE1	1:B:453:ARG:NH2	2.87	0.42
1:B:488:GLY:N	2:B:525:HOH:O	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:425:HIS:CE1	1:C:453:ARG:NH2	2.87	0.42
1:C:487:TRP:NE1	1:C:494:GLY:HA3	2.34	0.42
1:A:305:ASN:O	1:A:306:SER:C	2.58	0.42
1:A:408:VAL:N	1:A:431:ASN:HD21	2.17	0.42
1:B:108:GLN:HA	1:B:120:THR:O	2.19	0.42
1:C:122:LEU:HD22	1:C:257:LYS:HB2	2.00	0.42
1:C:300:ASN:C	1:C:300:ASN:ND2	2.73	0.42
1:C:300:ASN:C	1:C:300:ASN:HD22	2.20	0.42
1:B:83:ARG:NH1	1:D:421:GLU:OE1	2.51	0.42
1:D:487:TRP:HH2	1:D:496:SER:HB3	1.83	0.42
1:D:56:ASN:HD22	1:D:57:GLY:N	2.18	0.42
1:A:483:ASN:O	1:A:497:ILE:HA	2.19	0.42
1:B:360:ILE:HA	1:B:360:ILE:HD13	1.80	0.42
1:D:172:THR:HG22	1:D:173:HIS:N	2.34	0.42
1:A:407:GLU:HB3	1:A:455:LYS:HB3	2.01	0.42
1:C:107:LEU:CD1	1:C:126:ARG:HH21	2.25	0.42
1:C:204:GLU:HA	1:C:209:VAL:H	1.85	0.42
1:D:273:TYR:HA	1:D:358:TYR:O	2.19	0.42
1:B:180:GLN:HB2	1:B:227:LYS:HB3	2.01	0.42
1:A:144:ILE:HG21	1:A:157:ALA:HB1	2.02	0.42
1:B:230:PHE:CE2	1:B:274:GLY:HA2	2.54	0.42
1:B:291:GLN:O	1:B:295:LYS:HG3	2.20	0.42
1:C:303:ILE:CG1	1:C:304:LYS:H	2.33	0.42
1:D:107:LEU:HD23	1:D:267:MET:HB2	2.01	0.42
1:D:53:LEU:HD11	1:D:373:ALA:HB1	2.01	0.42
1:D:478:LEU:HD22	2:D:534:HOH:O	2.20	0.42
1:A:107:LEU:O	1:A:121:ILE:HA	2.19	0.42
1:A:230:PHE:CE2	1:A:274:GLY:HA2	2.55	0.42
1:A:464:TRP:O	1:A:466:TRP:N	2.47	0.42
1:C:273:TYR:HA	1:C:358:TYR:O	2.19	0.42
1:C:41:GLY:HA3	1:C:251:PHE:CE1	2.55	0.42
1:D:173:HIS:HB2	1:D:353:THR:OG1	2.20	0.42
1:D:199:ASN:OD1	1:D:201:LYS:HG2	2.20	0.42
1:A:407:GLU:HA	1:A:431:ASN:ND2	2.35	0.42
1:B:238:PRO:HB2	1:B:243:ASP:HB2	2.01	0.42
1:C:126:ARG:HB2	1:C:244:LEU:O	2.20	0.42
1:C:407:GLU:HG3	1:C:432:TYR:OH	2.20	0.42
1:D:295:LYS:HA	1:D:298:ILE:HD12	2.02	0.42
1:A:436:THR:O	1:A:437:ALA:C	2.57	0.41
1:A:52:VAL:HG21	1:A:366:PHE:CZ	2.54	0.41
1:A:52:VAL:CG2	1:A:53:LEU:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:LYS:HE2	1:B:282:GLU:OE2	2.19	0.41
1:C:226:TYR:HB2	1:C:277:ILE:HB	2.02	0.41
1:C:259:VAL:HG13	1:C:265:PRO:CD	2.41	0.41
1:C:265:PRO:CG	1:C:367:LEU:HD12	2.50	0.41
1:D:394:ILE:HB	1:D:443:ILE:HB	2.01	0.41
1:A:429:ASP:C	1:A:431:ASN:H	2.24	0.41
1:B:61:GLU:CG	1:B:61:GLU:O	2.68	0.41
1:C:500:ASN:ND2	2:C:525:HOH:O	2.54	0.41
1:D:258:GLY:O	1:D:263:ALA:HB3	2.20	0.41
1:D:457:ARG:HG2	1:D:467:TRP:HB2	2.01	0.41
1:B:110:ALA:HB2	1:B:266:LEU:CD2	2.50	0.41
1:B:192:ILE:HG23	1:B:193:SER:N	2.34	0.41
1:D:122:LEU:HD22	1:D:257:LYS:CB	2.50	0.41
1:D:310:LYS:HE2	1:D:310:LYS:HA	2.02	0.41
1:A:308:GLN:O	1:A:312:ILE:HG13	2.20	0.41
1:A:453:ARG:HG2	1:A:453:ARG:HH11	1.85	0.41
1:C:172:THR:HG22	1:C:173:HIS:N	2.36	0.41
1:C:274:GLY:O	1:C:360:ILE:HD11	2.21	0.41
1:C:295:LYS:HA	1:C:298:ILE:HD12	2.01	0.41
1:D:122:LEU:HD22	1:D:257:LYS:HB2	2.02	0.41
1:D:339:ASP:O	1:D:342:ARG:N	2.54	0.41
1:A:103:TYR:HB2	1:A:104:PRO:HD2	2.01	0.41
1:A:83:ARG:HB3	1:A:381:TYR:CZ	2.55	0.41
1:A:74:LYS:NZ	1:A:388:GLU:HG2	2.36	0.41
1:A:94:ILE:HD12	1:A:359:PRO:HB2	2.03	0.41
1:B:108:GLN:HE21	1:B:121:ILE:HD11	1.86	0.41
1:C:92:ILE:HG21	1:C:362:TYR:CZ	2.56	0.41
1:C:52:VAL:HG21	1:C:366:PHE:CZ	2.55	0.41
1:D:306:SER:O	1:D:307:GLN:C	2.58	0.41
1:A:413:VAL:HB	1:A:450:ARG:HD3	2.02	0.41
1:B:413:VAL:HB	1:B:450:ARG:HD3	2.02	0.41
1:D:476:VAL:CG1	1:D:482:ILE:HD13	2.50	0.41
1:B:38:ILE:HA	1:B:251:PHE:HB2	2.01	0.41
1:C:108:GLN:HB2	1:C:266:LEU:CD1	2.50	0.41
1:C:325:GLY:HA2	1:C:358:TYR:HD1	1.86	0.41
1:C:61:GLU:OE1	1:C:61:GLU:CA	2.66	0.41
1:D:108:GLN:HA	1:D:120:THR:O	2.21	0.41
1:D:204:GLU:HA	1:D:209:VAL:H	1.85	0.41
1:D:50:ASN:HA	1:D:376:HIS:CE1	2.56	0.41
1:A:189:LYS:O	1:A:193:SER:HB3	2.20	0.41
1:A:335:THR:HG21	1:A:337:ASP:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ASN:HA	1:A:376:HIS:NE2	2.35	0.41
1:B:198:VAL:HG11	1:B:278:TYR:CE2	2.56	0.41
1:C:407:GLU:HG3	1:C:432:TYR:CE2	2.56	0.41
1:D:265:PRO:HB2	1:D:367:LEU:CD1	2.51	0.41
1:D:78:VAL:HG22	1:D:386:SER:HB2	2.02	0.41
1:D:444:PRO:HD2	2:D:503:HOH:O	2.21	0.41
1:C:105:GLY:HA2	1:C:267:MET:CG	2.51	0.41
1:C:222:MET:CE	1:C:281:LEU:HD13	2.51	0.41
1:D:132:ASN:O	1:D:233:VAL:HA	2.21	0.41
1:D:274:GLY:O	1:D:360:ILE:HD11	2.21	0.41
1:D:96:ASP:CB	1:D:100:ASP:HB3	2.51	0.41
1:A:309:TYR:HA	1:A:312:ILE:HD12	2.02	0.41
1:A:491:LEU:C	1:A:493:PRO:HD3	2.41	0.41
1:B:337:ASP:OD1	1:B:339:ASP:HB2	2.20	0.41
1:C:64:VAL:CB	1:C:80:ARG:NH1	2.80	0.41
1:D:307:GLN:O	1:D:310:LYS:HB2	2.21	0.41
1:D:335:THR:CG2	1:D:336:LYS:N	2.80	0.41
1:B:144:ILE:HG21	1:B:157:ALA:HB1	2.03	0.40
1:B:212:ASN:O	1:B:215:ALA:N	2.54	0.40
1:C:254:LEU:C	1:C:256:GLN:H	2.25	0.40
1:C:310:LYS:HE2	1:C:313:TYR:HB2	2.03	0.40
1:B:436:THR:O	1:B:437:ALA:C	2.59	0.40
1:C:154:VAL:O	1:C:158:ILE:HG13	2.21	0.40
1:C:191:GLN:N	1:C:379:THR:HG21	2.35	0.40
1:D:238:PRO:CB	1:D:243:ASP:HB2	2.52	0.40
1:D:417:LYS:HB2	1:D:417:LYS:NZ	2.36	0.40
1:B:42:ILE:HD12	1:B:241:PRO:CB	2.51	0.40
1:B:83:ARG:HG3	1:B:383:GLU:HB2	2.03	0.40
1:C:228:GLN:OE1	1:C:348:ASN:O	2.39	0.40
1:C:350:THR:HG22	1:C:351:PHE:N	2.37	0.40
1:D:109:LEU:CD2	1:D:263:ALA:O	2.69	0.40
1:D:465:GLU:HG2	1:D:466:TRP:CE3	2.56	0.40
1:D:470:VAL:HG12	1:D:495:SER:HB3	2.04	0.40
1:D:53:LEU:HA	1:D:53:LEU:HD23	1.95	0.40
1:B:497:ILE:O	1:B:497:ILE:HG23	2.21	0.40
1:C:132:ASN:O	1:C:233:VAL:HA	2.21	0.40
1:C:189:LYS:HA	1:C:211:PHE:CE2	2.57	0.40
1:C:199:ASN:OD1	1:C:201:LYS:HG2	2.21	0.40
1:C:338:PHE:O	1:C:341:ILE:HB	2.22	0.40
1:A:335:THR:CG2	1:A:336:LYS:N	2.83	0.40
1:B:429:ASP:C	1:B:431:ASN:H	2.25	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:477:PRO:HG2	1:B:499:TYR:CE2	2.57	0.40
1:B:482:ILE:HG23	1:B:497:ILE:HD11	2.04	0.40
1:C:335:THR:CG2	1:C:336:LYS:N	2.82	0.40
1:C:476:VAL:CG1	1:C:482:ILE:HD13	2.51	0.40
1:D:228:GLN:OE1	1:D:348:ASN:O	2.40	0.40
1:D:297:LEU:HD21	1:D:318:PHE:CZ	2.56	0.40
1:D:411:ASP:O	1:D:449:ALA:HA	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	463/471 (98%)	421 (91%)	35 (8%)	7 (2%)	10 34
1	B	463/471 (98%)	417 (90%)	39 (8%)	7 (2%)	10 34
1	C	463/471 (98%)	416 (90%)	41 (9%)	6 (1%)	12 37
1	D	463/471 (98%)	424 (92%)	31 (7%)	8 (2%)	9 31
All	All	1852/1884 (98%)	1678 (91%)	146 (8%)	28 (2%)	10 34

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	462	LEU
1	B	58	ASP
1	D	38	ILE
1	D	62	SER
1	A	465	GLU
1	B	465	GLU
1	D	438	HIS
1	A	416	ASP

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Mol	Chain	Res	Type
1	B	416	ASP
1	C	90	VAL
1	C	368	LYS
1	C	437	ALA
1	C	438	HIS
1	D	368	LYS
1	D	437	ALA
1	A	437	ALA
1	B	437	ALA
1	D	307	GLN
1	A	330	HIS
1	B	65	PRO
1	C	141	GLU
1	D	106	ALA
1	D	141	GLU
1	A	430	GLY
1	C	38	ILE
1	A	290	VAL
1	B	290	VAL
1	B	430	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	412/418 (99%)	374 (91%)	38 (9%)	9	27
1	B	412/418 (99%)	372 (90%)	40 (10%)	8	25
1	C	412/418 (99%)	357 (87%)	55 (13%)	4	11
1	D	412/418 (99%)	364 (88%)	48 (12%)	5	16
All	All	1648/1672 (99%)	1467 (89%)	181 (11%)	6	19

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	SER

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Mol	Chain	Res	Type
1	A	43	SER
1	A	58	ASP
1	A	66	LYS
1	A	69	LYS
1	A	84	SER
1	A	108	GLN
1	A	112	LYS
1	A	126	ARG
1	A	130	ASN
1	A	132	ASN
1	A	153	LYS
1	A	159	ASP
1	A	171	SER
1	A	239	LYS
1	A	245	PHE
1	A	266	LEU
1	A	284	THR
1	A	286	SER
1	A	300	ASN
1	A	304	LYS
1	A	305	ASN
1	A	308	GLN
1	A	328	GLN
1	A	329	GLU
1	A	331	ASN
1	A	363	THR
1	A	370	ASN
1	A	385	THR
1	A	388	GLU
1	A	390	SER
1	A	391	LYS
1	A	393	LYS
1	A	398	HIS
1	A	414	SER
1	A	450	ARG
1	A	465	GLU
1	A	468	ARG
1	B	47	TYR
1	B	49	ARG
1	B	52	VAL
1	B	58	ASP
1	B	59	LYS

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Mol	Chain	Res	Type
1	B	60	ILE
1	B	79	GLU
1	B	87	THR
1	B	93	SER
1	B	101	ARG
1	B	108	GLN
1	B	112	LYS
1	B	126	ARG
1	B	130	ASN
1	B	132	ASN
1	B	153	LYS
1	B	159	ASP
1	B	171	SER
1	B	197	ASN
1	B	239	LYS
1	B	245	PHE
1	B	266	LEU
1	B	284	THR
1	B	286	SER
1	B	326	ASP
1	B	328	GLN
1	B	363	THR
1	B	370	ASN
1	B	375	VAL
1	B	377	ASN
1	B	380	ASP
1	B	383	GLU
1	B	384	THR
1	B	385	THR
1	B	387	THR
1	B	393	LYS
1	B	398	HIS
1	B	414	SER
1	B	450	ARG
1	B	458	GLU
1	C	45	LEU
1	C	49	ARG
1	C	52	VAL
1	C	53	LEU
1	C	58	ASP
1	C	64	VAL
1	C	69	LYS

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Mol	Chain	Res	Type
1	C	74	LYS
1	C	80	ARG
1	C	84	SER
1	C	85	LEU
1	C	86	THR
1	C	93	SER
1	C	100	ASP
1	C	126	ARG
1	C	130	ASN
1	C	131	ILE
1	C	132	ASN
1	C	163	SER
1	C	171	SER
1	C	194	SER
1	C	197	ASN
1	C	218	GLU
1	C	232	THR
1	C	239	LYS
1	C	243	ASP
1	C	266	LEU
1	C	286	SER
1	C	299	LYS
1	C	300	ASN
1	C	302	ASP
1	C	304	LYS
1	C	306	SER
1	C	308	GLN
1	C	310	LYS
1	C	311	ASP
1	C	317	SER
1	C	326	ASP
1	C	331	ASN
1	C	346	LYS
1	C	370	ASN
1	C	378	LYS
1	C	379	THR
1	C	384	THR
1	C	386	SER
1	C	387	THR
1	C	390	SER
1	C	393	LYS
1	C	398	HIS

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Mol	Chain	Res	Type
1	C	414	SER
1	C	440	SER
1	C	450	ARG
1	C	457	ARG
1	C	468	ARG
1	C	475	ASP
1	D	39	ASP
1	D	43	SER
1	D	44	SER
1	D	49	ARG
1	D	50	ASN
1	D	56	ASN
1	D	62	SER
1	D	63	PHE
1	D	64	VAL
1	D	69	LYS
1	D	73	ASN
1	D	96	ASP
1	D	101	ARG
1	D	108	GLN
1	D	126	ARG
1	D	130	ASN
1	D	131	ILE
1	D	132	ASN
1	D	163	SER
1	D	171	SER
1	D	194	SER
1	D	197	ASN
1	D	218	GLU
1	D	232	THR
1	D	239	LYS
1	D	243	ASP
1	D	266	LEU
1	D	286	SER
1	D	299	LYS
1	D	304	LYS
1	D	305	ASN
1	D	306	SER
1	D	308	GLN
1	D	311	ASP
1	D	328	GLN
1	D	330	HIS

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Mol	Chain	Res	Type
1	D	346	LYS
1	D	370	ASN
1	D	375	VAL
1	D	383	GLU
1	D	393	LYS
1	D	398	HIS
1	D	414	SER
1	D	440	SER
1	D	450	ARG
1	D	457	ARG
1	D	468	ARG
1	D	475	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	GLN
1	A	108	GLN
1	A	132	ASN
1	A	197	ASN
1	A	217	ASN
1	A	240	ASN
1	A	307	GLN
1	A	328	GLN
1	A	331	ASN
1	A	395	ASN
1	A	420	ASN
1	A	483	ASN
1	A	500	ASN
1	B	73	ASN
1	B	108	GLN
1	B	132	ASN
1	B	197	ASN
1	B	217	ASN
1	B	240	ASN
1	B	308	GLN
1	B	395	ASN
1	B	420	ASN
1	B	483	ASN
1	B	500	ASN
1	C	48	ASN
1	C	99	ASN

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Mol	Chain	Res	Type
1	C	108	GLN
1	C	117	ASN
1	C	197	ASN
1	C	205	ASN
1	C	217	ASN
1	C	308	GLN
1	C	315	ASN
1	C	331	ASN
1	C	370	ASN
1	C	377	ASN
1	C	395	ASN
1	C	420	ASN
1	C	483	ASN
1	D	56	ASN
1	D	73	ASN
1	D	99	ASN
1	D	108	GLN
1	D	117	ASN
1	D	180	GLN
1	D	197	ASN
1	D	205	ASN
1	D	217	ASN
1	D	308	GLN
1	D	330	HIS
1	D	395	ASN
1	D	420	ASN
1	D	451	ASN
1	D	483	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.