



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:48 PM GMT

PDB ID : 1M1J
Title : Crystal structure of native chicken fibrinogen with two different bound ligands
Authors : Yang, Z.; Kollman, J.M.; Pandi, L.; Doolittle, R.F.
Deposited on : 2002-06-19
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

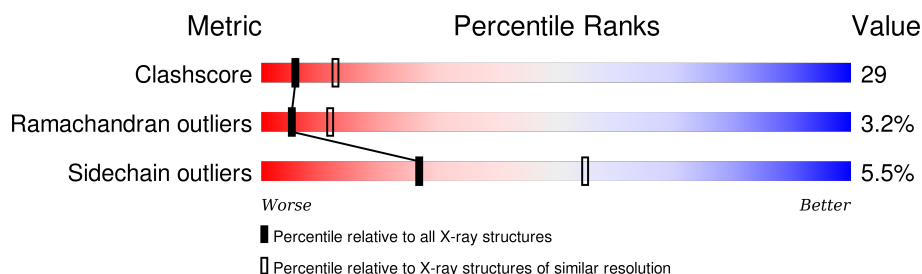
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)




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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	491	
1	D	491	
2	B	464	
2	E	464	
3	C	409	
3	F	409	
4	G	4	

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Mol	Chain	Length	Quality of chain
4	H	4	
5	I	4	
5	J	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NDG	B	470	-	-	X	-
6	NDG	C	420	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16117 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 Fibrinogen alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	192	Total	C	N	O	S	0	0	0
			1544	947	282	305	10			
1	D	194	Total	C	N	O	S	0	0	0
			1565	962	286	307	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	GLY	CYS	SEE REMARK 999	UNP P14448
D	49	GLY	CYS	SEE REMARK 999	UNP P14448

- Molecule 2 is a protein called Fibrinogen beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	402	Total	C	N	O	S	0	0	0
			3225	2023	554	623	25			
2	E	401	Total	C	N	O	S	0	0	0
			3216	2019	553	619	25			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLN	-	SEE REMARK 999	UNP Q02020
E	1	GLN	-	SEE REMARK 999	UNP Q02020

- Molecule 3 is a protein called Fibrinogen gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	390	Total	C	N	O	S	0	0	0
			3162	1987	539	620	16			
3	F	389	Total	C	N	O	S	0	0	0
			3155	1983	538	618	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	286	ALA	ARG	SEE REMARK 999	UNP O93568
F	286	ALA	ARG	SEE REMARK 999	UNP O93568

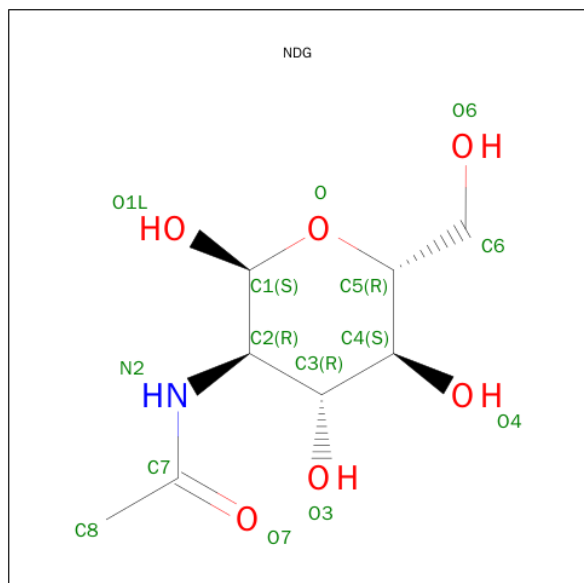
- Molecule 4 is a protein called GLY-PRO-ARG-PRO peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	4	Total	C	N	O	0	0	0
			30	18	7	5			
4	H	4	Total	C	N	O	0	0	0
			30	18	7	5			

- Molecule 5 is a protein called GLY-HIS-ARG-PRO peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	4	Total	C	N	O	0	0	0
			33	19	9	5			
5	J	4	Total	C	N	O	0	0	0
			33	19	9	5			

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



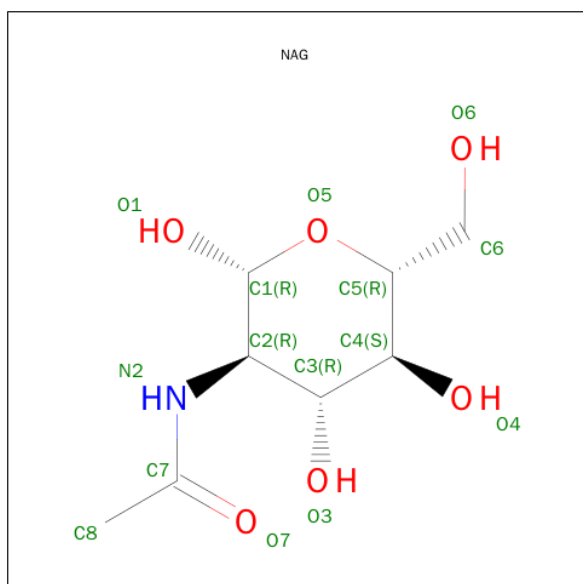
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			15	8	1	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	E	1	Total	C	N	O	0	0
			15	8	1	6		
6	J	1	Total	C	N	O	0	0
			15	8	1	6		
6	C	1	Total	C	N	O	0	0
			15	8	1	6		
6	F	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	I	1	Total	C	N	O	0	0
			15	8	1	6		
7	C	1	Total	C	N	O	0	0
			15	8	1	6		
7	F	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		
8	C	1	Total	Ca	0	0
			1	1		

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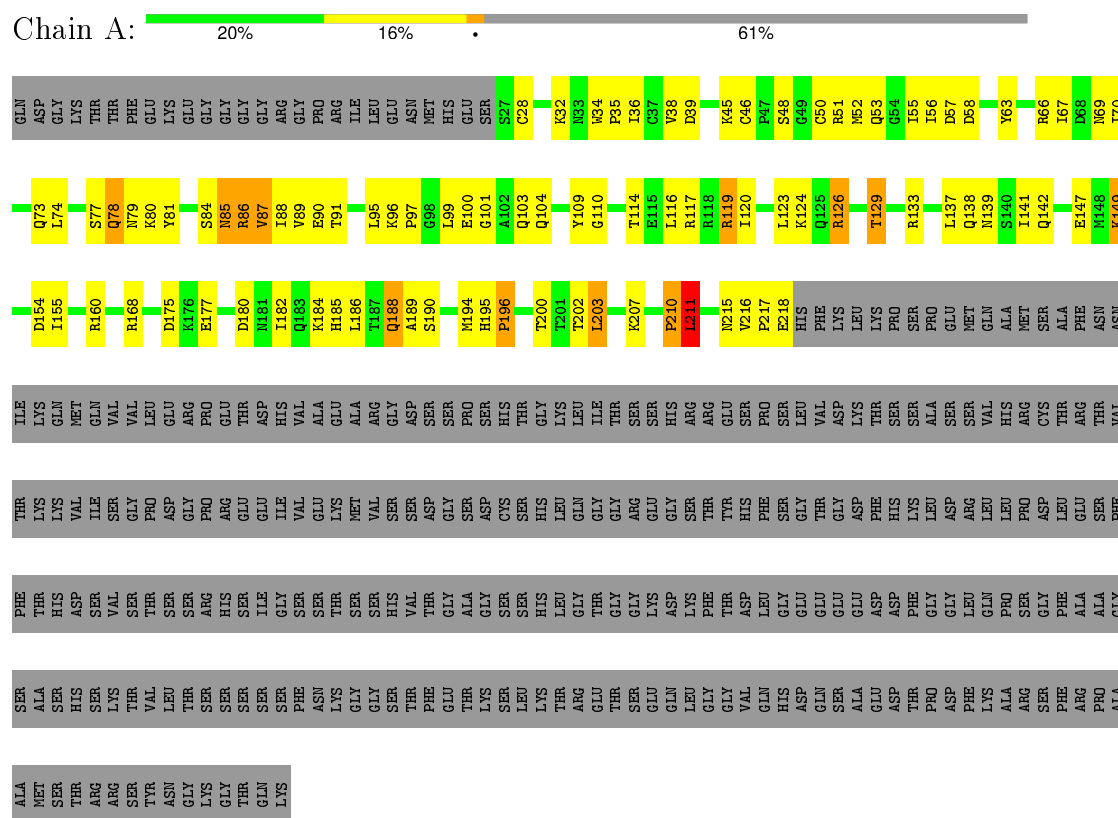
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	F	1	Total 1	Ca 1	0	0
8	E	1	Total 1	Ca 1	0	0

3 Residue-property plots

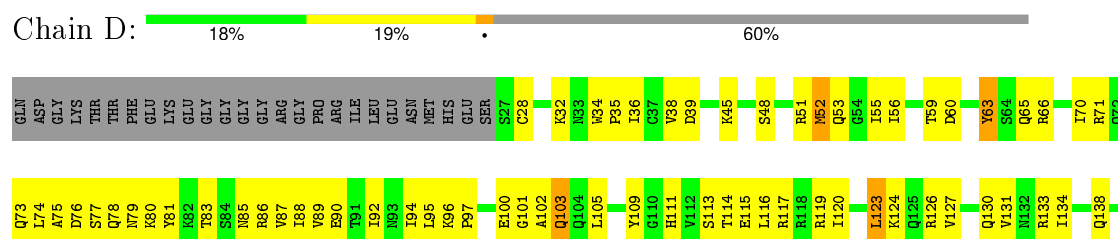
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: Fibrinogen alpha subunit



- Molecule 1: Fibrinogen alpha subunit







- Molecule 4: GLY-PRO-ARG-PRO peptide

Chain H:



- Molecule 5: GLY-HIS-ARG-PRO peptide

Chain I:



- Molecule 5: GLY-HIS-ARG-PRO peptide

Chain J:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	114.09Å 100.02Å 200.09Å 90.00° 105.79° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	93.1 (20.00-2.70)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.227 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16117	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NAG, NDG

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	0.33	0/1564	0.57	0/2108
1	D	0.30	0/1587	0.58	0/2139
2	B	0.39	0/3304	0.63	1/4467 (0.0%)
2	E	0.34	0/3295	0.61	1/4456 (0.0%)
3	C	0.42	0/3236	0.65	1/4374 (0.0%)
3	F	0.39	0/3229	0.65	1/4364 (0.0%)
4	G	0.62	0/31	0.80	0/40
4	H	0.60	0/31	0.69	0/40
5	I	0.55	0/34	0.69	0/43
5	J	0.46	0/34	0.52	0/43
All	All	0.37	0/16345	0.63	4/22074 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	338	ARG	N-CA-C	-6.79	92.66	111.00
3	C	338	ARG	N-CA-C	-6.79	92.67	111.00
2	B	403	GLY	N-CA-C	5.09	125.82	113.10
2	E	410	ARG	N-CA-C	-5.09	97.26	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	1544	0	1532	133	0
1	D	1565	0	1548	161	0
2	B	3225	0	3081	182	0
2	E	3216	0	3077	233	0
3	C	3162	0	2992	189	0
3	F	3155	0	2985	190	0
4	G	30	0	32	1	0
4	H	30	0	32	2	0
5	I	33	0	32	1	0
5	J	33	0	32	4	0
6	B	15	0	15	11	0
6	C	15	0	15	10	0
6	E	15	0	15	4	0
6	F	15	0	15	3	0
6	J	15	0	15	0	0
7	C	15	0	15	1	0
7	F	15	0	15	0	0
7	I	15	0	15	3	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
All	All	16117	0	15463	916	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 29.

All (916) 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:216:VAL:HG22	2:B:129:LYS:HE3	1.24	1.15
3:F:52:ASN:HD21	6:F:520:NDG:H8C3	1.01	1.13
2:E:443:ASN:H	2:E:443:ASN:HD22	1.05	1.01
2:E:371:MET:HB2	2:E:410:ARG:CB	1.92	0.99
3:F:356:ARG:HB3	3:F:356:ARG:NH1	1.79	0.97
1:D:142:GLN:HE22	1:D:183:GLN:HE22	1.12	0.96
2:B:371:MET:HB2	2:B:410:ARG:CB	1.96	0.96
2:E:371:MET:HB2	2:E:410:ARG:HB3	1.43	0.96
2:B:368:ASN:HD21	6:B:470:NDG:C1	1.80	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:64:TYR:HB3	2:E:65:PRO:HD2	1.48	0.95
2:E:368:ASN:HD21	6:E:570:NDG:H2	1.30	0.95
2:E:368:ASN:ND2	6:E:570:NDG:H2	1.82	0.94
1:A:117:ARG:HG3	1:A:203:LEU:HD13	1.49	0.94
1:D:192:ILE:HD11	2:E:165:ASN:HA	1.49	0.94
2:B:64:TYR:HB3	2:B:65:PRO:HD2	1.47	0.94
3:C:52:ASN:OD1	6:C:420:NDG:H4	1.68	0.93
2:B:371:MET:HB2	2:B:410:ARG:HB3	1.48	0.93
2:B:371:MET:SD	2:B:410:ARG:HG2	2.10	0.92
3:C:75:LEU:HG	3:C:76:PRO:HD2	1.52	0.92
1:D:96:LYS:HE2	1:D:217:PRO:HG3	1.53	0.91
3:C:69:PRO:HG2	3:C:73:GLN:HE21	1.35	0.91
3:C:304:TYR:HB3	3:C:338:ARG:HB3	1.53	0.91
3:F:304:TYR:HB3	3:F:338:ARG:HB3	1.52	0.90
2:B:443:ASN:HD22	2:B:443:ASN:H	1.01	0.90
3:F:356:ARG:HB3	3:F:356:ARG:HH11	1.33	0.90
3:F:52:ASN:ND2	6:F:520:NDG:H8C3	1.87	0.89
3:C:356:ARG:HB3	3:C:356:ARG:HH11	1.36	0.89
3:C:356:ARG:HB3	3:C:356:ARG:NH1	1.88	0.88
1:D:96:LYS:HB3	1:D:97:PRO:HD3	1.55	0.87
2:B:361:ALA:HB1	2:B:363:GLN:HE21	1.39	0.87
2:E:355:ASN:C	2:E:355:ASN:HD22	1.79	0.86
2:E:371:MET:SD	2:E:410:ARG:HG2	2.15	0.86
2:E:391:THR:HG22	2:E:393:ASP:H	1.37	0.86
2:B:443:ASN:HD22	2:B:443:ASN:N	1.74	0.85
1:A:84:SER:HB2	3:C:58:GLU:HG2	1.57	0.85
2:E:234:PRO:HB2	2:E:305:GLN:HE22	1.41	0.85
2:B:355:ASN:HD21	2:B:358:MET:H	1.24	0.85
2:E:355:ASN:HD21	2:E:358:MET:H	1.21	0.84
6:B:470:NDG:O4	7:I:471:NAG:H2	1.77	0.84
2:B:83:THR:HG22	2:B:84:GLY:H	1.45	0.82
2:B:355:ASN:ND2	2:B:358:MET:H	1.78	0.82
1:A:188:GLN:HE21	1:A:189:ALA:N	1.77	0.82
2:B:71:LYS:HE3	1:D:32:LYS:HG2	1.62	0.82
2:B:391:THR:HG22	2:B:393:ASP:H	1.42	0.81
2:B:234:PRO:HB2	2:B:305:GLN:HE22	1.45	0.81
3:F:151:ARG:HB3	3:F:239:GLN:HE22	1.46	0.81
1:D:53:GLN:HB2	2:E:87:LEU:HD21	1.63	0.81
1:A:188:GLN:C	1:A:188:GLN:HE21	1.84	0.80
2:E:127:ASP:HA	3:F:64:ILE:HD11	1.63	0.80
1:D:124:LYS:HB2	2:E:158:ILE:HD11	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:LYS:HZ3	1:D:200:THR:H	1.29	0.80
1:A:216:VAL:HB	1:A:217:PRO:HD3	1.65	0.79
2:E:83:THR:HG22	2:E:84:GLY:H	1.47	0.79
2:B:355:ASN:HD22	2:B:355:ASN:C	1.84	0.79
1:A:117:ARG:CG	1:A:203:LEU:HD13	2.13	0.79
2:E:355:ASN:ND2	2:E:358:MET:H	1.81	0.79
3:C:52:ASN:OD1	6:C:420:NDG:H2	1.83	0.79
2:E:443:ASN:HD22	2:E:443:ASN:N	1.79	0.78
3:F:247:ARG:HD3	3:F:261:ASP:OD1	1.82	0.78
1:A:123:LEU:HG	2:B:158:ILE:HD13	1.66	0.78
3:C:197:ARG:NH2	3:C:346:GLY:O	2.16	0.78
3:F:197:ARG:NH2	3:F:346:GLY:O	2.16	0.78
2:E:83:THR:HG22	2:E:84:GLY:N	1.99	0.78
1:A:32:LYS:HG2	2:E:71:LYS:HE3	1.66	0.78
3:C:151:ARG:HB3	3:C:239:GLN:HE22	1.47	0.77
2:B:138:LYS:NZ	2:B:138:LYS:HB3	2.00	0.77
3:C:4:THR:HG22	3:C:5:ARG:H	1.49	0.77
2:E:360:GLY:HA2	2:E:372:THR:O	1.84	0.77
2:B:129:LYS:O	2:B:132:LYS:HG2	1.85	0.77
3:F:197:ARG:HB2	3:F:382:THR:HB	1.67	0.77
2:E:155:TYR:CE2	2:E:159:LYS:HD2	2.20	0.77
2:B:83:THR:HG22	2:B:84:GLY:N	1.99	0.77
2:E:361:ALA:HB1	2:E:363:GLN:HE21	1.48	0.77
2:B:443:ASN:H	2:B:443:ASN:ND2	1.80	0.76
3:C:247:ARG:HD3	3:C:261:ASP:OD1	1.83	0.76
2:B:276:ARG:HB2	2:B:276:ARG:NH1	2.01	0.76
3:F:329:GLN:HE21	3:F:361:ASN:HD22	1.34	0.75
3:F:304:TYR:HB3	3:F:338:ARG:CB	2.16	0.75
3:C:56:SER:O	3:C:60:LEU:HD23	1.86	0.75
1:D:75:ALA:HA	1:D:78:GLN:HG2	1.69	0.75
2:B:409:ASN:C	2:B:411:CYS:H	1.90	0.75
1:D:142:GLN:NE2	1:D:183:GLN:HE22	1.84	0.74
1:D:142:GLN:HE22	1:D:183:GLN:NE2	1.85	0.74
3:F:96:TYR:O	3:F:100:ILE:HG13	1.87	0.74
3:F:37:ASP:O	3:F:41:LEU:HD13	1.86	0.74
3:F:172:GLN:HG3	3:F:239:GLN:HE21	1.51	0.74
3:F:356:ARG:HH11	3:F:356:ARG:CB	2.00	0.74
1:D:96:LYS:HG3	1:D:100:GLU:OE2	1.88	0.74
2:E:129:LYS:H	2:E:129:LYS:HD2	1.50	0.74
1:D:74:LEU:HD13	2:E:109:VAL:HG22	1.67	0.74
1:D:66:ARG:HH12	3:F:40:LEU:HD11	1.50	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:31:LYS:HA	3:C:31:LYS:HE2	1.70	0.74
2:B:137:ARG:HE	2:B:137:ARG:HA	1.53	0.74
1:D:138:GLN:HE22	1:D:190:SER:HB2	1.53	0.73
3:C:197:ARG:HB2	3:C:382:THR:HB	1.70	0.73
2:E:266:ASN:ND2	2:E:268:GLY:H	1.86	0.73
3:F:249:GLU:HB3	3:F:383:THR:HG23	1.71	0.73
2:B:368:ASN:ND2	6:B:470:NDG:C1	2.51	0.73
3:F:365:ASN:HD22	3:F:365:ASN:H	1.34	0.73
3:F:329:GLN:NE2	3:F:361:ASN:HD22	1.87	0.72
3:C:269:THR:HG22	3:C:272:ASP:H	1.55	0.72
3:C:329:GLN:HE21	3:C:361:ASN:HD22	1.37	0.72
1:D:96:LYS:O	1:D:100:GLU:HG3	1.89	0.72
1:D:133:ARG:HD2	3:F:107:ILE:HG21	1.71	0.72
2:B:368:ASN:ND2	6:B:470:NDG:H1	2.04	0.72
3:F:347:PRO:HD2	3:F:365:ASN:O	1.90	0.72
1:A:184:LYS:O	1:A:188:GLN:HB2	1.91	0.71
2:E:409:ASN:C	2:E:411:CYS:H	1.92	0.71
2:E:276:ARG:HB2	2:E:276:ARG:NH1	2.05	0.71
1:A:88:ILE:HD11	3:C:61:ILE:HG12	1.72	0.71
1:A:74:LEU:O	1:A:78:GLN:HB2	1.91	0.70
2:E:368:ASN:HD21	6:E:570:NDG:C2	2.03	0.70
1:D:66:ARG:HH12	3:F:40:LEU:CG	2.04	0.70
2:E:306:LEU:HD13	2:E:458:ILE:HD11	1.74	0.70
2:E:443:ASN:H	2:E:443:ASN:ND2	1.83	0.70
2:B:397:GLN:HE21	2:B:400:LYS:HE3	1.57	0.70
2:B:148:ASN:O	2:B:151:MET:HG3	1.91	0.69
2:E:106:LYS:HG2	3:F:43:ILE:HG12	1.73	0.69
3:C:347:PRO:HD2	3:C:365:ASN:O	1.93	0.69
1:A:129:THR:CG2	1:A:133:ARG:HH11	2.06	0.69
1:D:66:ARG:HH12	3:F:40:LEU:CD1	2.06	0.69
1:A:109:TYR:HD1	3:C:83:THR:HG22	1.58	0.69
3:C:52:ASN:HD21	6:C:420:NDG:C1	2.05	0.69
1:D:124:LYS:NZ	1:D:200:THR:H	1.92	0.68
1:A:96:LYS:HB3	1:A:97:PRO:HD3	1.74	0.68
1:A:195:HIS:HE1	2:B:160:ASP:OD1	1.76	0.68
2:B:368:ASN:OD1	6:B:470:NDG:H1	1.93	0.68
1:D:56:ILE:HD13	2:E:91:LEU:HD12	1.76	0.68
2:B:397:GLN:NE2	2:B:400:LYS:HE3	2.09	0.68
2:E:344:LEU:HD12	2:E:345:SER:H	1.59	0.68
2:B:106:LYS:HE2	3:C:42:GLU:OE2	1.94	0.68
1:D:215:ASN:HB3	2:E:129:LYS:HE3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:LEU:O	1:D:120:ILE:HG12	1.95	0.67
3:C:249:GLU:HB3	3:C:383:THR:HG23	1.74	0.67
2:B:159:LYS:HG3	3:C:96:TYR:OH	1.94	0.67
3:C:69:PRO:CG	3:C:73:GLN:HE21	2.05	0.67
3:F:276:LEU:C	3:F:276:LEU:HD23	2.15	0.67
1:D:152:GLU:HG2	1:D:174:VAL:HG12	1.77	0.67
2:E:123:VAL:HG12	2:E:123:VAL:O	1.94	0.67
2:E:83:THR:HG22	2:E:85:CYS:H	1.58	0.67
1:D:59:THR:O	1:D:63:TYR:HB2	1.96	0.66
3:C:304:TYR:HB3	3:C:338:ARG:CB	2.25	0.66
1:A:86:ARG:C	1:A:88:ILE:H	1.99	0.66
3:C:69:PRO:HG2	3:C:73:GLN:NE2	2.09	0.66
3:C:172:GLN:HG3	3:C:239:GLN:HE21	1.60	0.66
1:D:182:ILE:HG23	2:E:176:VAL:HG13	1.76	0.66
2:B:355:ASN:HD21	2:B:358:MET:N	1.94	0.66
2:E:161:ASN:HA	2:E:165:ASN:HB2	1.78	0.66
3:F:149:THR:HG23	3:F:168:PHE:O	1.96	0.65
2:B:266:ASN:ND2	2:B:268:GLY:H	1.94	0.65
1:A:34:TRP:CH2	2:E:67:ALA:HA	2.32	0.65
3:F:338:ARG:HH11	3:F:338:ARG:HG2	1.61	0.65
3:C:356:ARG:HH11	3:C:356:ARG:CB	2.08	0.65
2:E:146:GLU:HA	2:E:149:THR:HG22	1.79	0.65
1:D:144:GLN:HE21	2:E:180:LEU:HD13	1.60	0.64
2:B:371:MET:HB2	2:B:410:ARG:HB2	1.79	0.64
1:D:123:LEU:HD23	2:E:158:ILE:CG2	2.27	0.64
2:B:368:ASN:CG	6:B:470:NDG:H1	2.18	0.64
1:A:66:ARG:HH21	3:C:40:LEU:HD12	1.63	0.64
3:F:189:ASN:HD22	3:F:391:ARG:HD2	1.62	0.64
1:D:124:LYS:HZ3	1:D:200:THR:N	1.96	0.64
1:A:168:ARG:HB2	1:A:168:ARG:HH11	1.62	0.64
1:D:66:ARG:NH1	3:F:40:LEU:HD11	2.12	0.64
6:E:570:NDG:O6	5:J:4:PRO:HG2	1.98	0.64
1:D:201:THR:O	1:D:202:THR:HB	1.98	0.64
2:B:83:THR:HG22	2:B:85:CYS:H	1.63	0.63
2:B:306:LEU:HD13	2:B:458:ILE:HD11	1.80	0.63
3:F:337:ASN:C	3:F:339:CYS:H	2.02	0.63
1:D:178:GLY:O	1:D:182:ILE:HG12	1.98	0.63
1:D:193:ASP:O	1:D:194:MET:HB2	1.99	0.63
2:E:391:THR:HG22	2:E:392:THR:N	2.14	0.63
2:B:443:ASN:N	2:B:443:ASN:ND2	2.43	0.63
2:B:99:LYS:HB2	2:B:100:PRO:HD3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:338:ARG:HG2	3:C:338:ARG:HH11	1.64	0.63
2:E:355:ASN:HD21	2:E:358:MET:N	1.93	0.63
3:C:329:GLN:NE2	3:C:361:ASN:HD22	1.96	0.63
1:A:211:LEU:HD22	2:B:136:GLN:OE1	1.98	0.63
2:B:64:TYR:HB3	2:B:65:PRO:CD	2.26	0.63
1:A:66:ARG:HH21	3:C:40:LEU:CD1	2.12	0.63
3:C:52:ASN:CG	6:C:420:NDG:H2	2.19	0.62
2:E:119:MET:O	2:E:123:VAL:HG23	1.99	0.62
1:D:119:ARG:NH1	3:F:94:ILE:HG12	2.13	0.62
3:C:337:ASN:C	3:C:339:CYS:H	2.03	0.62
1:D:66:ARG:NH1	3:F:40:LEU:HD21	2.14	0.62
1:A:211:LEU:HG	2:B:133:THR:HG23	1.79	0.62
1:D:52:MET:HA	1:D:52:MET:CE	2.30	0.62
3:F:250:LEU:HB3	3:F:379:MET:HE1	1.81	0.62
2:B:391:THR:HG22	2:B:392:THR:N	2.14	0.62
1:A:155:ILE:HD12	2:B:191:ILE:HD11	1.82	0.62
2:B:170:LEU:HD13	3:C:106:THR:OG1	1.99	0.62
2:E:127:ASP:O	2:E:131:VAL:HG23	2.00	0.61
3:C:40:LEU:O	3:C:44:GLU:HG3	2.00	0.61
2:B:368:ASN:O	2:B:371:MET:HG2	2.00	0.61
1:D:70:ILE:HG22	1:D:70:ILE:O	1.99	0.61
3:C:7:ASN:HD21	3:F:11:LEU:CD2	2.13	0.61
3:F:153:CYS:SG	3:F:192:THR:HB	2.40	0.61
3:C:52:ASN:OD1	6:C:420:NDG:C4	2.43	0.61
2:B:361:ALA:HB1	2:B:363:GLN:NE2	2.13	0.61
2:B:67:ALA:HA	1:D:34:TRP:CH2	2.34	0.61
2:E:276:ARG:CB	2:E:276:ARG:HH11	2.14	0.61
3:F:269:THR:HG22	3:F:272:ASP:H	1.65	0.61
2:E:93:LYS:C	2:E:95:GLU:H	2.00	0.61
3:C:21:THR:C	3:C:23:CYS:H	2.04	0.61
3:C:111:THR:O	3:C:115:ILE:HG12	2.01	0.61
2:B:344:LEU:HD12	2:B:345:SER:H	1.66	0.61
1:D:123:LEU:HD23	2:E:158:ILE:HG21	1.83	0.61
2:E:318:MET:HB2	2:E:451:MET:HG2	1.83	0.61
2:B:119:MET:SD	3:C:57:ILE:HD13	2.41	0.61
3:C:276:LEU:C	3:C:276:LEU:HD23	2.20	0.61
2:E:129:LYS:HD2	2:E:129:LYS:N	2.15	0.61
3:F:71:GLU:HG2	3:F:71:GLU:O	2.01	0.61
1:D:219:HIS:HD1	2:E:122:TYR:HB3	1.64	0.61
1:A:155:ILE:HD13	3:C:128:ILE:HG13	1.81	0.61
1:D:123:LEU:HB3	2:E:158:ILE:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:325:ASN:HD22	3:C:325:ASN:C	2.04	0.60
3:F:48:GLN:O	3:F:52:ASN:HB2	2.01	0.60
1:A:34:TRP:HZ3	2:E:68:GLY:H	1.49	0.60
3:C:365:ASN:H	3:C:365:ASN:HD22	1.47	0.60
3:C:78:SER:H	3:C:81:GLN:NE2	1.99	0.60
2:E:99:LYS:HB2	2:E:100:PRO:HD3	1.83	0.60
3:C:30:ASN:O	3:C:34:LEU:HD13	2.02	0.60
2:E:65:PRO:O	2:E:66:ASP:HB2	2.00	0.60
2:B:276:ARG:CB	2:B:276:ARG:HH11	2.14	0.60
1:A:149:LYS:HB3	1:A:149:LYS:NZ	2.17	0.60
2:E:89:THR:C	2:E:91:LEU:H	2.04	0.60
1:D:127:VAL:O	1:D:131:VAL:HG23	2.01	0.60
2:B:166:ILE:HB	2:B:167:PRO:HD3	1.83	0.60
2:B:65:PRO:O	2:B:66:ASP:HB2	2.01	0.60
1:D:88:ILE:HG21	1:D:219:HIS:NE2	2.17	0.60
1:A:95:LEU:O	1:A:99:LEU:HD23	2.02	0.59
1:D:216:VAL:H	1:D:217:PRO:CD	2.15	0.59
3:C:24:GLY:HA3	3:F:15:PHE:O	2.02	0.59
3:C:357:ASP:HB3	3:C:362:SER:CB	2.32	0.59
1:A:34:TRP:CZ3	2:E:67:ALA:HA	2.37	0.59
2:B:138:LYS:HB3	2:B:138:LYS:HZ3	1.65	0.59
3:F:90:ILE:O	3:F:94:ILE:HG13	2.01	0.59
3:F:85:LYS:HA	3:F:88:LYS:HE2	1.84	0.59
2:E:165:ASN:H	2:E:167:PRO:HD2	1.67	0.59
2:B:112:PHE:HA	2:B:115:THR:HG22	1.85	0.59
1:A:69:ASN:N	1:A:69:ASN:HD22	2.01	0.59
1:D:127:VAL:HG21	2:E:158:ILE:HG23	1.84	0.59
3:C:250:LEU:HB3	3:C:379:MET:HE1	1.84	0.59
3:C:252:ASP:HB2	3:C:377:TYR:OH	2.02	0.59
1:A:195:HIS:N	1:A:196:PRO:HD3	2.17	0.59
3:F:9:CYS:O	3:F:17:SER:HA	2.02	0.59
3:C:288:ASP:OD2	3:C:291:ASP:HB2	2.03	0.59
2:B:397:GLN:HE21	2:B:400:LYS:CE	2.15	0.59
1:D:80:LYS:HA	1:D:83:THR:HG22	1.85	0.59
1:D:56:ILE:HG12	3:F:29:PHE:CE1	2.38	0.59
3:C:52:ASN:ND2	6:C:420:NDG:H2	2.18	0.59
1:A:85:ASN:HD22	1:A:86:ARG:HD2	1.68	0.58
1:D:155:ILE:HG23	3:F:128:ILE:HD13	1.84	0.58
3:C:217:HIS:O	3:C:224:THR:CG2	2.51	0.58
2:B:191:ILE:O	2:B:195:THR:HG23	2.03	0.58
3:F:47:LEU:O	3:F:51:THR:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:307:HIS:HD2	3:F:335:TRP:O	1.87	0.58
1:D:55:ILE:HD13	2:E:65:PRO:HG3	1.86	0.58
2:E:371:MET:HB2	2:E:410:ARG:HB2	1.82	0.58
2:B:68:GLY:H	1:D:34:TRP:HZ3	1.52	0.58
3:C:372:TRP:HZ3	3:C:379:MET:HE3	1.68	0.58
2:B:203:VAL:HG12	2:B:204:ALA:N	2.18	0.58
3:C:15:PHE:O	3:F:24:GLY:HA3	2.03	0.58
2:E:167:PRO:HG3	3:F:103:HIS:CE1	2.39	0.58
1:A:142:GLN:OE1	1:A:186:LEU:HD23	2.03	0.58
3:C:37:ASP:O	3:C:41:LEU:HD23	2.03	0.58
3:C:217:HIS:O	3:C:224:THR:HG23	2.03	0.58
2:E:83:THR:CG2	2:E:84:GLY:H	2.15	0.58
3:F:372:TRP:HZ3	3:F:379:MET:HE3	1.69	0.58
1:D:56:ILE:CD1	2:E:91:LEU:HD12	2.34	0.57
3:C:75:LEU:HG	3:C:76:PRO:CD	2.30	0.57
1:D:207:LYS:O	2:E:143:ILE:HG21	2.04	0.57
2:B:360:GLY:HA2	2:B:372:THR:O	2.04	0.57
2:E:316:ILE:HG12	2:E:456:MET:HG2	1.86	0.57
2:E:276:ARG:HB2	2:E:276:ARG:HH11	1.69	0.57
3:F:250:LEU:HB3	3:F:379:MET:CE	2.34	0.57
2:E:462:PHE:HD2	2:E:462:PHE:H	1.52	0.57
1:D:86:ARG:HG3	1:D:87:VAL:N	2.19	0.57
1:D:124:LYS:HG3	2:E:157:TYR:CE2	2.39	0.57
2:B:99:LYS:CB	2:B:100:PRO:HD3	2.35	0.57
3:C:153:CYS:SG	3:C:192:THR:HB	2.45	0.57
3:F:52:ASN:HD21	6:F:520:NDG:C8	1.95	0.57
2:B:83:THR:CG2	2:B:84:GLY:H	2.14	0.57
3:F:195:GLN:OE1	3:F:382:THR:HG22	2.05	0.57
1:D:66:ARG:HH11	1:D:66:ARG:HB2	1.69	0.57
2:E:130:LEU:O	3:F:67:ILE:HG12	2.05	0.57
2:B:83:THR:CG2	2:B:84:GLY:N	2.68	0.57
2:E:119:MET:HG3	3:F:57:ILE:HD13	1.87	0.57
2:B:332:GLY:O	2:B:346:VAL:HA	2.05	0.57
3:F:217:HIS:O	3:F:224:THR:HG23	2.05	0.56
1:D:186:LEU:HD21	2:E:176:VAL:HG11	1.86	0.56
1:D:85:ASN:O	1:D:89:VAL:HG23	2.06	0.56
3:F:390:ASN:HD22	3:F:390:ASN:C	2.09	0.56
2:E:260:ARG:NH1	2:E:439:ILE:HD11	2.20	0.56
1:A:188:GLN:C	1:A:188:GLN:NE2	2.55	0.56
3:C:329:GLN:OE1	4:G:3:ARG:NH1	2.37	0.56
2:B:67:ALA:HA	1:D:34:TRP:CZ3	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:149:THR:HG22	3:C:150:GLY:N	2.21	0.56
1:D:86:ARG:C	1:D:88:ILE:H	2.09	0.56
2:B:151:MET:SD	2:B:151:MET:C	2.84	0.56
2:B:355:ASN:C	2:B:355:ASN:ND2	2.56	0.56
2:B:318:MET:HB2	2:B:451:MET:HG2	1.88	0.56
2:E:368:ASN:O	2:E:371:MET:HG2	2.06	0.56
3:C:242:LEU:HD13	3:C:243:PRO:HD2	1.88	0.56
2:E:332:GLY:O	2:E:346:VAL:HA	2.06	0.56
1:A:85:ASN:O	1:A:88:ILE:HB	2.05	0.55
2:E:266:ASN:HD21	2:E:268:GLY:H	1.52	0.55
1:A:45:LYS:O	2:E:80:LEU:HD13	2.05	0.55
2:B:132:LYS:NZ	2:B:132:LYS:HB2	2.22	0.55
1:A:77:SER:OG	3:C:51:THR:HG22	2.06	0.55
1:A:79:ASN:C	1:A:81:TYR:H	2.10	0.55
3:F:116:MET:O	3:F:120:LYS:HG2	2.06	0.55
2:E:165:ASN:N	2:E:167:PRO:HD2	2.21	0.55
3:F:189:ASN:ND2	3:F:391:ARG:HH11	2.04	0.55
1:A:86:ARG:O	1:A:90:GLU:HG2	2.06	0.55
2:E:203:VAL:HG12	2:E:204:ALA:N	2.21	0.55
3:F:97:GLU:HA	3:F:100:ILE:CD1	2.36	0.55
2:B:80:LEU:HD13	1:D:45:LYS:O	2.06	0.55
1:A:117:ARG:CD	1:A:203:LEU:HA	2.37	0.55
2:E:391:THR:HG22	2:E:392:THR:H	1.72	0.55
2:B:119:MET:HE3	3:C:57:ILE:HD13	1.89	0.55
1:A:32:LYS:HA	1:A:34:TRP:CD1	2.42	0.55
3:C:189:ASN:ND2	3:C:391:ARG:HH11	2.04	0.55
1:A:117:ARG:HD2	1:A:203:LEU:HA	1.89	0.55
1:D:192:ILE:HD11	2:E:165:ASN:CA	2.32	0.55
1:D:32:LYS:HA	1:D:34:TRP:CD1	2.41	0.55
1:D:88:ILE:HD11	3:F:61:ILE:HD11	1.88	0.55
2:E:442:MET:SD	5:J:1:GLY:N	2.80	0.55
3:F:29:PHE:CE2	3:F:33:ARG:HD2	2.42	0.55
3:C:52:ASN:OD1	6:C:420:NDG:C2	2.53	0.55
3:C:96:TYR:O	3:C:100:ILE:HG13	2.06	0.55
1:A:155:ILE:CD1	3:C:128:ILE:HG13	2.37	0.55
1:A:211:LEU:HD21	2:B:133:THR:HA	1.89	0.55
2:B:391:THR:HG22	2:B:392:THR:H	1.70	0.55
3:F:172:GLN:HG3	3:F:239:GLN:NE2	2.22	0.55
1:D:66:ARG:O	1:D:70:ILE:HD13	2.07	0.55
3:F:357:ASP:HB3	3:F:362:SER:CB	2.37	0.55
3:F:325:ASN:HD22	3:F:325:ASN:C	2.09	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:LYS:HB2	3:F:128:ILE:HD11	1.87	0.54
1:A:86:ARG:C	1:A:88:ILE:N	2.60	0.54
1:D:95:LEU:HD23	2:E:130:LEU:HD11	1.88	0.54
1:D:73:GLN:HA	1:D:76:ASP:HB3	1.89	0.54
3:C:273:LYS:NZ	3:C:317:ASN:HD21	2.05	0.54
3:F:390:ASN:HD22	3:F:391:ARG:N	2.04	0.54
1:D:160:ARG:HG2	2:E:263:GLY:O	2.08	0.54
3:F:242:LEU:HD13	3:F:243:PRO:HD2	1.89	0.54
2:B:371:MET:CB	2:B:410:ARG:HB3	2.31	0.54
3:C:79:ILE:O	3:C:83:THR:HG23	2.07	0.54
3:C:77:GLN:HA	3:C:81:GLN:OE1	2.07	0.54
2:B:130:LEU:HD22	3:C:68:TYR:HE2	1.72	0.54
2:B:119:MET:CE	3:C:57:ILE:HD13	2.38	0.54
1:D:124:LYS:HD2	2:E:154:HIS:CE1	2.42	0.54
3:C:18:TYR:CZ	3:F:20:PRO:HG3	2.42	0.54
1:D:56:ILE:O	1:D:59:THR:HG22	2.06	0.54
2:B:64:TYR:CB	2:B:65:PRO:HD2	2.31	0.54
1:A:87:VAL:HG12	1:A:87:VAL:O	2.06	0.54
2:E:158:ILE:O	2:E:158:ILE:HG22	2.07	0.54
3:F:276:LEU:HD23	3:F:277:THR:N	2.23	0.54
2:E:98:VAL:O	2:E:98:VAL:HG12	2.07	0.54
2:B:391:THR:HG22	2:B:393:ASP:N	2.18	0.54
3:F:288:ASP:OD2	3:F:291:ASP:HB2	2.08	0.54
3:C:112:ASP:O	3:C:115:ILE:HB	2.08	0.54
2:E:409:ASN:C	2:E:411:CYS:N	2.61	0.54
1:D:124:LYS:HG3	2:E:157:TYR:HE2	1.73	0.54
1:A:129:THR:HG22	1:A:133:ARG:HH11	1.72	0.54
2:E:180:LEU:O	2:E:184:ILE:HG13	2.08	0.54
3:F:269:THR:CG2	3:F:271:GLU:H	2.21	0.54
1:D:210:PRO:HD2	1:D:212:LYS:HZ1	1.72	0.54
1:A:63:TYR:CE1	3:C:36:THR:HG21	2.43	0.54
2:E:166:ILE:O	2:E:170:LEU:HG	2.08	0.53
2:E:99:LYS:CB	2:E:100:PRO:HD3	2.37	0.53
3:C:357:ASP:HB3	3:C:362:SER:OG	2.07	0.53
3:C:250:LEU:HB3	3:C:379:MET:CE	2.38	0.53
1:D:182:ILE:HD11	2:E:179:SER:OG	2.08	0.53
2:B:409:ASN:C	2:B:411:CYS:N	2.62	0.53
2:E:271:TRP:HA	2:E:381:THR:HG21	1.89	0.53
3:C:78:SER:H	3:C:81:GLN:CD	2.12	0.53
2:B:303:ILE:HG22	2:B:335:ILE:HD12	1.90	0.53
1:D:197:ASP:C	1:D:199:GLN:H	2.11	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:161:ALA:O	3:F:162:ARG:HD2	2.08	0.53
2:B:154:HIS:O	2:B:157:TYR:HB3	2.08	0.53
2:B:259:ASN:HD21	2:B:261:GLN:NE2	2.06	0.53
1:A:56:ILE:HD13	2:B:91:LEU:HD21	1.89	0.53
3:F:101:LEU:HA	3:F:104:GLU:HB2	1.89	0.53
7:C:421:NAG:H82	7:C:421:NAG:O1	2.08	0.53
2:B:129:LYS:HB3	2:B:129:LYS:NZ	2.23	0.53
2:E:355:ASN:ND2	2:E:355:ASN:C	2.52	0.53
1:D:52:MET:HA	1:D:52:MET:HE2	1.91	0.53
3:F:12:ASP:OD1	3:F:14:ARG:HB2	2.08	0.53
2:B:368:ASN:HD21	6:B:470:NDG:C2	2.22	0.53
6:B:470:NDG:O4	7:I:471:NAG:H4	2.09	0.53
1:D:189:ALA:O	1:D:192:ILE:HG22	2.08	0.53
2:B:120:TYR:CE1	3:C:56:SER:HB3	2.44	0.53
3:C:273:LYS:HG2	3:C:319:ASN:ND2	2.24	0.53
2:E:64:TYR:HB3	2:E:65:PRO:CD	2.28	0.52
2:B:308:LYS:NZ	2:B:336:HIS:HA	2.23	0.52
3:F:253:TRP:CH2	3:F:350:ILE:HA	2.43	0.52
1:A:141:ILE:HD12	2:B:173:LEU:HD22	1.91	0.52
2:E:377:MET:HG3	2:E:409:ASN:HB2	1.92	0.52
3:C:11:LEU:O	3:C:12:ASP:CB	2.57	0.52
1:D:80:LYS:HA	1:D:83:THR:CG2	2.39	0.52
1:D:126:ARG:HH21	3:F:100:ILE:CD1	2.22	0.52
1:D:87:VAL:O	1:D:87:VAL:HG12	2.10	0.52
2:E:120:TYR:N	3:F:57:ILE:HD11	2.25	0.52
2:B:137:ARG:HA	2:B:137:ARG:NE	2.24	0.52
3:F:153:CYS:HB2	3:F:192:THR:HG22	1.92	0.52
2:E:397:GLN:HE21	2:E:400:LYS:HE3	1.75	0.52
3:F:149:THR:HG22	3:F:150:GLY:N	2.24	0.52
1:D:189:ALA:HB2	2:E:172:VAL:HG11	1.91	0.52
1:D:85:ASN:HD22	2:E:119:MET:CE	2.23	0.52
3:F:307:HIS:HE1	3:F:342:GLY:H	1.58	0.52
2:E:109:VAL:O	2:E:109:VAL:HG12	2.10	0.52
3:F:269:THR:HG23	3:F:271:GLU:H	1.74	0.52
3:C:189:ASN:HD22	3:C:391:ARG:HD2	1.74	0.52
1:A:86:ARG:O	1:A:88:ILE:N	2.43	0.52
6:B:470:NDG:O4	7:I:471:NAG:C2	2.55	0.52
2:E:123:VAL:HG12	3:F:60:LEU:HB3	1.91	0.52
1:D:134:ILE:HD11	2:E:166:ILE:HG23	1.92	0.52
1:D:201:THR:HG23	1:D:202:THR:H	1.75	0.52
3:C:21:THR:HG23	3:C:23:CYS:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:390:ASN:C	3:C:390:ASN:HD22	2.13	0.51
3:F:30:ASN:C	3:F:32:TYR:H	2.13	0.51
2:B:72:HIS:ND1	2:B:73:PRO:HD2	2.26	0.51
1:A:109:TYR:CD1	3:C:83:THR:HG22	2.43	0.51
1:D:168:ARG:HB3	2:E:197:TYR:CD2	2.44	0.51
3:C:304:TYR:CD2	3:C:338:ARG:HB2	2.46	0.51
3:C:372:TRP:HZ3	3:C:379:MET:CE	2.21	0.51
2:B:349:TYR:CG	2:B:350:LYS:N	2.78	0.51
2:E:443:ASN:N	2:E:443:ASN:ND2	2.47	0.51
2:B:89:THR:HG23	2:B:93:LYS:HE3	1.91	0.51
2:E:275:LYS:HE2	2:E:301:ASP:OD2	2.10	0.51
2:E:123:VAL:HG21	3:F:57:ILE:HG23	1.92	0.51
2:E:397:GLN:NE2	2:E:400:LYS:HE3	2.26	0.51
1:A:116:LEU:HD13	3:C:90:ILE:HG13	1.91	0.51
1:D:216:VAL:N	1:D:217:PRO:CD	2.73	0.51
1:D:80:LYS:HG3	3:F:58:GLU:OE2	2.10	0.51
3:C:29:PHE:O	3:C:33:ARG:HB2	2.11	0.51
1:A:160:ARG:HG2	2:B:263:GLY:O	2.11	0.51
1:A:154:ASP:OD2	2:B:432:LYS:HD3	2.10	0.51
2:B:276:ARG:HB2	2:B:276:ARG:HH11	1.67	0.51
2:B:303:ILE:CG2	2:B:335:ILE:HD12	2.40	0.51
3:F:252:ASP:HB2	3:F:377:TYR:OH	2.10	0.51
3:C:63:HIS:CE1	3:C:67:ILE:HD11	2.46	0.51
2:E:392:THR:O	2:E:394:PRO:HD3	2.11	0.51
1:A:73:GLN:OE1	3:C:47:LEU:HG	2.11	0.51
1:A:100:GLU:O	1:A:103:GLN:HB3	2.10	0.51
2:E:90:THR:O	2:E:90:THR:HG22	2.11	0.51
1:D:198:PHE:CZ	2:E:153:LEU:HD12	2.46	0.51
2:E:120:TYR:HA	3:F:57:ILE:HG12	1.93	0.51
3:C:152:ASP:C	3:C:152:ASP:OD1	2.49	0.51
3:F:227:TRP:HZ2	3:F:230:ASN:HD21	1.58	0.51
1:D:101:GLY:O	1:D:105:LEU:HD23	2.11	0.50
1:A:88:ILE:C	1:A:90:GLU:N	2.63	0.50
1:D:86:ARG:C	1:D:88:ILE:N	2.65	0.50
2:B:377:MET:HG3	2:B:409:ASN:HB2	1.93	0.50
3:F:365:ASN:N	3:F:365:ASN:HD22	1.99	0.50
2:E:72:HIS:ND1	2:E:73:PRO:HD2	2.26	0.50
1:D:92:ILE:O	1:D:96:LYS:HB2	2.12	0.50
1:D:74:LEU:O	1:D:78:GLN:HG2	2.10	0.50
3:C:357:ASP:HB3	3:C:362:SER:HB3	1.94	0.50
3:F:357:ASP:HB3	3:F:362:SER:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:GLN:HB3	2:B:67:ALA:O	2.12	0.50
2:B:70:CYS:HB2	1:D:35:PRO:O	2.12	0.50
3:C:57:ILE:O	3:C:61:ILE:HG13	2.12	0.50
1:D:211:LEU:O	1:D:213:ASP:N	2.42	0.50
1:A:36:ILE:N	1:A:36:ILE:HD12	2.27	0.50
2:B:297:TRP:HE1	2:B:300:ASN:ND2	2.09	0.50
1:D:66:ARG:HH11	1:D:66:ARG:CB	2.25	0.50
1:A:129:THR:CG2	1:A:133:ARG:NH1	2.74	0.50
2:B:203:VAL:HG12	2:B:204:ALA:H	1.75	0.50
2:E:299:GLY:O	2:E:303:ILE:HG13	2.12	0.50
1:A:117:ARG:HG2	1:A:203:LEU:HA	1.94	0.50
1:D:131:VAL:HG13	1:D:194:MET:SD	2.51	0.50
3:C:4:THR:O	3:C:8:CYS:HB3	2.12	0.50
2:E:276:ARG:NH1	2:E:276:ARG:CB	2.73	0.50
3:F:372:TRP:HZ3	3:F:379:MET:CE	2.24	0.50
3:C:161:ALA:O	3:C:162:ARG:HD2	2.11	0.50
2:B:271:TRP:HA	2:B:381:THR:HG21	1.93	0.50
3:C:4:THR:HG22	3:C:5:ARG:N	2.22	0.50
2:E:112:PHE:CE1	3:F:50:ALA:HB1	2.47	0.50
1:A:88:ILE:HG22	1:A:89:VAL:N	2.26	0.49
3:C:14:ARG:NH2	2:E:92:LEU:HD11	2.27	0.49
1:D:94:ILE:HG22	1:D:95:LEU:HD12	1.94	0.49
3:F:219:SER:OG	3:F:224:THR:HG22	2.13	0.49
2:E:135:LYS:NZ	2:E:135:LYS:HB2	2.26	0.49
2:E:204:ALA:O	3:F:141:ASP:HA	2.13	0.49
2:E:93:LYS:C	2:E:95:GLU:N	2.66	0.49
1:A:149:LYS:CB	1:A:149:LYS:NZ	2.76	0.49
3:C:273:LYS:NZ	3:C:319:ASN:HD21	2.10	0.49
2:E:118:THR:HG23	2:E:121:GLN:OE1	2.12	0.49
1:D:38:VAL:HG12	1:D:39:ASP:N	2.28	0.49
1:A:123:LEU:CG	2:B:158:ILE:HD13	2.41	0.49
2:E:106:LYS:NZ	2:E:106:LYS:HB3	2.28	0.49
1:D:210:PRO:HD2	1:D:212:LYS:NZ	2.26	0.49
1:D:148:MET:HG3	1:D:179:TYR:OH	2.13	0.49
3:F:325:ASN:O	3:F:329:GLN:HG3	2.12	0.49
1:D:75:ALA:HA	1:D:78:GLN:CG	2.40	0.49
2:E:106:LYS:HD2	2:E:106:LYS:O	2.13	0.49
1:D:120:ILE:HD13	3:F:93:ILE:HD11	1.95	0.49
2:B:266:ASN:HD21	2:B:268:GLY:H	1.61	0.49
2:E:100:PRO:HA	2:E:103:ARG:HD2	1.94	0.49
3:F:81:GLN:HG3	3:F:85:LYS:NZ	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:120:LYS:HA	3:F:120:LYS:HE2	1.94	0.49
3:C:10:ILE:O	3:C:10:ILE:HG13	2.13	0.49
3:C:390:ASN:HD22	3:C:391:ARG:N	2.10	0.49
2:B:144:LEU:O	2:B:146:GLU:N	2.46	0.49
1:A:38:VAL:HG12	1:A:39:ASP:N	2.28	0.49
3:F:337:ASN:C	3:F:339:CYS:N	2.64	0.49
3:F:67:ILE:HD12	3:F:67:ILE:N	2.28	0.49
2:E:129:LYS:C	2:E:131:VAL:H	2.16	0.48
3:C:195:GLN:OE1	3:C:382:THR:HG22	2.13	0.48
3:C:149:THR:HG23	3:C:168:PHE:O	2.12	0.48
2:B:132:LYS:CG	2:B:133:THR:N	2.76	0.48
1:D:100:GLU:O	1:D:103:GLN:HG3	2.13	0.48
2:E:156:ASN:HA	2:E:159:LYS:HD3	1.95	0.48
3:C:7:ASN:ND2	3:F:11:LEU:HD23	2.29	0.48
3:F:392:LEU:O	3:F:393:SER:HB2	2.14	0.48
2:E:72:HIS:CG	2:E:77:LEU:HD12	2.48	0.48
2:B:392:THR:O	2:B:394:PRO:HD3	2.14	0.48
1:A:194:MET:SD	2:B:165:ASN:HB3	2.53	0.48
2:B:208:ILE:HD12	2:B:208:ILE:N	2.28	0.48
2:E:166:ILE:N	2:E:167:PRO:CD	2.76	0.48
3:C:196:ARG:HD2	3:C:383:THR:HB	1.95	0.48
3:C:219:SER:OG	3:C:224:THR:HG22	2.12	0.48
2:E:397:GLN:HE21	2:E:400:LYS:CE	2.27	0.48
3:C:20:PRO:HG3	3:F:18:TYR:CZ	2.49	0.48
1:A:186:LEU:C	1:A:188:GLN:N	2.67	0.48
1:D:85:ASN:HD22	2:E:119:MET:HE3	1.77	0.48
3:C:229:GLY:O	3:C:233:ILE:HG13	2.13	0.48
3:F:273:LYS:HG2	3:F:319:ASN:ND2	2.28	0.48
1:D:130:GLN:NE2	3:F:104:GLU:HG2	2.28	0.48
1:D:88:ILE:HD13	2:E:123:VAL:HG22	1.95	0.48
3:C:11:LEU:HD12	3:C:18:TYR:CZ	2.49	0.48
1:A:100:GLU:HA	1:A:100:GLU:OE1	2.12	0.48
2:E:410:ARG:O	2:E:411:CYS:HB2	2.14	0.48
2:E:89:THR:O	2:E:91:LEU:N	2.42	0.48
2:E:83:THR:CG2	2:E:84:GLY:N	2.68	0.48
3:C:269:THR:HG23	3:C:271:GLU:H	1.79	0.48
2:B:275:LYS:HE2	2:B:301:ASP:OD2	2.13	0.48
3:C:212:LYS:HG3	3:C:274:TYR:OH	2.13	0.48
2:E:411:CYS:HB2	5:J:1:GLY:O	2.14	0.48
2:E:168:SER:O	2:E:172:VAL:HG12	2.14	0.48
2:E:88:GLN:O	2:E:92:LEU:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:276:LEU:HD23	3:C:277:THR:N	2.29	0.48
3:F:67:ILE:HG22	3:F:68:TYR:CD2	2.49	0.48
1:D:36:ILE:N	1:D:36:ILE:HD12	2.28	0.48
2:E:341:LYS:HB2	2:E:378:TYR:CD2	2.49	0.48
1:A:90:GLU:HG3	1:A:91:THR:N	2.29	0.47
3:F:249:GLU:HG3	3:F:259:THR:HG22	1.96	0.47
2:E:92:LEU:O	2:E:95:GLU:HB3	2.13	0.47
3:C:372:TRP:CZ3	3:C:379:MET:CE	2.96	0.47
2:B:72:HIS:CG	2:B:77:LEU:HD12	2.49	0.47
1:D:60:ASP:HA	1:D:63:TYR:HB2	1.96	0.47
1:A:123:LEU:HD21	2:B:158:ILE:HG21	1.96	0.47
3:C:7:ASN:HD21	3:F:11:LEU:HD23	1.78	0.47
1:D:216:VAL:H	1:D:217:PRO:HD3	1.78	0.47
1:D:116:LEU:HD21	2:E:151:MET:SD	2.54	0.47
3:F:217:HIS:O	3:F:224:THR:CG2	2.62	0.47
3:C:307:HIS:CE1	3:C:341:ALA:H	2.33	0.47
2:B:98:VAL:O	2:B:98:VAL:HG12	2.14	0.47
3:F:33:ARG:O	3:F:37:ASP:HB2	2.14	0.47
2:B:72:HIS:C	2:B:74:LEU:H	2.18	0.47
2:B:140:ASN:O	2:B:143:ILE:HG22	2.14	0.47
2:E:208:ILE:HG22	2:E:209:PRO:O	2.14	0.47
3:F:74:THR:O	3:F:75:LEU:HG	2.15	0.47
3:F:123:GLN:O	3:F:127:LYS:HG2	2.14	0.47
1:A:84:SER:CB	3:C:58:GLU:HG2	2.37	0.47
1:D:123:LEU:HD23	2:E:158:ILE:HG22	1.97	0.47
1:D:141:ILE:HG12	3:F:114:HIS:HD2	1.80	0.47
1:A:218:GLU:HB3	2:B:125:MET:HE2	1.96	0.47
1:A:211:LEU:HD21	2:B:136:GLN:HB3	1.96	0.47
3:C:249:GLU:HG3	3:C:259:THR:HG22	1.96	0.47
1:D:79:ASN:O	1:D:83:THR:HG22	2.14	0.47
3:C:307:HIS:HD2	3:C:335:TRP:O	1.96	0.47
1:A:211:LEU:HD11	2:B:132:LYS:HG3	1.97	0.47
2:E:391:THR:HG22	2:E:393:ASP:N	2.16	0.47
1:A:185:HIS:O	1:A:188:GLN:HB3	2.14	0.47
3:F:81:GLN:HG3	3:F:85:LYS:HZ2	1.80	0.47
1:A:216:VAL:CB	1:A:217:PRO:HD3	2.37	0.47
3:C:52:ASN:OD1	6:C:420:NDG:C3	2.63	0.47
3:F:365:ASN:ND2	3:F:365:ASN:H	2.07	0.47
1:D:141:ILE:HG12	3:F:114:HIS:CD2	2.50	0.47
3:F:143:ALA:HA	3:F:220:PRO:HG2	1.97	0.47
3:F:40:LEU:O	3:F:44:GLU:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:269:THR:HG22	3:F:271:GLU:N	2.29	0.47
1:A:101:GLY:O	1:A:104:GLN:N	2.47	0.47
2:E:199:ARG:HH11	2:E:199:ARG:HG2	1.79	0.47
3:F:92:GLU:N	3:F:95:ARG:HH21	2.13	0.47
1:D:66:ARG:NH1	1:D:66:ARG:CB	2.77	0.47
3:C:97:GLU:OE1	3:C:97:GLU:HA	2.14	0.47
3:F:269:THR:HG23	3:F:271:GLU:OE1	2.15	0.46
3:F:67:ILE:HD12	3:F:67:ILE:H	1.80	0.46
2:E:336:HIS:O	2:E:342:TYR:HA	2.14	0.46
2:E:166:ILE:HB	2:E:167:PRO:HD3	1.96	0.46
2:E:361:ALA:HB1	2:E:363:GLN:NE2	2.26	0.46
2:B:316:ILE:HG12	2:B:456:MET:HG2	1.96	0.46
2:B:368:ASN:ND2	6:B:470:NDG:O	2.46	0.46
2:B:112:PHE:HA	2:B:115:THR:CG2	2.45	0.46
2:B:246:ASP:HB3	2:B:254:TRP:HB2	1.96	0.46
3:C:28:PHE:CD1	3:F:14:ARG:HB3	2.50	0.46
3:F:273:LYS:NZ	3:F:317:ASN:HD21	2.13	0.46
3:F:97:GLU:HA	3:F:100:ILE:HD12	1.98	0.46
2:E:72:HIS:C	2:E:74:LEU:H	2.19	0.46
3:C:269:THR:CG2	3:C:271:GLU:HB2	2.46	0.46
3:C:21:THR:HG23	3:C:24:GLY:H	1.81	0.46
2:E:208:ILE:N	2:E:208:ILE:HD12	2.31	0.46
1:A:186:LEU:C	1:A:188:GLN:H	2.19	0.46
3:F:242:LEU:HD13	3:F:243:PRO:CD	2.44	0.46
2:E:319:GLU:OE1	2:E:325:LYS:HE2	2.15	0.46
2:E:355:ASN:HD21	2:E:358:MET:HB2	1.80	0.46
2:E:308:LYS:NZ	2:E:336:HIS:HA	2.30	0.46
1:A:207:LYS:NZ	2:B:143:ILE:HD13	2.31	0.46
2:E:382:TYR:C	2:E:382:TYR:CD1	2.89	0.46
2:B:150:GLU:O	2:B:150:GLU:HG2	2.16	0.46
1:A:81:TYR:CG	1:A:81:TYR:O	2.69	0.46
1:D:75:ALA:C	1:D:77:SER:H	2.19	0.46
2:E:333:PHE:CZ	2:E:335:ILE:HD11	2.50	0.46
3:C:9:CYS:SG	3:C:10:ILE:N	2.89	0.46
1:D:151:LEU:HD12	3:F:121:ILE:HG23	1.98	0.46
2:B:234:PRO:HB2	2:B:305:GLN:NE2	2.22	0.46
3:F:269:THR:CG2	3:F:271:GLU:N	2.79	0.46
3:F:307:HIS:CE1	3:F:341:ALA:H	2.34	0.46
2:B:144:LEU:C	2:B:146:GLU:N	2.68	0.46
3:C:227:TRP:HZ2	3:C:230:ASN:HD21	1.63	0.46
3:C:372:TRP:CZ3	3:C:379:MET:HE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ILE:O	1:A:56:ILE:HG22	2.16	0.46
1:D:203:LEU:H	1:D:203:LEU:HD22	1.81	0.46
1:D:109:TYR:CE1	1:D:113:SER:HB3	2.51	0.46
2:E:106:LYS:HZ2	2:E:106:LYS:HB3	1.81	0.45
3:C:337:ASN:C	3:C:339:CYS:N	2.65	0.45
1:A:55:ILE:C	1:A:57:ASP:N	2.70	0.45
1:A:137:LEU:HD23	1:A:137:LEU:HA	1.78	0.45
2:B:88:GLN:HG3	3:F:15:PHE:CE2	2.51	0.45
2:B:142:ILE:O	2:B:146:GLU:HB2	2.16	0.45
3:F:340:HIS:O	4:H:1:GLY:HA2	2.16	0.45
1:D:130:GLN:O	1:D:134:ILE:HG13	2.16	0.45
3:C:52:ASN:HD21	6:C:420:NDG:H2	1.81	0.45
2:E:349:TYR:HB2	2:E:358:MET:HE2	1.99	0.45
1:D:86:ARG:O	1:D:90:GLU:HG3	2.17	0.45
3:C:365:ASN:ND2	3:C:365:ASN:H	2.14	0.45
1:A:138:GLN:OE1	1:A:190:SER:HB2	2.16	0.45
1:A:51:ARG:NH1	2:E:76:GLU:O	2.49	0.45
3:C:11:LEU:HG	3:C:12:ASP:N	2.31	0.45
1:A:147:GLU:OE1	3:C:125:LYS:HE2	2.16	0.45
1:D:32:LYS:HA	1:D:34:TRP:NE1	2.31	0.45
1:A:32:LYS:HA	1:A:34:TRP:NE1	2.32	0.45
1:A:34:TRP:HZ3	2:E:68:GLY:N	2.13	0.45
3:F:357:ASP:HB3	3:F:362:SER:OG	2.17	0.45
2:E:303:ILE:HG22	2:E:335:ILE:HD12	1.97	0.45
1:D:80:LYS:HD2	1:D:83:THR:HG21	1.98	0.45
2:E:442:MET:O	2:E:444:TRP:N	2.50	0.45
2:E:349:TYR:CG	2:E:350:LYS:N	2.84	0.45
2:E:355:ASN:O	2:E:355:ASN:ND2	2.49	0.45
2:E:106:LYS:HG2	3:F:43:ILE:CG1	2.45	0.45
3:C:365:ASN:N	3:C:365:ASN:HD22	2.07	0.45
2:B:199:ARG:HG2	2:B:199:ARG:HH11	1.82	0.45
2:B:206:CYS:HB3	2:B:229:MET:HE3	1.99	0.45
1:D:101:GLY:C	1:D:103:GLN:H	2.20	0.45
3:F:82:LEU:HD23	3:F:85:LYS:NZ	2.32	0.45
3:F:191:TRP:CE3	3:F:385:LYS:HG3	2.52	0.45
2:E:123:VAL:CG1	2:E:123:VAL:O	2.64	0.45
1:A:123:LEU:CD2	2:B:158:ILE:HG21	2.46	0.45
3:F:329:GLN:NE2	3:F:361:ASN:ND2	2.61	0.45
3:C:21:THR:C	3:C:23:CYS:N	2.69	0.45
2:B:70:CYS:SG	1:D:45:LYS:HD2	2.57	0.45
3:C:325:ASN:ND2	3:C:325:ASN:C	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:307:HIS:CE1	3:F:342:GLY:H	2.35	0.45
3:C:275:ARG:NH2	3:C:311:ARG:HE	2.15	0.45
2:E:424:GLY:O	2:E:449:TYR:HA	2.18	0.45
2:E:170:LEU:HD13	3:F:106:THR:CG2	2.48	0.44
3:C:52:ASN:HD21	6:C:420:NDG:C2	2.30	0.44
2:E:157:TYR:C	2:E:159:LYS:H	2.19	0.44
1:A:126:ARG:HH11	1:A:126:ARG:HG2	1.82	0.44
3:F:75:LEU:N	3:F:76:PRO:HD3	2.32	0.44
3:C:253:TRP:CH2	3:C:350:ILE:HA	2.51	0.44
2:B:397:GLN:O	2:B:401:GLU:HG3	2.18	0.44
1:D:201:THR:HG23	1:D:202:THR:N	2.32	0.44
3:F:281:PHE:CD2	3:F:288:ASP:HB2	2.52	0.44
2:B:235:ASP:HB3	2:B:238:THR:HB	1.99	0.44
2:E:127:ASP:CA	3:F:64:ILE:HD11	2.42	0.44
3:C:82:LEU:HA	3:C:85:LYS:HE3	1.99	0.44
1:A:120:ILE:HD12	3:C:93:ILE:CD1	2.48	0.44
1:D:56:ILE:HG12	3:F:29:PHE:CD1	2.52	0.44
1:D:55:ILE:HG22	3:F:29:PHE:CE2	2.52	0.44
3:F:197:ARG:HD3	3:F:204:PHE:CE1	2.53	0.44
1:A:67:ILE:HD13	2:B:101:VAL:HG11	2.00	0.44
2:E:89:THR:C	2:E:91:LEU:N	2.70	0.44
2:E:72:HIS:CG	2:E:73:PRO:HD2	2.53	0.44
1:A:129:THR:HG22	1:A:133:ARG:NH1	2.31	0.44
3:F:67:ILE:HG22	3:F:68:TYR:N	2.31	0.44
2:B:72:HIS:CG	2:B:73:PRO:HD2	2.52	0.44
2:B:275:LYS:HG3	2:B:342:TYR:OH	2.17	0.44
2:E:426:TYR:O	2:E:448:TRP:HB3	2.18	0.44
3:C:58:GLU:O	3:C:62:GLN:HG3	2.17	0.44
1:D:219:HIS:HB2	2:E:126:ILE:HD11	1.99	0.44
2:E:314:VAL:HG11	2:E:333:PHE:CD1	2.52	0.44
1:D:141:ILE:O	1:D:145:VAL:HG23	2.17	0.44
2:E:125:MET:HA	2:E:128:ASN:HD22	1.83	0.44
2:E:235:ASP:HB3	2:E:238:THR:HB	1.98	0.44
2:E:246:ASP:HB3	2:E:254:TRP:HB2	1.98	0.44
1:D:70:ILE:O	2:E:105:LEU:HD11	2.17	0.44
3:C:242:LEU:HA	3:C:243:PRO:HD3	1.80	0.44
2:E:113:SER:OG	3:F:49:GLN:HG2	2.18	0.44
2:B:347:SER:HA	2:B:358:MET:SD	2.58	0.44
2:B:305:GLN:HB3	2:B:305:GLN:HE21	1.64	0.44
3:F:212:LYS:HG3	3:F:274:TYR:OH	2.16	0.44
1:D:208:MET:HA	2:E:140:ASN:OD1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:341:LYS:HB2	2:B:378:TYR:CD2	2.53	0.44
2:B:127:ASP:O	2:B:131:VAL:HG23	2.18	0.43
2:E:355:ASN:OD1	2:E:358:MET:HE2	2.18	0.43
2:B:67:ALA:HA	1:D:34:TRP:HH2	1.81	0.43
2:B:115:THR:HG23	2:B:116:SER:N	2.33	0.43
1:D:117:ARG:HH11	1:D:117:ARG:HG3	1.84	0.43
3:F:372:TRP:O	3:F:373:ARG:NH1	2.43	0.43
3:F:82:LEU:O	3:F:86:SER:HB2	2.17	0.43
3:F:80:GLU:O	3:F:84:GLN:HG2	2.18	0.43
3:F:372:TRP:CZ3	3:F:379:MET:CE	3.00	0.43
3:C:240:SER:OG	3:C:242:LEU:HB2	2.19	0.43
2:B:126:ILE:O	2:B:127:ASP:C	2.55	0.43
2:B:368:ASN:OD1	6:B:470:NDG:C1	2.63	0.43
1:A:88:ILE:O	1:A:90:GLU:N	2.51	0.43
2:E:88:GLN:O	2:E:88:GLN:HG2	2.18	0.43
3:C:307:HIS:HE1	3:C:341:ALA:H	1.66	0.43
3:F:211:TYR:CE2	3:F:333:GLY:HA3	2.52	0.43
3:F:295:PHE:CD2	4:H:2:PRO:HG3	2.54	0.43
3:C:50:ALA:O	3:C:54:THR:HB	2.18	0.43
2:B:126:ILE:O	2:B:129:LYS:N	2.51	0.43
1:A:117:ARG:HG3	1:A:203:LEU:CD1	2.35	0.43
1:A:168:ARG:NH1	1:A:168:ARG:HB2	2.30	0.43
3:C:21:THR:CG2	3:C:23:CYS:HB2	2.49	0.43
1:D:203:LEU:H	1:D:203:LEU:CD2	2.30	0.43
1:A:35:PRO:O	2:E:70:CYS:HB2	2.18	0.43
2:B:426:TYR:O	2:B:448:TRP:HB3	2.18	0.43
3:C:42:GLU:O	3:C:46:LEU:HD13	2.18	0.43
3:C:102:ALA:O	3:C:106:THR:HG23	2.19	0.43
3:C:11:LEU:HG	3:C:12:ASP:H	1.84	0.43
2:E:134:GLN:HA	3:F:68:TYR:OH	2.18	0.43
1:A:73:GLN:OE1	3:C:51:THR:HG21	2.18	0.43
2:E:308:LYS:HZ1	2:E:336:HIS:HA	1.82	0.43
1:D:195:HIS:HB3	1:D:198:PHE:HB2	1.99	0.43
2:E:118:THR:O	2:E:121:GLN:HG2	2.18	0.43
1:A:80:LYS:O	1:A:80:LYS:HG2	2.19	0.43
2:E:442:MET:C	2:E:444:TRP:H	2.22	0.43
2:E:64:TYR:CB	2:E:65:PRO:HD2	2.31	0.43
3:C:53:SER:O	3:C:57:ILE:HG13	2.18	0.43
1:A:186:LEU:HA	1:A:186:LEU:HD12	1.82	0.43
1:D:119:ARG:HH12	3:F:94:ILE:HG12	1.84	0.43
3:C:153:CYS:HB2	3:C:192:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:168:ARG:HB3	2:E:197:TYR:CG	2.54	0.43
3:C:367:ILE:O	3:C:379:MET:HG2	2.18	0.43
3:F:83:THR:O	3:F:83:THR:HG22	2.19	0.43
1:A:88:ILE:CD1	3:C:61:ILE:HG12	2.45	0.43
3:C:344:LEU:HB3	3:C:382:THR:HG21	2.01	0.43
1:D:70:ILE:N	1:D:70:ILE:HD12	2.33	0.43
2:B:76:GLU:O	1:D:51:ARG:NH1	2.51	0.43
3:F:21:THR:C	3:F:23:CYS:H	2.21	0.43
1:A:117:ARG:CG	1:A:203:LEU:HA	2.49	0.43
2:E:172:VAL:O	2:E:176:VAL:HG23	2.19	0.43
3:F:96:TYR:C	3:F:98:ASN:H	2.22	0.43
2:E:88:GLN:OE1	3:F:20:PRO:HG2	2.19	0.43
2:B:308:LYS:HZ1	2:B:336:HIS:HA	1.83	0.43
1:A:124:LYS:HE2	1:A:200:THR:O	2.19	0.43
3:C:392:LEU:O	3:C:393:SER:HB2	2.19	0.43
3:F:367:ILE:O	3:F:379:MET:HG2	2.19	0.42
2:B:80:LEU:HB3	1:D:45:LYS:C	2.39	0.42
1:A:84:SER:OG	3:C:57:ILE:HG22	2.18	0.42
1:D:182:ILE:O	1:D:186:LEU:HD23	2.19	0.42
1:A:85:ASN:HD21	1:A:89:VAL:CG2	2.32	0.42
1:A:186:LEU:O	1:A:188:GLN:N	2.52	0.42
3:C:269:THR:HG21	3:C:271:GLU:HB2	2.01	0.42
2:B:98:VAL:O	2:B:102:LEU:HG	2.20	0.42
2:E:208:ILE:HD12	2:E:208:ILE:H	1.83	0.42
1:A:119:ARG:HD2	1:A:119:ARG:HA	1.78	0.42
2:B:125:MET:CE	2:B:126:ILE:HG13	2.50	0.42
2:B:355:ASN:OD1	2:B:358:MET:HE2	2.20	0.42
3:F:196:ARG:HD2	3:F:383:THR:HB	2.01	0.42
2:E:266:ASN:HD22	2:E:267:PHE:N	2.17	0.42
2:E:133:THR:O	2:E:133:THR:HG22	2.19	0.42
3:C:307:HIS:CE1	3:C:342:GLY:H	2.38	0.42
2:B:424:GLY:O	2:B:449:TYR:HA	2.20	0.42
2:E:349:TYR:CD2	2:E:355:ASN:HB2	2.55	0.42
2:E:391:THR:CG2	2:E:392:THR:N	2.82	0.42
2:B:355:ASN:OD1	2:B:358:MET:CE	2.68	0.42
3:F:388:PRO:O	3:F:391:ARG:HB2	2.19	0.42
2:E:95:GLU:OE1	2:E:95:GLU:HA	2.19	0.42
3:C:281:PHE:CD2	3:C:288:ASP:HB2	2.54	0.42
2:E:297:TRP:HE1	2:E:300:ASN:ND2	2.17	0.42
3:F:92:GLU:O	3:F:96:TYR:HD1	2.03	0.42
3:C:68:TYR:HA	3:C:69:PRO:HD3	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:269:THR:CG2	3:C:271:GLU:H	2.33	0.42
3:F:85:LYS:O	3:F:89:ILE:HG13	2.20	0.42
1:A:69:ASN:N	1:A:69:ASN:ND2	2.65	0.42
1:D:211:LEU:HD22	1:D:211:LEU:N	2.34	0.42
2:E:334:THR:HG22	2:E:335:ILE:N	2.34	0.42
2:E:349:TYR:CG	2:E:355:ASN:HB2	2.53	0.42
3:C:33:ARG:O	3:C:37:ASP:OD2	2.37	0.42
1:D:95:LEU:CD2	2:E:130:LEU:HD11	2.48	0.42
1:D:182:ILE:CG2	2:E:176:VAL:HG13	2.47	0.42
2:E:87:LEU:HD13	3:F:25:ILE:HG21	2.01	0.42
3:F:185:ASP:OD2	3:F:189:ASN:HB2	2.20	0.42
1:A:149:LYS:HG3	2:B:429:ASP:O	2.20	0.42
2:E:275:LYS:HG3	2:E:342:TYR:OH	2.19	0.42
2:E:402:ASP:HA	2:E:437:ASP:HB3	2.02	0.42
2:E:221:ARG:HD3	2:E:221:ARG:HA	1.87	0.42
1:D:96:LYS:CB	1:D:97:PRO:HD3	2.36	0.42
2:B:68:GLY:N	1:D:34:TRP:HZ3	2.17	0.42
3:F:59:TYR:C	3:F:61:ILE:H	2.21	0.42
3:F:242:LEU:HA	3:F:243:PRO:HD3	1.81	0.42
3:F:21:THR:OG1	3:F:23:CYS:SG	2.58	0.42
2:B:216:CYS:SG	2:B:255:THR:HA	2.60	0.42
2:E:170:LEU:HD13	3:F:106:THR:HG21	2.02	0.42
3:C:172:GLN:HG3	3:C:239:GLN:NE2	2.29	0.42
3:F:240:SER:OG	3:F:242:LEU:HB2	2.19	0.42
2:B:144:LEU:O	2:B:147:TYR:N	2.52	0.42
1:A:210:PRO:O	1:A:211:LEU:HB2	2.20	0.41
1:A:51:ARG:HE	2:B:66:ASP:CG	2.24	0.41
1:A:88:ILE:C	1:A:90:GLU:H	2.23	0.41
1:A:88:ILE:HG13	3:C:61:ILE:HD13	2.01	0.41
3:F:60:LEU:O	3:F:64:ILE:HG12	2.20	0.41
3:F:67:ILE:CD1	3:F:67:ILE:H	2.33	0.41
2:B:80:LEU:O	2:B:81:CYS:SG	2.78	0.41
3:C:28:PHE:CE1	3:F:14:ARG:HB3	2.54	0.41
1:A:55:ILE:C	1:A:57:ASP:H	2.22	0.41
1:A:182:ILE:HG23	2:B:176:VAL:HG13	2.01	0.41
1:A:52:MET:HA	1:A:52:MET:CE	2.50	0.41
2:B:234:PRO:CB	2:B:305:GLN:HE22	2.22	0.41
1:A:34:TRP:HH2	2:E:67:ALA:HA	1.79	0.41
2:E:259:ASN:HD21	2:E:261:GLN:NE2	2.18	0.41
2:E:74:LEU:O	2:E:76:GLU:N	2.53	0.41
1:A:66:ARG:NH2	3:C:40:LEU:CB	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:238:THR:HG22	2:B:239:THR:N	2.34	0.41
1:D:208:MET:CE	1:D:209:ARG:HH11	2.33	0.41
5:I:2:HIS:NE2	5:I:4:PRO:HG3	2.35	0.41
2:E:377:MET:HA	2:E:377:MET:CE	2.50	0.41
1:A:202:THR:O	1:A:203:LEU:C	2.59	0.41
2:B:167:PRO:HG3	3:C:103:HIS:CE1	2.56	0.41
3:C:252:ASP:OD2	3:C:256:LYS:HB2	2.20	0.41
3:C:47:LEU:O	3:C:48:GLN:C	2.58	0.41
2:B:149:THR:O	2:B:153:LEU:HG	2.19	0.41
1:A:175:ASP:C	1:A:177:GLU:H	2.23	0.41
1:A:110:GLY:O	1:A:114:THR:HG23	2.21	0.41
3:F:171:PRO:O	3:F:174:ALA:HB3	2.20	0.41
2:E:127:ASP:OD2	3:F:63:HIS:ND1	2.53	0.41
2:B:138:LYS:HZ2	2:B:138:LYS:HB3	1.81	0.41
3:F:68:TYR:O	3:F:69:PRO:O	2.39	0.41
2:E:203:VAL:HG12	2:E:204:ALA:H	1.85	0.41
2:B:144:LEU:O	2:B:145:SER:C	2.58	0.41
2:B:208:ILE:HD12	2:B:208:ILE:H	1.85	0.41
1:D:86:ARG:O	1:D:88:ILE:N	2.53	0.41
3:F:307:HIS:HE1	3:F:341:ALA:H	1.68	0.41
1:D:111:HIS:O	1:D:114:THR:HB	2.19	0.41
3:C:101:LEU:O	3:C:104:GLU:HB2	2.20	0.41
5:J:2:HIS:HD2	5:J:4:PRO:HG3	1.85	0.41
1:D:130:GLN:HE22	3:F:100:ILE:HG22	1.86	0.41
1:A:126:ARG:O	1:A:129:THR:HB	2.21	0.41
1:A:45:LYS:C	2:E:80:LEU:HB3	2.41	0.41
1:D:211:LEU:HG	2:E:133:THR:HA	2.01	0.41
3:F:45:GLY:O	3:F:48:GLN:HB2	2.21	0.41
3:F:382:THR:C	3:F:383:THR:HG22	2.41	0.41
2:E:266:ASN:ND2	2:E:267:PHE:N	2.69	0.41
2:E:406:TRP:CH2	2:E:416:PRO:HG2	2.55	0.41
3:C:198:LEU:C	3:C:198:LEU:HD12	2.41	0.41
3:C:63:HIS:HE1	3:C:67:ILE:HD11	1.83	0.41
3:F:304:TYR:CD2	3:F:338:ARG:HB2	2.56	0.41
2:E:155:TYR:CD2	2:E:159:LYS:HD2	2.55	0.41
1:D:66:ARG:HH12	3:F:40:LEU:CD2	2.34	0.41
3:F:38:GLY:C	3:F:40:LEU:H	2.24	0.41
3:C:269:THR:HG23	3:C:271:GLU:OE1	2.21	0.41
2:E:106:LYS:O	2:E:110:ALA:HB2	2.20	0.41
3:F:269:THR:CG2	3:F:271:GLU:HB2	2.51	0.41
3:C:11:LEU:O	3:C:12:ASP:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:462:PHE:O	2:E:462:PHE:CD2	2.74	0.41
1:D:211:LEU:HD22	1:D:211:LEU:H	1.86	0.41
2:E:406:TRP:CG	2:E:407:TRP:N	2.89	0.41
2:B:131:VAL:HG22	3:C:67:ILE:CD1	2.51	0.41
2:B:132:LYS:HZ2	2:B:132:LYS:HB2	1.85	0.41
2:E:377:MET:HE3	2:E:377:MET:HA	2.03	0.41
2:E:123:VAL:O	3:F:60:LEU:HD13	2.21	0.41
1:A:34:TRP:HB3	2:E:69:GLY:O	2.21	0.41
1:D:75:ALA:CA	1:D:78:GLN:HG2	2.46	0.41
2:E:146:GLU:HA	2:E:149:THR:CG2	2.50	0.41
1:A:46:CYS:SG	3:C:21:THR:OG1	2.79	0.41
1:A:149:LYS:HB3	1:A:149:LYS:HZ3	1.84	0.41
1:A:207:LYS:HZ2	2:B:143:ILE:HD13	1.86	0.41
2:B:406:TRP:CG	2:B:407:TRP:N	2.89	0.41
1:A:99:LEU:HD11	3:C:68:TYR:OH	2.21	0.40
3:C:185:ASP:OD2	3:C:189:ASN:HB2	2.21	0.40
2:E:196:ASP:O	2:E:199:ARG:HB2	2.21	0.40
3:C:6:GLU:OE1	3:C:6:GLU:N	2.54	0.40
1:D:101:GLY:C	1:D:103:GLN:N	2.75	0.40
1:D:124:LYS:HD2	2:E:154:HIS:HE1	1.85	0.40
1:A:81:TYR:O	1:A:85:ASN:HB2	2.22	0.40
1:D:52:MET:HB3	2:E:87:LEU:CD1	2.52	0.40
2:B:334:THR:HG22	2:B:335:ILE:N	2.35	0.40
2:B:143:ILE:HA	2:B:143:ILE:HD12	1.98	0.40
2:E:215:GLU:OE1	2:E:217:GLU:HB3	2.21	0.40
2:B:162:LEU:HA	2:B:162:LEU:HD23	1.91	0.40
3:F:97:GLU:HG3	3:F:97:GLU:O	2.21	0.40
2:B:377:MET:HA	2:B:377:MET:CE	2.52	0.40
3:C:269:THR:CG2	3:C:271:GLU:N	2.84	0.40
3:C:7:ASN:HD21	3:F:11:LEU:HD21	1.84	0.40
3:C:379:MET:HE2	3:C:379:MET:HB3	1.93	0.40
3:C:242:LEU:HA	3:C:242:LEU:HD22	1.88	0.40
3:F:242:LEU:HA	3:F:242:LEU:HD22	1.83	0.40
2:B:94:GLN:O	2:B:98:VAL:HG23	2.22	0.40
1:D:203:LEU:N	1:D:203:LEU:HD22	2.37	0.40
1:A:139:ASN:HD22	1:A:139:ASN:N	2.18	0.40
2:E:409:ASN:CG	2:E:410:ARG:H	2.25	0.40
3:C:338:ARG:NH1	3:C:338:ARG:HG2	2.35	0.40
1:A:91:THR:HG22	1:A:91:THR:O	2.21	0.40
3:C:325:ASN:ND2	3:C:328:GLU:H	2.20	0.40
1:D:80:LYS:HD2	1:D:80:LYS:HA	1.81	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:GLY:O	3:C:48:GLN:HB3	2.22	0.40
1:D:76:ASP:O	1:D:76:ASP:OD1	2.40	0.40
1:D:211:LEU:HG	2:E:133:THR:HG23	2.04	0.40
2:B:140:ASN:O	2:B:144:LEU:HG	2.22	0.40
1:A:70:ILE:HG22	2:B:105:LEU:HD11	2.02	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	190/491 (39%)	159 (84%)	24 (13%)	7 (4%)	4	9
1	D	192/491 (39%)	147 (77%)	32 (17%)	13 (7%)	1	2
2	B	400/464 (86%)	353 (88%)	39 (10%)	8 (2%)	9	24
2	E	399/464 (86%)	335 (84%)	52 (13%)	12 (3%)	5	13
3	C	388/409 (95%)	350 (90%)	27 (7%)	11 (3%)	6	15
3	F	387/409 (95%)	342 (88%)	34 (9%)	11 (3%)	6	15
4	G	2/4 (50%)	2 (100%)	0	0	100	100
4	H	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
5	I	2/4 (50%)	2 (100%)	0	0	100	100
5	J	2/4 (50%)	2 (100%)	0	0	100	100
All	All	1964/2744 (72%)	1693 (86%)	209 (11%)	62 (3%)	5	12

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	203	LEU
1	A	210	PRO

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Mol	Chain	Res	Type
1	A	211	LEU
2	B	65	PRO
2	B	411	CYS
1	D	193	ASP
1	D	201	THR
1	D	208	MET
1	D	214	SER
2	E	65	PRO
2	E	411	CYS
3	F	69	PRO
3	F	74	THR
3	F	172	GLN
1	A	28	CYS
2	B	75	ASP
2	B	443	ASN
3	C	12	ASP
3	C	172	GLN
3	C	339	CYS
1	D	71	ARG
1	D	203	LEU
1	D	212	LYS
2	E	75	ASP
2	E	355	ASN
2	E	443	ASN
3	F	67	ILE
3	F	72	LYS
3	F	78	SER
3	F	339	CYS
3	F	375	ARG
1	A	48	SER
2	B	261	GLN
2	B	418	GLY
3	C	76	PRO
3	C	77	GLN
1	D	198	PHE
2	E	90	THR
2	E	261	GLN
3	F	13	GLU
3	F	198	LEU
1	A	87	VAL
2	B	145	SER
3	C	22	THR

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Mol	Chain	Res	Type
3	C	198	LEU
3	C	356	ARG
3	C	375	ARG
2	E	105	LEU
2	E	418	GLY
1	A	196	PRO
3	C	78	SER
3	C	98	ASN
1	D	28	CYS
1	D	48	SER
1	D	102	ALA
1	D	202	THR
2	E	164	ASN
3	F	199	ASP
2	E	91	LEU
2	E	158	ILE
2	B	463	PRO
1	D	216	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	177/430 (41%)	164 (93%)	13 (7%)	17	39
1	D	179/430 (42%)	167 (93%)	12 (7%)	20	44
2	B	350/402 (87%)	335 (96%)	15 (4%)	35	66
2	E	349/402 (87%)	335 (96%)	14 (4%)	38	69
3	C	341/355 (96%)	317 (93%)	24 (7%)	19	42
3	F	340/355 (96%)	322 (95%)	18 (5%)	28	57
4	G	3/3 (100%)	3 (100%)	0	100	100
4	H	3/3 (100%)	3 (100%)	0	100	100
5	I	3/3 (100%)	3 (100%)	0	100	100
5	J	3/3 (100%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1748/2386 (73%)	1652 (94%)	96 (6%)	27 55

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	CYS
1	A	58	ASP
1	A	78	GLN
1	A	85	ASN
1	A	86	ARG
1	A	119	ARG
1	A	126	ARG
1	A	129	THR
1	A	149	LYS
1	A	180	ASP
1	A	188	GLN
1	A	211	LEU
1	A	215	ASN
2	B	132	LYS
2	B	137	ARG
2	B	139	ASP
2	B	150	GLU
2	B	178	ASP
2	B	187	LEU
2	B	199	ARG
2	B	215	GLU
2	B	258	GLN
2	B	288	LYS
2	B	305	GLN
2	B	355	ASN
2	B	384	ARG
2	B	443	ASN
2	B	451	MET
3	C	6	GLU
3	C	30	ASN
3	C	31	LYS
3	C	54	THR
3	C	88	LYS
3	C	96	TYR
3	C	99	THR
3	C	124	LEU
3	C	128	ILE

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Mol	Chain	Res	Type
3	C	173	LYS
3	C	192	THR
3	C	242	LEU
3	C	247	ARG
3	C	250	LEU
3	C	269	THR
3	C	317	ASN
3	C	325	ASN
3	C	338	ARG
3	C	347	PRO
3	C	350	ILE
3	C	356	ARG
3	C	365	ASN
3	C	383	THR
3	C	390	ASN
1	D	52	MET
1	D	63	TYR
1	D	65	GLN
1	D	81	TYR
1	D	103	GLN
1	D	115	GLU
1	D	123	LEU
1	D	151	LEU
1	D	168	ARG
1	D	181	ASN
1	D	193	ASP
1	D	208	MET
2	E	106	LYS
2	E	124	ASN
2	E	150	GLU
2	E	153	LEU
2	E	199	ARG
2	E	215	GLU
2	E	258	GLN
2	E	288	LYS
2	E	305	GLN
2	E	355	ASN
2	E	384	ARG
2	E	443	ASN
2	E	451	MET
2	E	462	PHE
3	F	23	CYS

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Mol	Chain	Res	Type
3	F	42	GLU
3	F	131	LEU
3	F	173	LYS
3	F	192	THR
3	F	242	LEU
3	F	247	ARG
3	F	250	LEU
3	F	269	THR
3	F	317	ASN
3	F	325	ASN
3	F	338	ARG
3	F	347	PRO
3	F	350	ILE
3	F	356	ARG
3	F	365	ASN
3	F	383	THR
3	F	390	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	78	GLN
1	A	85	ASN
1	A	108	ASN
1	A	132	ASN
1	A	139	ASN
1	A	173	GLN
1	A	188	GLN
1	A	195	HIS
1	A	215	ASN
2	B	94	GLN
2	B	134	GLN
2	B	154	HIS
2	B	185	GLN
2	B	258	GLN
2	B	261	GLN
2	B	266	ASN
2	B	300	ASN
2	B	305	GLN
2	B	322	ASN
2	B	343	GLN

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Mol	Chain	Res	Type
2	B	355	ASN
2	B	363	GLN
2	B	368	ASN
2	B	397	GLN
2	B	409	ASN
2	B	412	HIS
2	B	443	ASN
3	C	7	ASN
3	C	30	ASN
3	C	73	GLN
3	C	81	GLN
3	C	84	GLN
3	C	98	ASN
3	C	114	HIS
3	C	117	ASN
3	C	136	GLN
3	C	189	ASN
3	C	230	ASN
3	C	239	GLN
3	C	307	HIS
3	C	317	ASN
3	C	319	ASN
3	C	325	ASN
3	C	361	ASN
3	C	365	ASN
3	C	390	ASN
1	D	33	ASN
1	D	69	ASN
1	D	73	GLN
1	D	85	ASN
1	D	93	ASN
1	D	103	GLN
1	D	130	GLN
1	D	132	ASN
1	D	138	GLN
1	D	142	GLN
1	D	144	GLN
1	D	173	GLN
1	D	181	ASN
1	D	215	ASN
2	E	124	ASN
2	E	128	ASN

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Mol	Chain	Res	Type
2	E	154	HIS
2	E	165	ASN
2	E	185	GLN
2	E	189	ASN
2	E	258	GLN
2	E	261	GLN
2	E	266	ASN
2	E	300	ASN
2	E	305	GLN
2	E	322	ASN
2	E	343	GLN
2	E	355	ASN
2	E	363	GLN
2	E	397	GLN
2	E	409	ASN
2	E	412	HIS
2	E	443	ASN
3	F	52	ASN
3	F	103	HIS
3	F	114	HIS
3	F	189	ASN
3	F	230	ASN
3	F	239	GLN
3	F	307	HIS
3	F	317	ASN
3	F	319	ASN
3	F	325	ASN
3	F	329	GLN
3	F	365	ASN
3	F	390	ASN

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

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NDG	B	470	-	15,15,15	0.49	0	17,21,21	0.71	0
6	NDG	C	420	-	15,15,15	0.41	0	17,21,21	0.53	0
7	NAG	C	421	-	15,15,15	0.47	0	17,21,21	0.56	0
6	NDG	E	570	-	15,15,15	0.44	0	17,21,21	0.59	0
6	NDG	F	520	-	15,15,15	0.44	0	17,21,21	0.52	0
7	NAG	F	521	-	15,15,15	0.42	0	17,21,21	0.53	0
7	NAG	I	471	-	15,15,15	0.47	0	17,21,21	0.53	0
6	NDG	J	571	-	15,15,15	0.54	0	17,21,21	0.53	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NDG	B	470	-	-	0/6/26/26	0/1/1/1
6	NDG	C	420	-	-	0/6/26/26	0/1/1/1
7	NAG	C	421	-	-	0/6/26/26	0/1/1/1
6	NDG	E	570	-	-	0/6/26/26	0/1/1/1
6	NDG	F	520	-	-	0/6/26/26	0/1/1/1
7	NAG	F	521	-	-	0/6/26/26	0/1/1/1
7	NAG	I	471	-	-	1/6/26/26	0/1/1/1
6	NDG	J	571	-	-	0/6/26/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	I	471	NAG	O7-C7-N2-C2

There are no ring outliers.

6 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	470	NDG	11	0
6	C	420	NDG	10	0
7	C	421	NAG	1	0
6	E	570	NDG	4	0
6	F	520	NDG	3	0
7	I	471	NAG	3	0

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.