



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:25 AM GMT

PDB ID : 2H2P
Title : Crystal structure of CLC-ec1 in complex with Fab fragment in SeCN-
Authors : Nguitragool, W.; Miller, C.
Deposited on : 2006-05-19
Resolution : 3.10 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

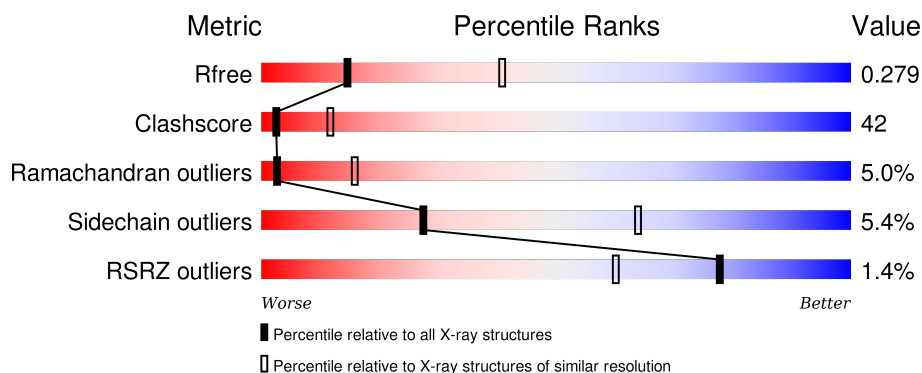
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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.

Mol	Chain	Length	Quality of chain
1	A	465	<div> <div>2%</div> <div>46%</div> <div>47%</div> <div>5%</div> </div>
1	B	465	<div> <div>2%</div> <div>42%</div> <div>49%</div> <div>5%</div> </div>
2	C	221	<div> <div>2%</div> <div>51%</div> <div>44%</div> <div>5%</div> </div>
2	E	221	<div> <div>52%</div> <div>39%</div> <div>8%</div> </div>
3	D	211	<div> <div>29%</div> <div>61%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	211	

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
4	SEK	A	466	-	-	X	X
4	SEK	B	466	-	-	X	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13231 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 CLC Cl transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3333	2190	560	563	20			
1	B	441	Total	C	N	O	S	0	0	0
			3304	2174	553	557	20			

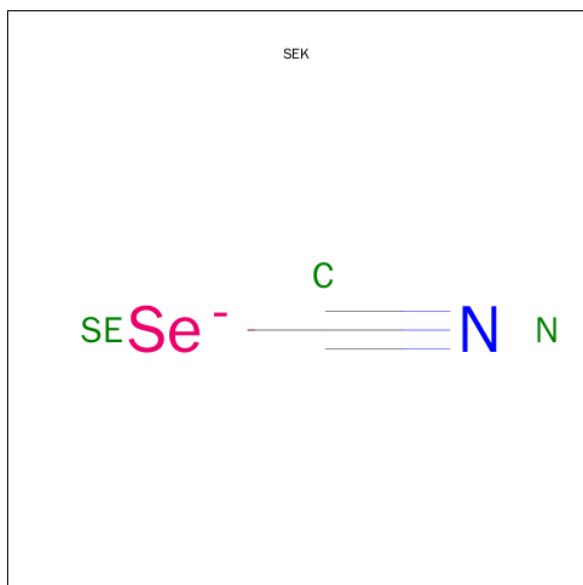
- Molecule 2 is a protein called FAB fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			
2	E	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			

- Molecule 3 is a protein called FAB fragment, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			
3	F	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			

- Molecule 4 is SELENOCYANATE ION (three-letter code: SEK) (formula: CNSe).

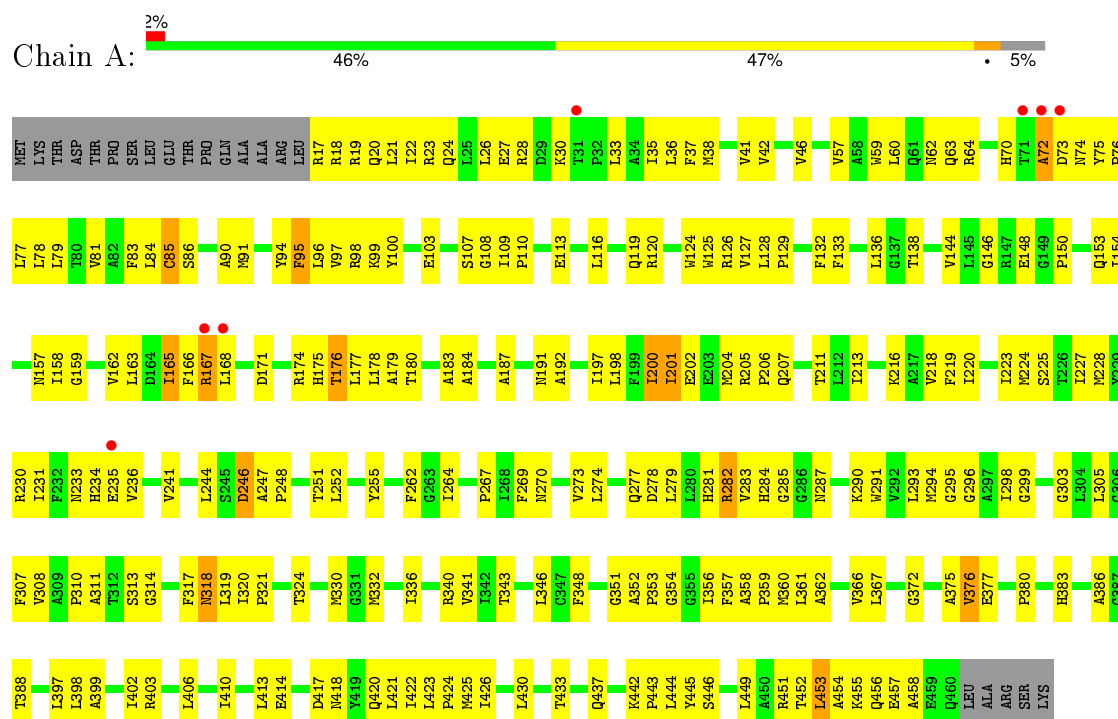


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Se 1	0	0
4	B	1	Total 1	Se 1	0	0
4	A	1	Total 1	Se 1	1	0
4	B	1	Total 1	Se 1	1	0
4	A	1	Total 1	Se 1	1	0
4	B	1	Total 1	Se 1	1	0
4	A	1	Total 1	Se 1	1	0
4	B	1	Total 1	Se 1	1	0

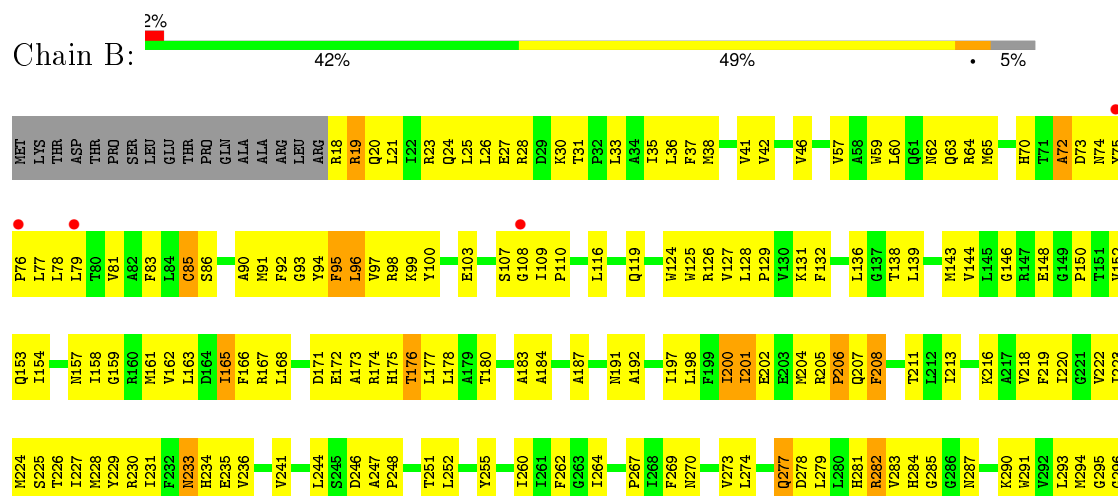
3 Residue-property plots

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.

• Molecule 1: CLC Cl transporter

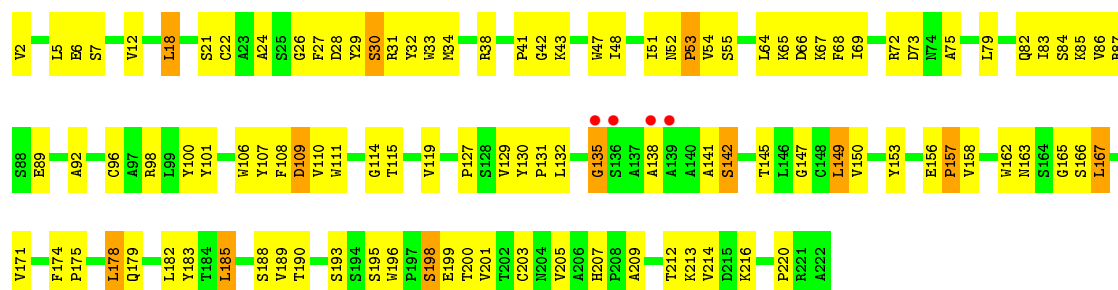


• Molecule 1: CLC Cl transporter

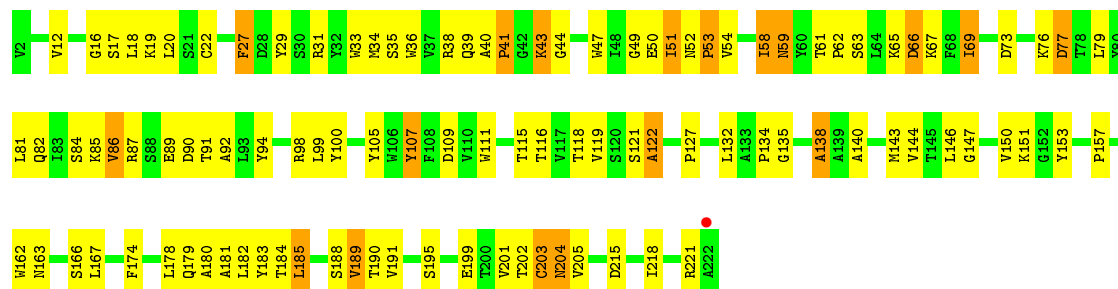




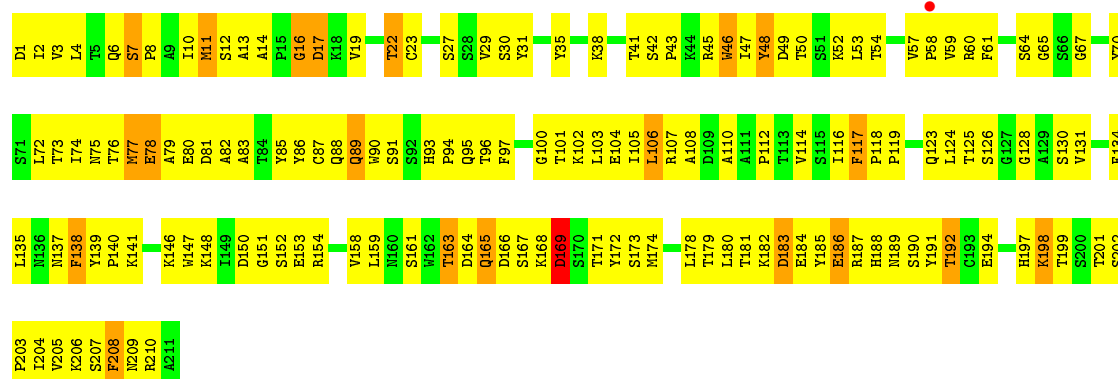
• Molecule 2: FAB fragment, heavy chain



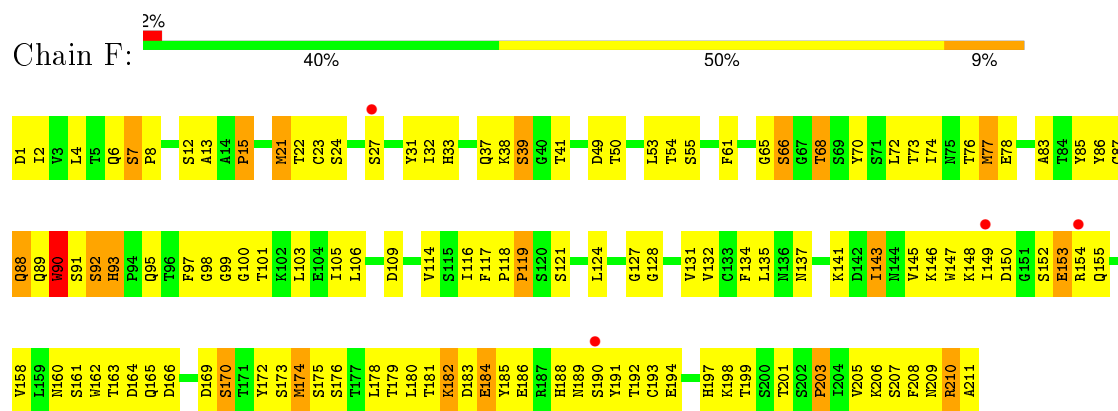
• Molecule 2: FAB fragment, heavy chain



• Molecule 3: FAB fragment, light chain



• Molecule 3: FAB fragment, light chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	220.58Å 121.58Å 151.24Å 90.00° 128.25° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 37.67 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-3.10) 98.0 (37.67-3.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.278 , 0.280 0.274 , 0.279	Depositor DCC
R_{free} test set	2835 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.676	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 61342 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	13231	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.48	0/3405	0.64	0/4621
1	B	0.48	0/3376	0.63	0/4583
2	C	0.52	0/1721	0.76	0/2355
2	E	0.52	0/1721	0.78	0/2355
3	D	0.48	0/1660	0.73	1/2257 (0.0%)
3	F	0.52	0/1660	0.77	0/2257
All	All	0.49	0/13543	0.70	1/18428 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	16	GLY	N-CA-C	-6.80	96.11	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3333	0	3482	267	0
1	B	3304	0	3456	274	0
2	C	1672	0	1654	122	0
2	E	1672	0	1654	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1621	0	1544	230	0
3	F	1621	0	1546	172	0
4	A	4	0	0	2	0
4	B	4	0	0	2	0
All	All	13231	0	13336	1109	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 42.

All (1109) 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)
2:C:107:TYR:CE1	3:D:45:ARG:NH1	1.70	1.56
1:A:274:LEU:CD2	1:A:451:ARG:NH1	1.71	1.53
3:D:186:GLU:HA	3:D:210:ARG:NH2	1.27	1.45
2:E:163:ASN:HD22	2:E:167:LEU:CD1	1.35	1.39
1:A:18:ARG:NH1	1:B:456:GLN:OE1	1.62	1.30
1:A:274:LEU:HD22	1:A:451:ARG:NH1	0.94	1.25
3:D:75:ASN:O	3:D:76:THR:HG22	1.35	1.22
2:E:143:MET:CE	2:E:190:THR:HG22	1.70	1.21
3:D:188:HIS:O	3:D:210:ARG:HD2	1.36	1.20
1:A:119:GLN:NE2	1:B:18:ARG:HD3	1.55	1.19
3:F:38:LYS:O	3:F:41:THR:HG22	1.01	1.18
3:D:107:ARG:HG2	3:D:108:ALA:H	1.06	1.18
3:D:6:GLN:HG3	3:D:100:GLY:H	1.01	1.18
1:A:171:ASP:O	1:A:175:HIS:CD2	2.02	1.12
3:F:38:LYS:O	3:F:41:THR:CG2	1.97	1.12
3:D:16:GLY:HA2	3:D:76:THR:OG1	1.49	1.10
3:D:186:GLU:CA	3:D:210:ARG:NH2	2.14	1.10
1:B:171:ASP:O	1:B:175:HIS:ND1	1.82	1.09
2:E:163:ASN:ND2	2:E:167:LEU:HD13	1.67	1.09
3:D:74:ILE:HG21	3:D:77:MET:CB	1.81	1.09
3:D:186:GLU:CA	3:D:210:ARG:HH22	1.66	1.08
3:D:74:ILE:HG21	3:D:77:MET:HB2	1.07	1.07
2:E:35:SER:HB2	2:E:99:LEU:HD11	1.35	1.07
3:F:7:SER:HB2	3:F:22:THR:HB	1.10	1.07
3:D:192:THR:HA	3:D:207:SER:HB3	1.36	1.06
3:D:107:ARG:HG2	3:D:108:ALA:N	1.60	1.05
2:E:143:MET:HE3	2:E:190:THR:HG22	1.37	1.04
3:D:74:ILE:CG2	3:D:77:MET:HB2	1.86	1.04
2:E:143:MET:HE3	2:E:190:THR:CG2	1.88	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:38:ARG:HD3	2:C:48:ILE:HD11	1.39	1.02
2:E:163:ASN:ND2	2:E:167:LEU:CD1	2.18	1.02
2:E:143:MET:CE	2:E:190:THR:CG2	2.37	1.02
1:A:171:ASP:O	1:A:175:HIS:HD2	1.41	1.00
2:E:163:ASN:HD22	2:E:167:LEU:HD13	0.87	1.00
2:C:167:LEU:HD23	2:C:189:VAL:HG21	1.42	0.99
3:F:2:ILE:CD1	3:F:27:SER:OG	2.11	0.99
3:D:6:GLN:HG3	3:D:100:GLY:N	1.78	0.98
3:D:107:ARG:CG	3:D:108:ALA:H	1.75	0.98
3:F:191:TYR:O	3:F:207:SER:HB2	1.63	0.98
3:F:188:HIS:O	3:F:210:ARG:HD3	1.64	0.97
3:D:17:ASP:H	3:D:76:THR:HA	1.26	0.97
3:D:188:HIS:C	3:D:210:ARG:HD2	1.86	0.95
3:F:158:VAL:HG22	3:F:178:LEU:HD13	1.49	0.94
2:E:204:ASN:HB3	2:E:215:ASP:OD1	1.67	0.93
3:F:150:ASP:OD2	3:F:188:HIS:HB3	1.68	0.93
1:B:75:TYR:HB3	1:B:76:PRO:HD3	1.50	0.93
2:C:127:PRO:HB3	2:C:153:TYR:HB3	1.50	0.93
3:D:75:ASN:O	3:D:76:THR:CG2	2.16	0.93
1:B:107:SER:H	4:B:466:SEK:SE	2.01	0.93
3:F:7:SER:HB2	3:F:22:THR:CB	1.97	0.92
1:A:75:TYR:HB3	1:A:76:PRO:HD3	1.48	0.92
1:A:220:ILE:HG12	1:B:430:LEU:HD21	1.52	0.92
3:F:7:SER:CB	3:F:22:THR:HB	1.99	0.92
3:D:7:SER:HB3	3:D:8:PRO:HD3	1.51	0.92
3:F:2:ILE:HD12	3:F:27:SER:OG	1.70	0.91
3:D:89:GLN:NE2	3:D:91:SER:H	1.68	0.90
3:D:79:ALA:HA	3:D:105:ILE:HD11	1.54	0.90
1:A:119:GLN:NE2	1:B:18:ARG:CD	2.34	0.90
3:F:54:THR:HG22	3:F:55:SER:H	1.34	0.89
3:F:32:ILE:HD11	3:F:70:TYR:CG	2.07	0.89
3:F:90:TRP:HH2	3:F:93:HIS:HD1	1.16	0.89
3:D:188:HIS:O	3:D:210:ARG:CD	2.20	0.89
2:E:91:THR:OG1	2:E:119:VAL:HG23	1.73	0.89
2:C:6:GLU:OE1	2:C:114:GLY:HA2	1.70	0.88
3:F:201:THR:O	3:F:203:PRO:HD3	1.74	0.88
2:E:163:ASN:HD22	2:E:167:LEU:HD11	1.38	0.88
2:C:132:LEU:HB2	2:C:147:GLY:O	1.73	0.88
2:C:6:GLU:HG2	2:C:96:CYS:SG	2.14	0.88
3:D:141:LYS:HB3	3:D:172:TYR:CD1	2.07	0.87
3:D:112:PRO:HG2	3:D:204:ILE:HD12	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:THR:HG22	1:B:218:VAL:HA	1.55	0.87
3:F:7:SER:CB	3:F:8:PRO:HD3	2.05	0.87
1:B:244:LEU:H	1:B:418:ASN:HD21	1.23	0.87
3:D:6:GLN:NE2	3:D:86:TYR:HA	1.90	0.86
3:F:146:LYS:HB3	3:F:194:GLU:HB2	1.54	0.86
2:E:201:VAL:HG13	2:E:218:ILE:HB	1.57	0.86
3:D:185:TYR:O	3:D:210:ARG:NH1	2.08	0.86
1:B:287:ASN:ND2	1:B:290:LYS:H	1.73	0.85
3:F:95:GLN:OE1	3:F:95:GLN:N	2.10	0.85
2:E:91:THR:HG23	2:E:118:THR:HA	1.59	0.85
1:A:207:GLN:HG3	1:B:28:ARG:HH11	1.41	0.85
3:D:166:ASP:OD2	3:D:169:ASP:HB3	1.77	0.85
2:C:7:SER:HA	2:C:115:THR:HG21	1.59	0.85
2:E:29:TYR:HD1	2:E:34:MET:HE3	1.41	0.84
1:A:28:ARG:HH11	1:B:207:GLN:HG3	1.40	0.84
2:E:29:TYR:CD1	2:E:34:MET:CE	2.60	0.84
3:D:202:SER:HB3	3:D:203:PRO:HD2	1.60	0.84
1:A:107:SER:H	4:A:466:SEK:SE	2.11	0.84
2:C:107:TYR:HE1	3:D:45:ARG:NH1	1.35	0.84
3:F:143:ILE:HG13	3:F:197:HIS:HD2	1.42	0.84
3:F:191:TYR:HB2	3:F:208:PHE:CE2	2.12	0.84
1:A:274:LEU:HD23	1:A:451:ARG:NH1	1.88	0.83
2:E:29:TYR:CD1	2:E:34:MET:HE3	2.13	0.83
2:E:29:TYR:HD1	2:E:34:MET:CE	1.90	0.83
1:A:274:LEU:HA	1:A:277:GLN:HE21	1.43	0.83
3:D:192:THR:HA	3:D:207:SER:CB	2.08	0.83
1:B:59:TRP:O	1:B:63:GLN:HG2	1.78	0.83
1:A:287:ASN:ND2	1:A:290:LYS:H	1.75	0.83
3:D:201:THR:HG23	3:D:202:SER:N	1.94	0.83
3:F:38:LYS:C	3:F:41:THR:HG22	1.99	0.82
3:F:7:SER:HB3	3:F:8:PRO:HD3	1.61	0.82
3:D:89:GLN:HE22	3:D:91:SER:H	1.21	0.82
3:D:146:LYS:HD3	3:D:153:GLU:HG3	1.60	0.82
1:A:124:TRP:HA	1:A:157:ASN:HD22	1.44	0.82
2:E:107:TYR:HB3	3:F:33:HIS:CD2	2.15	0.82
3:F:194:GLU:HA	3:F:205:VAL:HG12	1.60	0.82
1:A:423:LEU:HB3	1:A:424:PRO:HD3	1.62	0.81
3:D:114:VAL:HG22	3:D:135:LEU:HD13	1.63	0.81
1:B:124:TRP:HA	1:B:157:ASN:HD22	1.45	0.81
2:E:143:MET:HE2	2:E:190:THR:HG22	1.57	0.81
1:B:234:HIS:ND1	1:B:235:GLU:HG2	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:GLU:HB3	1:B:19:ARG:CZ	2.10	0.80
1:A:234:HIS:ND1	1:A:235:GLU:HG2	1.95	0.80
2:C:87:ARG:O	2:C:119:VAL:HG11	1.82	0.80
2:C:171:VAL:HG22	2:C:189:VAL:HG23	1.64	0.80
3:D:54:THR:O	3:D:57:VAL:HG23	1.82	0.80
2:E:143:MET:HE2	2:E:190:THR:CG2	2.08	0.80
1:A:244:LEU:H	1:A:418:ASN:HD21	1.25	0.80
3:D:139:TYR:CD1	3:D:140:PRO:HA	2.16	0.79
3:D:107:ARG:NH1	3:D:108:ALA:O	2.16	0.79
1:B:449:LEU:HD12	1:B:452:THR:HG21	1.62	0.79
3:D:182:LYS:O	3:D:186:GLU:HG2	1.83	0.79
3:D:125:THR:HG22	3:D:125:THR:O	1.83	0.79
3:F:7:SER:HB3	3:F:8:PRO:CD	2.12	0.79
1:A:180:THR:HG22	1:A:218:VAL:HA	1.63	0.79
2:E:29:TYR:CD2	2:E:77:ASP:HA	2.16	0.79
1:A:430:LEU:HD21	1:B:220:ILE:HG12	1.62	0.79
1:A:59:TRP:O	1:A:63:GLN:HG2	1.83	0.79
1:B:423:LEU:HB3	1:B:424:PRO:HD3	1.64	0.78
3:D:140:PRO:HD3	3:D:198:LYS:HD3	1.65	0.77
1:A:216:LYS:HE2	1:B:433:THR:CG2	2.15	0.77
2:C:107:TYR:CD1	3:D:45:ARG:NH1	2.49	0.77
3:D:31:TYR:HA	3:D:50:THR:OG1	1.84	0.77
1:A:332:MET:O	1:A:336:ILE:HG13	1.85	0.77
1:A:273:VAL:O	1:A:277:GLN:HG3	1.85	0.76
2:C:52:ASN:HB2	2:C:53:PRO:CD	2.16	0.76
2:E:162:TRP:CZ3	2:E:203:CYS:HB3	2.20	0.76
1:A:274:LEU:HA	1:A:277:GLN:NE2	2.01	0.75
3:D:74:ILE:HG21	3:D:77:MET:CA	2.16	0.75
1:B:99:LYS:HG2	1:B:100:TYR:CE2	2.20	0.75
1:A:18:ARG:NH1	1:B:456:GLN:CD	2.39	0.75
1:B:154:ILE:O	1:B:158:ILE:HG12	1.87	0.75
1:A:154:ILE:O	1:A:158:ILE:HG12	1.87	0.75
1:A:119:GLN:HE22	1:B:18:ARG:HD3	1.52	0.74
1:A:99:LYS:HG2	1:A:100:TYR:CE2	2.22	0.74
1:A:287:ASN:HD22	1:A:290:LYS:HG3	1.51	0.74
3:D:61:PHE:CE2	3:D:74:ILE:HG12	2.22	0.74
2:E:31:ARG:HH11	2:E:31:ARG:HG2	1.52	0.74
2:C:107:TYR:CZ	3:D:45:ARG:NH1	2.52	0.74
3:F:88:GLN:HG2	3:F:89:GLN:N	2.02	0.74
2:E:38:ARG:HD3	2:E:94:TYR:HE1	1.52	0.74
3:F:89:GLN:NE2	3:F:95:GLN:HA	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:36:TRP:CE2	2:E:81:LEU:HB2	2.22	0.73
3:F:38:LYS:HB2	3:F:41:THR:HG21	1.68	0.73
3:F:2:ILE:HD11	3:F:27:SER:OG	1.88	0.73
2:E:73:ASP:OD2	2:E:76:LYS:HD2	1.86	0.73
3:F:121:SER:HA	3:F:124:LEU:HD12	1.70	0.73
2:C:66:ASP:OD1	2:C:69:ILE:HD11	1.89	0.73
3:F:188:HIS:O	3:F:210:ARG:CD	2.36	0.73
2:C:5:LEU:O	2:C:22:CYS:HA	1.89	0.73
1:A:230:ARG:HG3	1:A:230:ARG:HH11	1.54	0.73
3:D:124:LEU:HD23	3:D:128:GLY:O	1.89	0.73
3:D:154:ARG:NH2	3:D:184:GLU:OE2	2.16	0.72
2:C:149:LEU:O	2:C:149:LEU:HD23	1.89	0.72
1:B:311:ALA:O	1:B:340:ARG:NH1	2.21	0.72
2:E:144:VAL:HG13	2:E:191:VAL:HG23	1.71	0.72
1:B:287:ASN:HD22	1:B:290:LYS:HG3	1.53	0.72
2:E:73:ASP:OD2	2:E:76:LYS:CD	2.36	0.72
3:D:186:GLU:HA	3:D:210:ARG:CZ	2.16	0.72
3:F:119:PRO:HD3	3:F:131:VAL:HG12	1.71	0.72
3:D:7:SER:CB	3:D:8:PRO:HD3	2.18	0.72
1:A:216:LYS:HE2	1:B:433:THR:HG22	1.71	0.72
1:B:449:LEU:O	1:B:452:THR:HG22	1.89	0.72
2:E:39:GLN:O	2:E:92:ALA:HB1	1.89	0.72
2:C:145:THR:HG22	2:C:190:THR:OG1	1.91	0.71
3:D:74:ILE:CG2	3:D:77:MET:CA	2.68	0.71
3:D:90:TRP:CH2	3:D:95:GLN:NE2	2.59	0.71
3:D:79:ALA:C	3:D:81:ASP:H	1.94	0.71
2:E:29:TYR:CD1	2:E:34:MET:HE2	2.25	0.71
3:F:7:SER:OG	3:F:8:PRO:HD3	1.91	0.71
1:A:94:TYR:CZ	1:A:352:ALA:HB2	2.26	0.71
3:D:74:ILE:CG2	3:D:77:MET:CB	2.58	0.70
1:B:235:GLU:OE1	2:C:100:TYR:HE2	1.72	0.70
3:F:182:LYS:HG2	3:F:186:GLU:OE1	1.92	0.70
3:D:138:PHE:N	3:D:171:THR:HB	2.07	0.70
1:B:332:MET:O	1:B:336:ILE:HG13	1.91	0.70
2:E:127:PRO:HB3	2:E:153:TYR:HB3	1.74	0.70
3:D:6:GLN:HE21	3:D:86:TYR:HA	1.54	0.70
3:D:12:SER:HA	3:D:104:GLU:O	1.92	0.69
3:F:186:GLU:HA	3:F:210:ARG:HD2	1.73	0.69
2:C:130:TYR:HB2	2:C:149:LEU:CD2	2.22	0.69
1:A:311:ALA:O	1:A:340:ARG:NH2	2.25	0.69
1:B:94:TYR:CZ	1:B:352:ALA:HB2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:146:LEU:HD12	2:E:201:VAL:HG11	1.73	0.69
3:F:189:ASN:ND2	3:F:210:ARG:HB3	2.08	0.69
3:D:7:SER:HB3	3:D:8:PRO:CD	2.22	0.69
3:F:90:TRP:HH2	3:F:93:HIS:ND1	1.89	0.69
3:F:89:GLN:HE21	3:F:95:GLN:HA	1.57	0.69
2:C:131:PRO:HD3	2:C:216:LYS:NZ	2.07	0.69
1:A:443:PRO:HB2	1:A:446:SER:HB2	1.73	0.69
1:A:372:GLY:O	1:A:376:VAL:HG23	1.92	0.69
1:A:219:PHE:HB3	1:B:430:LEU:HD13	1.75	0.69
3:D:6:GLN:NE2	3:D:87:CYS:H	1.90	0.68
3:D:13:ALA:HB3	3:D:77:MET:SD	2.33	0.68
3:D:201:THR:HG23	3:D:202:SER:H	1.56	0.68
1:A:81:VAL:O	1:A:85:CYS:HB2	1.94	0.68
3:F:4:LEU:HD22	3:F:23:CYS:SG	2.34	0.68
3:F:54:THR:HG22	3:F:55:SER:N	2.07	0.68
2:C:147:GLY:HA2	2:C:162:TRP:CZ2	2.28	0.68
3:D:74:ILE:CG2	3:D:77:MET:HA	2.23	0.68
3:F:88:GLN:HB2	3:F:97:PHE:CD1	2.29	0.68
2:C:178:LEU:HD12	2:C:179:GLN:N	2.09	0.68
3:F:77:MET:HG2	3:F:78:GLU:N	2.07	0.68
2:E:163:ASN:ND2	2:E:167:LEU:HD11	1.99	0.68
2:E:61:THR:O	2:E:63:SER:N	2.27	0.67
1:A:442:LYS:HE3	1:B:26:LEU:O	1.94	0.67
1:B:78:LEU:HA	1:B:81:VAL:HG22	1.75	0.67
3:F:32:ILE:HG22	3:F:89:GLN:HA	1.76	0.67
1:A:282:ARG:O	1:A:285:GLY:N	2.27	0.67
1:A:192:ALA:HB1	1:A:414:GLU:OE1	1.93	0.67
3:D:90:TRP:CZ2	3:D:95:GLN:NE2	2.63	0.67
3:D:79:ALA:O	3:D:81:ASP:N	2.28	0.67
2:E:201:VAL:CG1	2:E:218:ILE:HB	2.24	0.67
1:A:78:LEU:HA	1:A:81:VAL:HG22	1.77	0.67
3:D:201:THR:CG2	3:D:202:SER:H	2.06	0.67
3:F:169:ASP:O	3:F:170:SER:HB2	1.94	0.67
2:C:42:GLY:O	2:C:43:LYS:HG2	1.94	0.67
2:C:207:HIS:NE2	2:C:209:ALA:HB3	2.10	0.67
3:D:81:ASP:O	3:D:103:LEU:HD23	1.95	0.67
3:D:201:THR:CG2	3:D:202:SER:N	2.57	0.67
2:E:143:MET:HE3	2:E:190:THR:HG23	1.75	0.67
1:B:449:LEU:HA	1:B:452:THR:HG22	1.74	0.67
1:B:330:MET:HE3	1:B:330:MET:HA	1.77	0.67
1:A:287:ASN:HD22	1:A:290:LYS:H	1.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:305:LEU:C	1:B:307:PHE:H	1.97	0.67
1:A:305:LEU:HA	1:A:308:VAL:HG22	1.77	0.67
1:B:281:HIS:ND1	1:B:284:HIS:HE1	1.93	0.66
2:C:87:ARG:HH11	2:C:87:ARG:HG3	1.59	0.66
1:A:274:LEU:HD23	1:A:277:GLN:NE2	2.09	0.66
3:D:89:GLN:HE22	3:D:91:SER:N	1.93	0.66
1:A:26:LEU:O	1:B:442:LYS:HE3	1.96	0.66
1:A:433:THR:CG2	1:B:216:LYS:HE2	2.26	0.66
1:B:443:PRO:HB2	1:B:446:SER:HB2	1.76	0.66
3:D:146:LYS:HD3	3:D:153:GLU:CG	2.26	0.66
2:C:166:SER:O	2:C:167:LEU:HD12	1.95	0.66
1:A:305:LEU:C	1:A:307:PHE:H	1.99	0.66
2:E:17:SER:HB3	2:E:84:SER:HA	1.78	0.66
3:D:138:PHE:H	3:D:171:THR:HB	1.60	0.66
2:E:121:SER:O	2:E:122:ALA:O	2.13	0.66
1:B:287:ASN:HD22	1:B:290:LYS:H	1.41	0.65
3:F:189:ASN:HA	3:F:210:ARG:HB2	1.77	0.65
3:F:77:MET:HE3	3:F:103:LEU:HD21	1.78	0.65
2:C:51:ILE:HD13	2:C:72:ARG:HG2	1.78	0.65
3:F:116:ILE:HD12	3:F:193:CYS:HB2	1.78	0.65
3:D:205:VAL:O	3:D:206:LYS:HG2	1.97	0.65
3:D:8:PRO:O	3:D:101:THR:HG23	1.97	0.65
3:D:150:ASP:HA	3:D:190:SER:HB3	1.78	0.65
3:F:33:HIS:CE1	3:F:49:ASP:H	2.15	0.65
1:B:282:ARG:O	1:B:285:GLY:N	2.29	0.65
2:E:132:LEU:HB2	2:E:147:GLY:O	1.97	0.65
1:A:75:TYR:HB3	1:A:76:PRO:CD	2.25	0.65
3:F:90:TRP:HA	3:F:95:GLN:HB3	1.78	0.65
3:F:7:SER:CB	3:F:8:PRO:CD	2.70	0.65
2:E:47:TRP:CZ2	2:E:49:GLY:HA2	2.30	0.65
1:A:281:HIS:ND1	1:A:284:HIS:HE1	1.94	0.65
2:E:163:ASN:HB2	2:E:166:SER:OG	1.98	0.64
2:C:6:GLU:OE1	2:C:114:GLY:CA	2.45	0.64
3:F:158:VAL:CG2	3:F:178:LEU:HD13	2.25	0.64
1:A:18:ARG:NH2	1:B:457:GLU:OE1	2.28	0.64
1:B:305:LEU:HA	1:B:308:VAL:HG22	1.80	0.64
2:E:195:SER:O	2:E:199:GLU:HB2	1.97	0.64
2:E:132:LEU:HD11	3:F:132:VAL:HG21	1.79	0.64
2:E:38:ARG:HD3	2:E:94:TYR:CE1	2.33	0.64
2:E:105:TYR:CE1	3:F:31:TYR:HD2	2.15	0.64
3:D:89:GLN:NE2	3:D:90:TRP:N	2.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:VAL:HG12	1:A:244:LEU:HD21	1.79	0.63
1:B:81:VAL:O	1:B:85:CYS:HB2	1.97	0.63
1:B:241:VAL:HG12	1:B:244:LEU:HD21	1.80	0.63
3:F:143:ILE:HG13	3:F:197:HIS:CD2	2.30	0.63
3:D:123:GLN:HE22	3:D:130:SER:HB2	1.64	0.63
3:F:37:GLN:O	3:F:83:ALA:HB1	1.99	0.63
2:C:32:TYR:CE2	2:C:98:ARG:HD2	2.33	0.63
3:D:192:THR:CA	3:D:207:SER:HB3	2.23	0.63
3:F:149:ILE:HD12	3:F:154:ARG:CZ	2.27	0.63
3:F:146:LYS:CB	3:F:194:GLU:HB2	2.28	0.63
1:A:330:MET:HE3	1:A:330:MET:HA	1.79	0.63
3:F:72:LEU:HD23	3:F:72:LEU:C	2.19	0.63
1:B:294:MET:O	1:B:298:ILE:HG13	1.99	0.63
1:A:18:ARG:O	1:A:18:ARG:HG2	1.97	0.62
3:D:141:LYS:HB3	3:D:172:TYR:CG	2.34	0.62
2:E:162:TRP:HA	2:E:202:THR:O	1.99	0.62
2:C:30:SER:C	2:C:32:TYR:H	2.03	0.62
3:D:74:ILE:HG21	3:D:77:MET:HA	1.80	0.62
2:C:6:GLU:OE2	2:C:96:CYS:N	2.27	0.62
3:F:149:ILE:HD13	3:F:191:TYR:HE2	1.65	0.62
1:A:430:LEU:HD13	1:B:219:PHE:HB3	1.81	0.62
1:B:281:HIS:HA	1:B:284:HIS:CE1	2.35	0.62
3:D:117:PHE:CD1	3:D:117:PHE:N	2.66	0.62
3:D:17:ASP:N	3:D:76:THR:HA	2.09	0.62
3:D:110:ALA:HB3	3:D:138:PHE:HA	1.82	0.62
3:D:31:TYR:HB3	3:D:49:ASP:HA	1.80	0.62
1:A:120:ARG:NH1	1:A:452:THR:HG22	2.14	0.62
3:F:197:HIS:O	3:F:199:THR:N	2.32	0.61
1:B:336:ILE:O	1:B:340:ARG:HG3	1.99	0.61
1:A:281:HIS:HA	1:A:284:HIS:CE1	2.35	0.61
2:C:18:LEU:HD21	2:C:83:ILE:HD12	1.82	0.61
3:F:13:ALA:HB3	3:F:77:MET:HE1	1.82	0.61
1:A:205:ARG:HG2	1:A:206:PRO:HD2	1.81	0.61
3:D:138:PHE:CE1	3:D:172:TYR:HB2	2.35	0.61
1:A:294:MET:O	1:A:298:ILE:HG13	2.00	0.61
2:C:6:GLU:HA	2:C:21:SER:O	2.01	0.61
2:E:132:LEU:CD1	3:F:132:VAL:HG21	2.30	0.61
1:B:75:TYR:HB3	1:B:76:PRO:CD	2.28	0.61
1:A:433:THR:HG22	1:B:216:LYS:HE2	1.82	0.61
1:B:205:ARG:HG2	1:B:206:PRO:HD2	1.82	0.61
1:A:274:LEU:HD23	1:A:277:GLN:HE22	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:118:PRO:HG3	3:D:208:PHE:CD2	2.36	0.61
1:B:38:MET:O	1:B:41:VAL:HG12	2.01	0.61
2:E:67:LYS:NZ	2:E:85:LYS:O	2.34	0.61
1:A:198:LEU:HD12	1:A:406:LEU:HG	1.83	0.61
1:A:274:LEU:O	1:A:277:GLN:HB2	2.01	0.60
3:D:107:ARG:HH21	3:D:171:THR:CG2	2.13	0.60
3:F:190:SER:HB2	3:F:209:ASN:OD1	2.01	0.60
1:A:360:MET:HG2	1:A:397:LEU:HD23	1.83	0.60
3:D:184:GLU:HA	3:D:187:ARG:HH21	1.65	0.60
3:F:32:ILE:HD11	3:F:70:TYR:CB	2.31	0.60
1:B:241:VAL:HG11	1:B:324:THR:HG21	1.83	0.60
1:A:37:PHE:HD2	1:A:38:MET:HE2	1.66	0.60
1:A:457:GLU:OE1	1:B:19:ARG:NH2	2.33	0.60
3:F:186:GLU:O	3:F:210:ARG:HD2	2.01	0.60
1:B:159:GLY:O	1:B:162:VAL:HG22	2.01	0.60
1:B:163:LEU:HD12	1:B:168:LEU:HB2	1.83	0.60
1:A:241:VAL:HG11	1:A:324:THR:HG21	1.82	0.60
1:A:109:ILE:HG21	1:A:445:TYR:CD2	2.36	0.60
1:A:205:ARG:HG3	1:A:213:ILE:HD12	1.81	0.60
1:A:91:MET:HG3	1:A:296:GLY:HA3	1.84	0.60
3:F:12:SER:HB3	3:F:106:LEU:HD21	1.84	0.60
2:C:178:LEU:HB2	2:C:183:TYR:CE2	2.37	0.60
1:A:287:ASN:ND2	1:A:290:LYS:HG3	2.16	0.60
2:C:109:ASP:OD1	2:C:110:VAL:HG23	2.01	0.60
2:C:52:ASN:HB2	2:C:53:PRO:HD2	1.83	0.59
3:D:38:LYS:HB2	3:D:41:THR:CG2	2.31	0.59
3:F:141:LYS:HD3	3:F:172:TYR:CE2	2.37	0.59
1:B:372:GLY:O	1:B:376:VAL:HG23	2.02	0.59
2:C:6:GLU:O	2:C:115:THR:HG23	2.02	0.59
1:B:358:ALA:HB3	1:B:359:PRO:HD3	1.84	0.59
1:B:205:ARG:CG	1:B:206:PRO:HD2	2.33	0.59
1:B:360:MET:HG2	1:B:397:LEU:HD23	1.85	0.59
3:D:6:GLN:NE2	3:D:87:CYS:N	2.50	0.59
3:F:186:GLU:O	3:F:210:ARG:CD	2.50	0.59
1:B:205:ARG:HG3	1:B:213:ILE:HD12	1.84	0.59
3:F:131:VAL:HG23	3:F:178:LEU:HB3	1.83	0.59
1:A:358:ALA:HB3	1:A:359:PRO:HD3	1.84	0.59
1:A:90:ALA:HB2	1:A:299:GLY:HA3	1.85	0.59
1:B:198:LEU:HD12	1:B:406:LEU:HG	1.83	0.59
3:D:179:THR:O	3:D:180:LEU:HD23	2.03	0.59
1:B:287:ASN:ND2	1:B:290:LYS:HG3	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:VAL:O	1:A:46:VAL:HG23	2.02	0.59
1:A:127:VAL:HB	1:A:157:ASN:ND2	2.18	0.58
1:B:449:LEU:HD12	1:B:452:THR:CG2	2.32	0.58
1:A:270:ASN:OD1	1:A:444:LEU:HD13	2.03	0.58
1:B:127:VAL:HB	1:B:157:ASN:ND2	2.18	0.58
2:C:2:VAL:O	2:C:2:VAL:HG23	2.02	0.58
3:D:7:SER:CB	3:D:8:PRO:CD	2.80	0.58
2:E:43:LYS:HD3	2:E:44:GLY:H	1.68	0.58
3:F:31:TYR:HA	3:F:50:THR:OG1	2.03	0.58
1:B:91:MET:HG3	1:B:296:GLY:HA3	1.85	0.58
3:D:58:PRO:HB2	3:D:60:ARG:NH1	2.18	0.58
3:D:79:ALA:CA	3:D:105:ILE:HD11	2.31	0.58
1:A:216:LYS:HE2	1:B:433:THR:HG21	1.85	0.58
1:B:42:VAL:O	1:B:46:VAL:HG23	2.03	0.58
1:B:90:ALA:HB2	1:B:299:GLY:HA3	1.85	0.58
1:B:109:ILE:HG21	1:B:445:TYR:CD2	2.39	0.58
3:F:33:HIS:HD2	3:F:88:GLN:OE1	1.84	0.58
3:D:130:SER:HA	3:D:178:LEU:O	2.03	0.58
1:A:163:LEU:HD12	1:A:168:LEU:HB2	1.84	0.58
2:C:163:ASN:HD21	2:C:201:VAL:HA	1.69	0.58
3:F:90:TRP:CE3	3:F:90:TRP:O	2.57	0.58
2:C:64:LEU:O	2:C:66:ASP:N	2.37	0.58
1:A:205:ARG:CG	1:A:206:PRO:HD2	2.33	0.58
3:F:24:SER:HA	3:F:68:THR:O	2.03	0.58
3:F:180:LEU:HD13	3:F:184:GLU:HG3	1.85	0.58
1:B:136:LEU:HD12	1:B:136:LEU:H	1.67	0.58
1:B:319:LEU:HD12	1:B:319:LEU:C	2.24	0.58
1:B:18:ARG:O	1:B:21:LEU:N	2.37	0.58
2:E:31:ARG:NH1	2:E:31:ARG:HG2	2.17	0.58
1:A:94:TYR:OH	1:A:352:ALA:HB2	2.04	0.58
1:A:380:PRO:HG2	3:D:93:HIS:HB2	1.85	0.58
3:F:145:VAL:HA	3:F:194:GLU:O	2.03	0.58
3:D:48:TYR:HE1	3:D:52:LYS:HE3	1.69	0.58
2:E:65:LYS:O	2:E:66:ASP:HB2	2.02	0.58
2:E:22:CYS:SG	2:E:22:CYS:O	2.61	0.58
1:A:125:TRP:CD1	1:A:126:ARG:HG3	2.39	0.57
1:B:270:ASN:OD1	1:B:444:LEU:HD13	2.03	0.57
1:B:192:ALA:HB1	1:B:414:GLU:OE1	2.03	0.57
2:C:30:SER:O	2:C:32:TYR:N	2.37	0.57
1:A:18:ARG:HB2	1:B:119:GLN:NE2	2.19	0.57
3:F:150:ASP:OD2	3:F:188:HIS:CB	2.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:130:TYR:HB2	2:C:149:LEU:HD23	1.87	0.57
1:B:358:ALA:O	1:B:361:LEU:HB2	2.05	0.57
3:F:114:VAL:O	3:F:206:LYS:HE2	2.04	0.57
3:D:107:ARG:HH21	3:D:171:THR:HG23	1.69	0.57
3:D:125:THR:O	3:D:125:THR:CG2	2.53	0.57
1:B:413:LEU:HD22	1:B:422:ILE:HD13	1.86	0.57
1:A:383:HIS:HD2	2:C:33:TRP:CE3	2.22	0.57
1:B:125:TRP:CD1	1:B:126:ARG:HG3	2.40	0.57
1:B:305:LEU:C	1:B:307:PHE:N	2.58	0.57
3:D:148:LYS:HB3	3:D:151:GLY:O	2.05	0.57
2:E:35:SER:CB	2:E:99:LEU:HD11	2.22	0.57
2:C:131:PRO:HD3	2:C:216:LYS:HE2	1.87	0.57
2:C:87:ARG:HG3	2:C:87:ARG:NH1	2.18	0.56
1:A:305:LEU:HA	1:A:308:VAL:CG2	2.34	0.56
3:F:141:LYS:HD3	3:F:172:TYR:CD2	2.40	0.56
3:D:6:GLN:NE2	3:D:86:TYR:CA	2.67	0.56
1:B:180:THR:HG22	1:B:218:VAL:CA	2.33	0.56
1:A:216:LYS:CE	1:B:433:THR:HG22	2.34	0.56
3:F:124:LEU:O	3:F:127:GLY:N	2.36	0.56
2:C:131:PRO:HD3	2:C:216:LYS:CE	2.36	0.56
1:B:73:ASP:OD1	1:B:74:ASN:N	2.34	0.56
2:C:32:TYR:CZ	2:C:98:ARG:HD2	2.40	0.56
1:A:97:VAL:HG21	1:A:353:PRO:HD3	1.87	0.56
2:E:151:LYS:HG3	2:E:184:THR:OG1	2.05	0.56
3:D:208:PHE:CD1	3:D:208:PHE:C	2.78	0.56
3:D:118:PRO:HG3	3:D:208:PHE:CE2	2.40	0.56
3:F:146:LYS:HD3	3:F:194:GLU:OE1	2.05	0.56
1:A:202:GLU:O	1:A:202:GLU:HG2	2.06	0.56
1:A:159:GLY:O	1:A:162:VAL:HG22	2.06	0.56
2:E:87:ARG:HG3	2:E:89:GLU:H	1.70	0.56
3:D:107:ARG:HG2	3:D:107:ARG:HH11	1.70	0.56
3:D:58:PRO:HG2	3:D:61:PHE:CD1	2.40	0.56
1:B:33:LEU:HD23	1:B:33:LEU:O	2.06	0.56
2:E:39:GLN:HE22	3:F:37:GLN:HE22	1.51	0.56
2:E:146:LEU:CD1	2:E:201:VAL:HG11	2.35	0.56
2:E:73:ASP:OD2	2:E:76:LYS:CE	2.54	0.56
2:E:29:TYR:CE2	2:E:77:ASP:HA	2.41	0.56
3:F:22:THR:CG2	3:F:23:CYS:N	2.68	0.56
3:D:140:PRO:CD	3:D:198:LYS:HD3	2.34	0.56
1:A:248:PRO:HB2	1:A:251:THR:HG23	1.88	0.56
3:D:4:LEU:HD11	3:D:89:GLN:CG	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:82:ALA:HB2	3:D:105:ILE:HG13	1.88	0.56
3:D:139:TYR:HA	3:D:140:PRO:O	2.06	0.56
2:C:129:VAL:HG12	2:C:205:VAL:HG21	1.88	0.55
1:A:38:MET:O	1:A:41:VAL:HG12	2.06	0.55
3:D:76:THR:HG23	3:D:76:THR:O	2.06	0.55
1:A:223:ILE:HD12	1:B:430:LEU:HD22	1.88	0.55
1:A:100:TYR:O	1:A:126:ARG:HD3	2.06	0.55
3:F:6:GLN:NE2	3:F:100:GLY:H	2.05	0.55
1:A:211:THR:HG22	1:A:213:ILE:HG13	1.89	0.55
1:A:437:GLN:NE2	1:B:30:LYS:HA	2.21	0.55
1:A:28:ARG:HD2	1:B:207:GLN:HG3	1.87	0.55
1:B:100:TYR:O	1:B:126:ARG:HD3	2.07	0.55
3:F:189:ASN:CG	3:F:210:ARG:HB3	2.26	0.55
1:B:421:LEU:O	1:B:424:PRO:HD2	2.07	0.55
3:D:50:THR:HG22	3:D:64:SER:HA	1.87	0.55
1:B:305:LEU:HA	1:B:308:VAL:CG2	2.36	0.55
3:D:154:ARG:NH2	3:D:180:LEU:HD22	2.20	0.55
2:E:73:ASP:OD2	2:E:76:LYS:HE3	2.07	0.55
1:B:99:LYS:CG	1:B:100:TYR:CE2	2.89	0.55
2:E:69:ILE:HB	2:E:82:GLN:HB2	1.88	0.55
1:B:18:ARG:O	1:B:20:GLN:N	2.40	0.55
3:D:107:ARG:HG2	3:D:107:ARG:NH1	2.22	0.55
1:A:421:LEU:O	1:A:424:PRO:HD2	2.07	0.55
1:A:99:LYS:CG	1:A:100:TYR:CE2	2.90	0.55
3:F:15:PRO:HD3	3:F:105:ILE:HG23	1.89	0.55
2:C:185:LEU:HD12	2:C:185:LEU:C	2.27	0.55
1:B:94:TYR:OH	1:B:352:ALA:HB2	2.07	0.55
3:F:92:SER:O	3:F:93:HIS:C	2.45	0.54
3:F:209:ASN:O	3:F:211:ALA:N	2.40	0.54
3:D:90:TRP:CZ3	3:D:95:GLN:OE1	2.60	0.54
1:A:33:LEU:O	1:A:33:LEU:HD23	2.07	0.54
1:B:455:LYS:C	1:B:457:GLU:H	2.10	0.54
3:F:166:ASP:HB3	3:F:169:ASP:OD1	2.06	0.54
1:A:205:ARG:HG3	1:A:213:ILE:CD1	2.37	0.54
2:C:196:TRP:HA	2:C:198:SER:N	2.22	0.54
3:F:146:LYS:HB3	3:F:194:GLU:CB	2.33	0.54
1:A:413:LEU:HD22	1:A:422:ILE:HD13	1.88	0.54
1:B:227:ILE:O	1:B:231:ILE:HG13	2.08	0.54
2:E:29:TYR:CE1	2:E:34:MET:CE	2.90	0.54
1:A:235:GLU:OE1	2:E:100:TYR:HE2	1.90	0.54
1:A:305:LEU:C	1:A:307:PHE:N	2.60	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:GLU:H	1:B:148:GLU:CD	2.09	0.54
1:B:362:ALA:O	1:B:366:VAL:HG23	2.06	0.54
2:C:167:LEU:HD23	2:C:189:VAL:CG2	2.28	0.54
1:A:223:ILE:HD11	1:B:426:ILE:HG22	1.90	0.54
2:C:147:GLY:HA2	2:C:162:TRP:CH2	2.41	0.54
1:B:198:LEU:HG	1:B:410:ILE:HD12	1.90	0.54
1:A:273:VAL:O	1:A:277:GLN:NE2	2.39	0.54
3:D:16:GLY:HA2	3:D:76:THR:HG1	1.66	0.54
1:B:202:GLU:HG2	1:B:202:GLU:O	2.07	0.54
1:A:28:ARG:HH11	1:B:207:GLN:CG	2.18	0.54
3:F:90:TRP:HA	3:F:95:GLN:CB	2.38	0.53
2:C:142:SER:O	2:C:193:SER:HB2	2.08	0.53
1:A:148:GLU:H	1:A:148:GLU:CD	2.10	0.53
2:E:163:ASN:HB2	2:E:167:LEU:HD13	1.90	0.53
3:D:58:PRO:HG2	3:D:61:PHE:CE1	2.43	0.53
2:C:212:THR:HG22	2:C:213:LYS:N	2.23	0.53
2:C:51:ILE:CD1	2:C:72:ARG:HG2	2.37	0.53
3:F:77:MET:CE	3:F:103:LEU:HD21	2.38	0.53
3:D:10:ILE:O	3:D:11:MET:HB3	2.09	0.53
1:A:340:ARG:O	1:A:341:VAL:C	2.47	0.53
3:D:19:VAL:O	3:D:73:THR:HA	2.09	0.53
2:C:171:VAL:CG2	2:C:189:VAL:HG23	2.37	0.53
1:A:73:ASP:OD1	1:A:74:ASN:N	2.36	0.53
1:B:211:THR:HG22	1:B:213:ILE:HG13	1.90	0.53
2:E:51:ILE:HG13	2:E:58:ILE:HG12	1.91	0.53
1:A:136:LEU:HD12	1:A:136:LEU:H	1.72	0.53
2:C:127:PRO:HB3	2:C:153:TYR:CB	2.30	0.53
2:C:127:PRO:CB	2:C:153:TYR:HB3	2.31	0.53
3:D:53:LEU:HD22	3:D:57:VAL:HB	1.91	0.53
1:A:223:ILE:HD11	1:B:426:ILE:CG2	2.38	0.53
3:D:48:TYR:CE1	3:D:52:LYS:HE3	2.44	0.53
2:C:174:PHE:H	2:C:174:PHE:HD2	1.56	0.53
3:D:189:ASN:HA	3:D:210:ARG:CD	2.39	0.53
3:F:109:ASP:HB3	3:F:199:THR:HG22	1.91	0.53
1:A:358:ALA:O	1:A:361:LEU:HB2	2.09	0.53
1:A:357:PHE:CE1	1:A:398:LEU:HD22	2.43	0.53
2:C:2:VAL:HG12	2:C:26:GLY:O	2.09	0.53
1:B:449:LEU:CA	1:B:452:THR:HG22	2.39	0.53
1:B:38:MET:HG3	1:B:168:LEU:HD11	1.90	0.52
3:D:146:LYS:CD	3:D:153:GLU:HG3	2.37	0.52
3:D:146:LYS:NZ	3:D:153:GLU:OE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ASN:ND2	1:A:420:GLN:HE22	2.06	0.52
2:E:87:ARG:CZ	2:E:89:GLU:HB2	2.40	0.52
2:E:33:TRP:O	2:E:99:LEU:HD12	2.09	0.52
2:E:204:ASN:CB	2:E:215:ASP:OD1	2.49	0.52
2:C:131:PRO:HD3	2:C:216:LYS:HZ1	1.74	0.52
3:D:186:GLU:C	3:D:210:ARG:NH2	2.62	0.52
3:D:79:ALA:C	3:D:81:ASP:N	2.62	0.52
3:F:134:PHE:O	3:F:135:LEU:HG	2.09	0.52
3:F:131:VAL:CG2	3:F:178:LEU:HB3	2.40	0.52
1:A:319:LEU:C	1:A:319:LEU:HD12	2.28	0.52
1:A:171:ASP:C	1:A:175:HIS:HD2	2.12	0.52
3:F:180:LEU:HD22	3:F:184:GLU:HG2	1.91	0.52
3:F:65:GLY:O	3:F:66:SER:HB3	2.09	0.52
1:B:163:LEU:HD22	1:B:174:ARG:HA	1.92	0.52
1:B:241:VAL:O	1:B:241:VAL:HG12	2.10	0.52
1:B:163:LEU:CD1	1:B:168:LEU:HB2	2.38	0.52
3:D:53:LEU:HD22	3:D:57:VAL:CG1	2.40	0.52
3:F:153:GLU:OE2	3:F:155:GLN:HG3	2.10	0.52
3:D:186:GLU:HA	3:D:210:ARG:HH22	0.71	0.51
3:F:149:ILE:HD12	3:F:154:ARG:NE	2.25	0.51
3:F:183:ASP:O	3:F:186:GLU:N	2.43	0.51
3:D:89:GLN:NE2	3:D:91:SER:N	2.50	0.51
2:E:47:TRP:CG	3:F:95:GLN:NE2	2.77	0.51
1:B:418:ASN:ND2	1:B:420:GLN:HE22	2.08	0.51
1:A:150:PRO:HD3	1:A:354:GLY:HA2	1.90	0.51
1:B:357:PHE:CE1	1:B:398:LEU:HD22	2.45	0.51
2:E:163:ASN:CB	2:E:166:SER:OG	2.58	0.51
2:C:129:VAL:HG21	2:C:214:VAL:HG21	1.90	0.51
1:B:150:PRO:HD3	1:B:354:GLY:HA2	1.91	0.51
1:A:22:ILE:HG12	1:B:453:LEU:HB3	1.93	0.51
3:D:48:TYR:C	3:D:48:TYR:CD1	2.83	0.51
1:A:317:PHE:O	1:A:319:LEU:N	2.43	0.51
3:D:46:TRP:CE3	3:D:46:TRP:HA	2.45	0.51
3:D:180:LEU:HD22	3:D:184:GLU:OE2	2.11	0.51
3:D:11:MET:HG3	3:D:11:MET:O	2.10	0.51
3:D:60:ARG:NE	3:D:78:GLU:HG2	2.26	0.51
3:F:90:TRP:CH2	3:F:93:HIS:ND1	2.66	0.51
1:A:388:THR:HG22	1:A:421:LEU:HD21	1.92	0.51
1:A:278:ASP:O	1:A:281:HIS:N	2.43	0.51
1:B:248:PRO:HB2	1:B:251:THR:HG23	1.92	0.51
1:B:183:ALA:HB2	1:B:200:ILE:CG1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:65:GLY:HA3	3:D:70:TYR:HA	1.92	0.51
2:E:143:MET:HA	2:E:191:VAL:O	2.10	0.51
3:F:89:GLN:O	3:F:91:SER:N	2.43	0.51
1:A:150:PRO:O	1:A:154:ILE:HG13	2.11	0.51
2:C:178:LEU:HB2	2:C:183:TYR:HE2	1.73	0.51
2:E:98:ARG:NH2	2:E:109:ASP:OD2	2.40	0.51
2:C:29:TYR:OH	2:C:79:LEU:HB2	2.10	0.51
2:C:53:PRO:HA	2:C:72:ARG:NH1	2.25	0.51
1:A:90:ALA:CB	1:A:299:GLY:HA3	2.41	0.51
1:A:17:ARG:C	1:A:19:ARG:N	2.64	0.51
2:E:144:VAL:N	2:E:191:VAL:O	2.35	0.51
2:E:51:ILE:O	2:E:51:ILE:HG23	2.11	0.51
1:A:362:ALA:O	1:A:366:VAL:HG23	2.10	0.51
1:B:205:ARG:HG3	1:B:213:ILE:CD1	2.40	0.50
1:A:198:LEU:HG	1:A:410:ILE:HD12	1.92	0.50
1:B:148:GLU:CD	1:B:357:PHE:HB3	2.31	0.50
2:E:40:ALA:O	2:E:43:LYS:HB2	2.10	0.50
1:B:317:PHE:O	1:B:319:LEU:N	2.45	0.50
2:E:189:VAL:HG13	2:E:189:VAL:O	2.11	0.50
2:E:179:GLN:O	2:E:180:ALA:HB3	2.12	0.50
3:D:117:PHE:N	3:D:117:PHE:HD1	2.08	0.50
3:D:123:GLN:HE22	3:D:130:SER:CB	2.23	0.50
3:D:10:ILE:HA	3:D:102:LYS:HB3	1.93	0.50
1:A:426:ILE:CG2	1:B:223:ILE:HD11	2.42	0.50
1:B:388:THR:HG22	1:B:421:LEU:HD21	1.93	0.50
2:E:40:ALA:HA	2:E:92:ALA:CB	2.42	0.50
1:A:399:ALA:O	1:A:403:ARG:HA	2.10	0.50
1:A:433:THR:HG21	1:B:216:LYS:HE2	1.92	0.50
2:C:174:PHE:N	2:C:174:PHE:CD2	2.79	0.50
3:D:47:ILE:HD13	3:D:72:LEU:HD11	1.92	0.50
3:D:185:TYR:C	3:D:187:ARG:H	2.15	0.50
1:A:241:VAL:HG12	1:A:241:VAL:O	2.11	0.50
1:B:340:ARG:O	1:B:341:VAL:C	2.49	0.50
3:D:189:ASN:OD1	3:D:209:ASN:HB3	2.12	0.50
3:F:191:TYR:HB2	3:F:208:PHE:HE2	1.73	0.50
1:B:83:PHE:CD1	1:B:83:PHE:C	2.84	0.50
1:B:171:ASP:HB3	1:B:175:HIS:CE1	2.47	0.50
3:F:145:VAL:HG11	3:F:176:SER:OG	2.12	0.50
3:F:72:LEU:HD23	3:F:73:THR:N	2.27	0.50
1:B:252:LEU:HD11	1:B:423:LEU:HD23	1.93	0.50
1:A:70:HIS:O	1:A:70:HIS:ND1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:ILE:HG22	1:B:402:ILE:O	2.11	0.50
3:F:27:SER:O	3:F:68:THR:HG22	2.11	0.49
1:B:107:SER:N	4:B:466:SEK:SE	2.83	0.49
3:D:88:GLN:HG2	3:D:89:GLN:N	2.27	0.49
2:C:6:GLU:CG	2:C:96:CYS:SG	2.96	0.49
1:A:207:GLN:HG3	1:B:28:ARG:HD2	1.93	0.49
2:C:53:PRO:O	2:C:55:SER:N	2.45	0.49
1:A:163:LEU:HD22	1:A:174:ARG:HA	1.93	0.49
3:F:38:LYS:H	3:F:41:THR:CG2	2.25	0.49
3:D:74:ILE:HG22	3:D:77:MET:CA	2.40	0.49
1:A:360:MET:CG	1:A:397:LEU:HD23	2.42	0.49
1:A:163:LEU:CD1	1:A:168:LEU:HB2	2.42	0.49
1:B:399:ALA:O	1:B:403:ARG:HA	2.13	0.49
1:A:38:MET:HG3	1:A:168:LEU:HD11	1.93	0.49
2:C:24:ALA:HB1	2:C:27:PHE:CZ	2.48	0.49
3:D:16:GLY:O	3:D:17:ASP:HB2	2.13	0.49
2:C:156:GLU:HG2	2:C:183:TYR:CE1	2.47	0.49
2:C:195:SER:C	2:C:198:SER:HB2	2.32	0.49
3:D:208:PHE:HD1	3:D:209:ASN:N	2.10	0.49
1:B:457:GLU:O	1:B:458:ALA:HB2	2.13	0.49
3:D:166:ASP:C	3:D:168:LYS:H	2.16	0.49
1:A:17:ARG:C	1:A:19:ARG:H	2.15	0.49
1:B:131:LYS:HE2	1:B:153:GLN:NE2	2.28	0.49
3:D:188:HIS:O	3:D:210:ARG:CG	2.60	0.49
1:B:422:ILE:HG23	1:B:423:LEU:N	2.27	0.49
2:C:156:GLU:OE1	2:C:157:PRO:HA	2.12	0.49
1:B:330:MET:HE3	1:B:330:MET:CA	2.42	0.49
1:A:298:ILE:HG23	1:A:346:LEU:HD23	1.95	0.49
1:B:205:ARG:CD	1:B:213:ILE:HD12	2.43	0.49
1:B:97:VAL:HG21	1:B:353:PRO:HD3	1.95	0.49
2:E:143:MET:HB3	2:E:190:THR:HG23	1.93	0.49
3:F:192:THR:HA	3:F:207:SER:CB	2.43	0.49
2:C:207:HIS:CD2	2:C:209:ALA:HB3	2.47	0.49
3:F:32:ILE:HG22	3:F:89:GLN:CA	2.42	0.49
1:B:163:LEU:HD21	1:B:174:ARG:HG3	1.95	0.49
3:F:148:LYS:HA	3:F:152:SER:O	2.12	0.49
1:B:75:TYR:CE2	1:B:79:LEU:HD11	2.47	0.49
3:D:85:TYR:HE1	3:D:103:LEU:HD23	1.78	0.49
3:D:35:TYR:O	3:D:85:TYR:HA	2.12	0.49
3:F:90:TRP:O	3:F:90:TRP:HE3	1.94	0.49
3:F:143:ILE:HG22	3:F:174:MET:CE	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:ILE:HG23	1:A:423:LEU:N	2.27	0.49
2:C:30:SER:C	2:C:32:TYR:N	2.65	0.49
1:A:163:LEU:HD21	1:A:174:ARG:HG3	1.95	0.49
1:B:165:ILE:HG22	1:B:166:PHE:N	2.26	0.49
1:A:98:ARG:HD2	1:A:291:TRP:CD2	2.47	0.49
3:D:189:ASN:O	3:D:209:ASN:HA	2.13	0.49
1:A:18:ARG:O	1:A:22:ILE:HG13	2.13	0.49
1:B:449:LEU:HA	1:B:452:THR:CG2	2.42	0.49
1:B:360:MET:CG	1:B:397:LEU:HD23	2.43	0.49
1:A:108:GLY:CA	1:A:153:GLN:NE2	2.76	0.49
1:A:383:HIS:CE1	3:D:90:TRP:CZ2	3.01	0.49
1:B:90:ALA:CB	1:B:299:GLY:HA3	2.43	0.49
1:B:98:ARG:HD2	1:B:291:TRP:CD2	2.48	0.49
3:F:8:PRO:O	3:F:101:THR:HG23	2.13	0.48
1:A:75:TYR:CE2	1:A:79:LEU:HD11	2.48	0.48
3:F:32:ILE:HG22	3:F:88:GLN:O	2.13	0.48
2:E:36:TRP:CZ2	2:E:81:LEU:HB2	2.48	0.48
2:E:127:PRO:CB	2:E:153:TYR:HB3	2.42	0.48
1:A:165:ILE:HG22	1:A:166:PHE:N	2.28	0.48
1:A:183:ALA:HB2	1:A:200:ILE:CG1	2.42	0.48
3:F:189:ASN:HA	3:F:210:ARG:CB	2.41	0.48
3:D:114:VAL:HG22	3:D:135:LEU:CD1	2.39	0.48
1:A:205:ARG:CD	1:A:213:ILE:HD12	2.43	0.48
1:B:38:MET:HA	1:B:41:VAL:HG12	1.95	0.48
3:D:47:ILE:CD1	3:D:72:LEU:HD11	2.43	0.48
1:B:95:PHE:O	1:B:97:VAL:N	2.45	0.48
3:D:29:VAL:HG23	3:D:70:TYR:CE1	2.47	0.48
1:B:320:ILE:HB	1:B:321:PRO:HD3	1.95	0.48
3:F:76:THR:HG22	3:F:76:THR:O	2.12	0.48
3:D:107:ARG:NH1	3:D:108:ALA:HB3	2.29	0.48
2:C:150:VAL:HG22	2:C:205:VAL:HG21	1.94	0.48
1:A:426:ILE:HG22	1:B:223:ILE:HD11	1.94	0.48
1:B:150:PRO:O	1:B:154:ILE:HG13	2.13	0.48
1:A:86:SER:OG	1:A:303:GLY:HA3	2.13	0.48
1:B:356:ILE:O	1:B:356:ILE:HG12	2.13	0.48
1:A:330:MET:CA	1:A:330:MET:HE3	2.44	0.48
3:D:6:GLN:HE22	3:D:87:CYS:N	2.10	0.48
2:C:158:VAL:HG12	2:C:207:HIS:HB2	1.95	0.48
3:F:77:MET:CE	3:F:103:LEU:HD11	2.44	0.48
2:E:16:GLY:O	2:E:85:LYS:N	2.47	0.48
1:A:36:LEU:HD13	1:B:434:LEU:CD2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:150:VAL:HG22	2:E:205:VAL:HG21	1.96	0.48
3:F:186:GLU:O	3:F:210:ARG:NE	2.47	0.48
1:B:278:ASP:O	1:B:281:HIS:N	2.42	0.48
3:D:102:LYS:HG3	3:D:104:GLU:HG3	1.96	0.48
1:A:433:THR:HG22	1:B:216:LYS:CE	2.43	0.48
2:E:135:GLY:O	2:E:138:ALA:HB2	2.14	0.48
2:C:106:TRP:HD1	2:C:106:TRP:H	1.56	0.48
1:A:356:ILE:HG12	1:A:356:ILE:O	2.13	0.48
1:A:230:ARG:CG	1:A:230:ARG:HH11	2.26	0.48
1:A:37:PHE:HD2	1:A:38:MET:CE	2.27	0.48
1:A:320:ILE:HB	1:A:321:PRO:HD3	1.96	0.48
1:A:270:ASN:HA	1:A:273:VAL:HG12	1.95	0.48
3:D:17:ASP:O	3:D:76:THR:HA	2.13	0.48
2:C:185:LEU:CD1	2:C:185:LEU:C	2.83	0.48
2:C:72:ARG:O	2:C:72:ARG:HG3	2.14	0.48
1:B:126:ARG:HH11	1:B:126:ARG:HG2	1.79	0.48
1:B:108:GLY:CA	1:B:153:GLN:NE2	2.77	0.48
1:B:93:GLY:O	1:B:97:VAL:HG23	2.13	0.48
1:A:262:PHE:CZ	1:A:367:LEU:HD23	2.49	0.48
3:F:53:LEU:HD21	3:F:61:PHE:O	2.13	0.48
3:D:146:LYS:HD3	3:D:153:GLU:CD	2.34	0.47
1:B:144:VAL:HG12	1:B:144:VAL:O	2.14	0.47
2:C:200:THR:HG23	2:C:200:THR:O	2.14	0.47
1:A:119:GLN:HA	1:A:119:GLN:NE2	2.28	0.47
1:B:86:SER:HB3	1:B:299:GLY:O	2.14	0.47
1:A:83:PHE:C	1:A:83:PHE:CD1	2.86	0.47
3:F:6:GLN:NE2	3:F:98:GLY:HA3	2.29	0.47
1:B:183:ALA:HB2	1:B:200:ILE:HG12	1.95	0.47
1:A:183:ALA:HB2	1:A:200:ILE:HG12	1.95	0.47
1:B:229:TYR:CE1	1:B:233:ASN:ND2	2.78	0.47
3:D:135:LEU:HG	3:D:174:MET:CE	2.44	0.47
1:A:430:LEU:HD22	1:B:223:ILE:HD12	1.96	0.47
1:A:77:LEU:O	1:A:81:VAL:HG13	2.14	0.47
3:D:164:ASP:O	3:D:165:GLN:O	2.31	0.47
3:F:143:ILE:HG12	3:F:197:HIS:HB2	1.96	0.47
1:A:180:THR:HG22	1:A:218:VAL:CA	2.39	0.47
1:B:247:ALA:CB	1:B:424:PRO:HG2	2.44	0.47
1:B:298:ILE:HG23	1:B:346:LEU:HD23	1.95	0.47
3:D:181:THR:O	3:D:182:LYS:C	2.53	0.47
3:D:57:VAL:CG1	3:D:58:PRO:HD2	2.45	0.47
1:A:247:ALA:CB	1:A:424:PRO:HG2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ASN:HD22	1:A:420:GLN:HE22	1.62	0.47
3:F:169:ASP:OD1	3:F:170:SER:N	2.48	0.47
2:E:174:PHE:CD1	3:F:163:THR:HG23	2.50	0.47
2:C:18:LEU:CD2	2:C:18:LEU:H	2.27	0.47
2:C:165:GLY:C	2:C:167:LEU:H	2.18	0.47
3:F:186:GLU:CA	3:F:210:ARG:HD2	2.41	0.47
1:A:219:PHE:HB3	1:B:430:LEU:CD1	2.42	0.47
3:D:194:GLU:HG2	3:D:205:VAL:HG12	1.96	0.47
3:D:106:LEU:HA	3:D:139:TYR:OH	2.14	0.47
3:D:139:TYR:HA	3:D:140:PRO:C	2.35	0.47
2:C:69:ILE:N	2:C:69:ILE:HD12	2.30	0.47
1:A:202:GLU:OE2	1:A:406:LEU:HB3	2.15	0.47
1:B:86:SER:OG	1:B:303:GLY:HA3	2.15	0.47
2:E:181:ALA:O	2:E:182:LEU:HD23	2.15	0.47
1:A:144:VAL:HG21	1:A:343:THR:HB	1.96	0.47
2:E:18:LEU:HG	2:E:19:LYS:N	2.29	0.47
1:B:226:THR:O	1:B:230:ARG:HG3	2.14	0.47
2:E:146:LEU:HD23	2:E:146:LEU:N	2.30	0.47
3:F:143:ILE:HG22	3:F:174:MET:HE3	1.96	0.47
3:D:154:ARG:NH2	3:D:180:LEU:CD2	2.78	0.47
3:F:54:THR:CG2	3:F:55:SER:H	2.17	0.47
1:A:148:GLU:CD	1:A:357:PHE:HB3	2.35	0.47
1:A:144:VAL:O	1:A:144:VAL:HG12	2.15	0.47
3:D:158:VAL:HG12	3:D:159:LEU:N	2.30	0.47
2:C:12:VAL:HG23	2:C:119:VAL:HG22	1.96	0.47
1:B:24:GLN:O	1:B:27:GLU:N	2.40	0.47
2:C:129:VAL:CG2	2:C:214:VAL:HG21	2.44	0.46
2:C:178:LEU:CD1	2:C:182:LEU:H	2.28	0.46
2:E:50:GLU:OE2	2:E:59:ASN:ND2	2.48	0.46
1:A:27:GLU:HA	1:A:27:GLU:OE1	2.15	0.46
3:D:75:ASN:C	3:D:76:THR:HG22	2.24	0.46
1:A:421:LEU:O	1:A:425:MET:HG3	2.15	0.46
1:A:255:TYR:CD2	1:A:424:PRO:HB3	2.50	0.46
2:C:178:LEU:HD12	2:C:178:LEU:C	2.36	0.46
1:A:457:GLU:HB3	1:B:19:ARG:NH2	2.30	0.46
3:F:4:LEU:HA	3:F:24:SER:O	2.15	0.46
3:D:114:VAL:HG11	3:D:206:LYS:HB2	1.97	0.46
1:A:38:MET:HA	1:A:41:VAL:HG12	1.96	0.46
3:D:107:ARG:NH2	3:D:171:THR:CG2	2.78	0.46
1:A:108:GLY:HA3	1:A:153:GLN:NE2	2.30	0.46
2:E:190:THR:O	2:E:191:VAL:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:183:ASP:O	3:F:184:GLU:C	2.54	0.46
3:F:33:HIS:O	3:F:87:CYS:HA	2.16	0.46
1:A:62:ASN:O	1:A:63:GLN:C	2.54	0.46
3:D:123:GLN:HG2	3:D:128:GLY:C	2.36	0.46
1:B:108:GLY:HA3	1:B:153:GLN:NE2	2.30	0.46
1:B:35:ILE:CG2	1:B:176:THR:HG21	2.45	0.46
1:A:201:ILE:HG13	1:A:201:ILE:O	2.16	0.46
1:A:22:ILE:CD1	1:B:453:LEU:HB3	2.46	0.46
1:B:456:GLN:O	1:B:456:GLN:HG2	2.15	0.46
3:F:21:MET:HG2	3:F:21:MET:H	1.66	0.46
3:F:188:HIS:O	3:F:210:ARG:NE	2.47	0.46
2:C:147:GLY:HA2	2:C:162:TRP:HZ2	1.79	0.46
1:A:207:GLN:CG	1:B:28:ARG:HH11	2.19	0.46
1:B:309:ALA:O	1:B:311:ALA:N	2.49	0.46
2:E:105:TYR:CE1	3:F:31:TYR:CD2	3.02	0.46
1:B:148:GLU:OE1	1:B:357:PHE:CB	2.64	0.46
2:E:143:MET:HE3	2:E:191:VAL:N	2.30	0.46
1:A:423:LEU:HB3	1:A:424:PRO:CD	2.42	0.46
1:B:70:HIS:ND1	1:B:70:HIS:O	2.49	0.46
1:A:270:ASN:HA	1:A:273:VAL:CG1	2.45	0.46
1:B:451:ARG:C	1:B:453:LEU:H	2.20	0.46
3:D:107:ARG:HH11	3:D:108:ALA:HB3	1.81	0.46
1:B:376:VAL:HG12	1:B:376:VAL:O	2.16	0.46
2:E:22:CYS:HB3	2:E:79:LEU:HB3	1.97	0.46
1:A:35:ILE:CG2	1:A:176:THR:HG21	2.46	0.46
3:D:163:THR:OG1	3:D:173:SER:HB2	2.16	0.46
3:D:14:ALA:O	3:D:17:ASP:HB3	2.16	0.45
3:D:16:GLY:CA	3:D:76:THR:OG1	2.42	0.45
3:F:6:GLN:HE21	3:F:98:GLY:HA3	1.81	0.45
2:E:40:ALA:O	2:E:43:LYS:CB	2.65	0.45
1:A:116:LEU:HD23	1:A:178:LEU:HD23	1.97	0.45
1:B:262:PHE:CZ	1:B:367:LEU:HD23	2.50	0.45
2:C:175:PRO:HD2	3:D:161:SER:OG	2.16	0.45
1:A:124:TRP:CA	1:A:157:ASN:HD22	2.24	0.45
1:B:109:ILE:N	1:B:110:PRO:CD	2.79	0.45
1:B:136:LEU:N	1:B:136:LEU:HD12	2.31	0.45
1:B:274:LEU:O	1:B:277:GLN:HB2	2.16	0.45
3:D:77:MET:HE2	3:D:77:MET:O	2.16	0.45
1:B:127:VAL:O	1:B:128:LEU:C	2.55	0.45
1:A:146:GLY:HA3	1:A:148:GLU:OE2	2.16	0.45
3:F:6:GLN:HE21	3:F:99:GLY:N	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ARG:HG2	1:A:126:ARG:HH11	1.82	0.45
1:A:205:ARG:CG	1:A:213:ILE:HD12	2.47	0.45
1:B:116:LEU:HD23	1:B:178:LEU:HD23	1.99	0.45
3:F:73:THR:CG2	3:F:74:ILE:N	2.79	0.45
1:A:269:PHE:O	1:A:273:VAL:HG12	2.16	0.45
3:F:188:HIS:N	3:F:188:HIS:ND1	2.64	0.45
2:E:36:TRP:NE1	2:E:81:LEU:HB2	2.32	0.45
1:A:30:LYS:HA	1:B:437:GLN:NE2	2.31	0.45
1:B:77:LEU:O	1:B:81:VAL:HG13	2.17	0.45
1:B:27:GLU:HA	1:B:27:GLU:OE1	2.16	0.45
1:B:312:THR:HG22	1:B:339:ALA:CB	2.46	0.45
3:F:6:GLN:O	3:F:7:SER:O	2.34	0.45
1:A:197:ILE:HD13	1:A:219:PHE:CE1	2.52	0.45
1:B:269:PHE:O	1:B:273:VAL:HG12	2.17	0.45
3:D:2:ILE:HG22	3:D:3:VAL:N	2.32	0.45
3:F:38:LYS:O	3:F:39:SER:C	2.55	0.45
3:D:53:LEU:HD22	3:D:57:VAL:HG11	1.99	0.45
1:A:109:ILE:HG21	1:A:445:TYR:CE2	2.51	0.45
1:B:455:LYS:C	1:B:457:GLU:N	2.70	0.45
2:C:68:PHE:CE2	2:C:83:ILE:HG23	2.51	0.45
3:F:205:VAL:O	3:F:205:VAL:HG23	2.16	0.45
1:A:287:ASN:HD22	1:A:290:LYS:CG	2.23	0.45
1:A:252:LEU:HD11	1:A:423:LEU:HD23	1.98	0.45
1:B:200:ILE:HD13	1:B:204:MET:HG3	1.98	0.45
3:D:89:GLN:C	3:D:89:GLN:NE2	2.71	0.44
1:B:235:GLU:OE1	2:C:100:TYR:CE2	2.61	0.44
3:D:54:THR:HB	3:D:57:VAL:CG2	2.47	0.44
3:F:149:ILE:HD13	3:F:191:TYR:CE2	2.48	0.44
3:F:192:THR:HA	3:F:207:SER:HB2	1.98	0.44
3:F:33:HIS:CD2	3:F:88:GLN:OE1	2.69	0.44
3:F:124:LEU:HD23	3:F:128:GLY:O	2.17	0.44
1:A:230:ARG:NH1	1:A:230:ARG:HG3	2.27	0.44
1:A:317:PHE:O	1:A:318:ASN:C	2.54	0.44
1:B:176:THR:HG22	1:B:177:LEU:N	2.31	0.44
2:C:158:VAL:HG23	2:C:185:LEU:HD21	2.00	0.44
1:B:59:TRP:CE3	1:B:60:LEU:HD23	2.52	0.44
1:A:150:PRO:CD	1:A:354:GLY:HA2	2.47	0.44
2:E:174:PHE:CE1	3:F:163:THR:HG23	2.53	0.44
2:E:221:ARG:NH1	3:F:118:PRO:HG2	2.32	0.44
1:A:223:ILE:CD1	1:B:430:LEU:HD22	2.47	0.44
2:E:47:TRP:CD2	3:F:95:GLN:NE2	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:29:VAL:HG23	3:D:70:TYR:HE1	1.81	0.44
1:A:24:GLN:O	1:A:27:GLU:N	2.39	0.44
1:B:260:ILE:HG23	1:B:435:LEU:HG	2.00	0.44
1:A:313:SER:OG	1:A:314:GLY:N	2.51	0.44
3:D:141:LYS:CB	3:D:172:TYR:CD1	2.93	0.44
2:C:132:LEU:CB	2:C:147:GLY:O	2.57	0.44
2:E:29:TYR:CE1	2:E:34:MET:HE2	2.52	0.44
1:A:74:ASN:O	1:A:78:LEU:HD13	2.17	0.44
2:C:109:ASP:C	2:C:109:ASP:OD1	2.56	0.44
1:A:264:ILE:O	1:A:267:PRO:HD2	2.18	0.44
3:D:60:ARG:HG2	3:D:60:ARG:HH11	1.82	0.44
2:E:47:TRP:CZ2	2:E:49:GLY:CA	3.01	0.44
3:D:189:ASN:HA	3:D:210:ARG:HD3	2.00	0.44
3:D:17:ASP:C	3:D:17:ASP:OD1	2.56	0.44
1:B:421:LEU:O	1:B:425:MET:HG3	2.18	0.44
2:E:86:VAL:HG12	2:E:90:ASP:HB2	2.00	0.44
3:F:154:ARG:HE	3:F:154:ARG:HB2	1.71	0.44
3:F:192:THR:HG22	3:F:207:SER:CB	2.48	0.44
2:C:127:PRO:HB2	2:C:150:VAL:HG13	1.99	0.44
3:D:7:SER:HB2	3:D:22:THR:HB	1.99	0.44
1:B:287:ASN:HD22	1:B:290:LYS:CG	2.24	0.44
1:B:62:ASN:O	1:B:63:GLN:C	2.56	0.44
2:E:153:TYR:CE1	2:E:183:TYR:HB2	2.53	0.44
1:B:74:ASN:O	1:B:78:LEU:HD13	2.18	0.44
1:B:224:MET:O	1:B:228:MET:HG2	2.17	0.44
2:C:18:LEU:HD22	2:C:18:LEU:H	1.81	0.44
1:A:60:LEU:O	1:A:64:ARG:HG3	2.17	0.44
3:D:46:TRP:HB3	3:D:47:ILE:H	1.61	0.44
1:B:35:ILE:HG21	1:B:176:THR:HG21	1.99	0.44
2:C:135:GLY:N	2:C:138:ALA:HB2	2.33	0.44
2:C:86:VAL:O	2:C:86:VAL:HG23	2.17	0.44
3:F:164:ASP:O	3:F:165:GLN:C	2.55	0.44
1:B:18:ARG:O	1:B:19:ARG:C	2.54	0.43
3:F:135:LEU:HB2	3:F:174:MET:HB3	2.00	0.43
3:D:10:ILE:HG22	3:D:11:MET:N	2.33	0.43
1:B:37:PHE:HD2	1:B:38:MET:CE	2.31	0.43
3:D:6:GLN:HE22	3:D:86:TYR:CA	2.32	0.43
3:D:6:GLN:HG3	3:D:100:GLY:CA	2.46	0.43
3:F:21:MET:HB3	3:F:101:THR:HG21	2.00	0.43
1:A:59:TRP:CE3	1:A:60:LEU:HD23	2.53	0.43
1:B:255:TYR:CD2	1:B:424:PRO:HB3	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:LYS:CG	1:B:100:TYR:CD2	3.01	0.43
1:B:270:ASN:OD1	1:B:444:LEU:HB2	2.18	0.43
1:A:227:ILE:O	1:A:231:ILE:HG13	2.18	0.43
2:E:163:ASN:ND2	2:E:167:LEU:CD2	2.81	0.43
3:D:57:VAL:HG13	3:D:58:PRO:HD2	2.00	0.43
1:A:128:LEU:HB2	1:A:129:PRO:CD	2.48	0.43
3:D:38:LYS:O	3:D:41:THR:HG22	2.17	0.43
1:A:86:SER:HB3	1:A:299:GLY:O	2.18	0.43
3:F:90:TRP:CE3	3:F:90:TRP:HA	2.54	0.43
2:C:52:ASN:CB	2:C:53:PRO:CD	2.89	0.43
2:E:162:TRP:CZ3	2:E:203:CYS:CB	2.96	0.43
1:A:376:VAL:HG12	1:A:376:VAL:O	2.17	0.43
1:B:270:ASN:HA	1:B:273:VAL:HG12	1.99	0.43
2:C:34:MET:HB3	2:C:79:LEU:HD22	2.01	0.43
2:C:67:LYS:NZ	2:C:85:LYS:O	2.52	0.43
3:D:185:TYR:O	3:D:187:ARG:N	2.51	0.43
2:C:18:LEU:CD2	2:C:18:LEU:N	2.81	0.43
3:F:109:ASP:HB3	3:F:199:THR:CG2	2.48	0.43
3:F:134:PHE:O	3:F:135:LEU:CG	2.66	0.43
1:B:37:PHE:HD2	1:B:38:MET:HE2	1.84	0.43
2:C:84:SER:O	2:C:85:LYS:C	2.55	0.43
3:D:150:ASP:OD2	3:D:188:HIS:HB3	2.19	0.43
1:A:207:GLN:HE21	1:B:28:ARG:HD2	1.84	0.43
1:A:107:SER:HB2	1:A:348:PHE:CZ	2.53	0.43
1:A:216:LYS:NZ	1:B:433:THR:HG22	2.33	0.43
3:F:169:ASP:O	3:F:170:SER:CB	2.64	0.43
1:B:205:ARG:CG	1:B:213:ILE:HD12	2.49	0.43
1:A:176:THR:O	1:A:179:ALA:N	2.52	0.43
1:A:116:LEU:CD2	1:A:178:LEU:HD23	2.48	0.43
2:E:185:LEU:O	2:E:185:LEU:HD12	2.19	0.43
1:B:208:PHE:CD1	1:B:208:PHE:N	2.87	0.43
1:A:184:ALA:HB1	1:A:225:SER:HB2	2.00	0.43
3:D:208:PHE:HD1	3:D:208:PHE:C	2.22	0.43
3:D:53:LEU:HD22	3:D:57:VAL:CB	2.49	0.43
1:B:270:ASN:HA	1:B:273:VAL:CG1	2.49	0.43
1:A:36:LEU:HD13	1:B:434:LEU:HD21	2.01	0.43
1:A:402:ILE:O	1:A:402:ILE:HG22	2.19	0.43
1:B:128:LEU:HB2	1:B:129:PRO:CD	2.48	0.43
1:B:150:PRO:CD	1:B:354:GLY:HA2	2.49	0.43
2:C:2:VAL:CG2	2:C:2:VAL:O	2.67	0.43
1:B:109:ILE:HG21	1:B:445:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:TRP:CA	1:B:157:ASN:HD22	2.25	0.43
1:B:270:ASN:O	1:B:273:VAL:CG1	2.67	0.43
1:B:264:ILE:O	1:B:267:PRO:HD2	2.19	0.43
1:B:423:LEU:HB3	1:B:424:PRO:CD	2.43	0.42
2:C:69:ILE:HB	2:C:82:GLN:HB2	2.01	0.42
1:B:317:PHE:O	1:B:318:ASN:C	2.57	0.42
1:A:246:ASP:O	1:A:248:PRO:HD3	2.19	0.42
3:D:47:ILE:HD13	3:D:72:LEU:CD1	2.49	0.42
2:C:111:TRP:N	2:C:111:TRP:CD1	2.86	0.42
1:A:433:THR:HG22	1:B:216:LYS:NZ	2.34	0.42
2:E:16:GLY:C	2:E:86:VAL:HG23	2.39	0.42
1:A:91:MET:HG3	1:A:296:GLY:CA	2.48	0.42
1:B:116:LEU:CD2	1:B:178:LEU:HD23	2.49	0.42
1:B:378:LEU:HD23	1:B:378:LEU:N	2.33	0.42
2:C:108:PHE:CE1	3:D:97:PHE:CZ	3.08	0.42
1:A:136:LEU:HD12	1:A:136:LEU:N	2.34	0.42
1:A:449:LEU:O	1:A:453:LEU:HB2	2.19	0.42
3:D:6:GLN:HE22	3:D:86:TYR:HA	1.80	0.42
1:B:418:ASN:HD22	1:B:420:GLN:HE22	1.66	0.42
3:D:30:SER:O	3:D:31:TYR:HB2	2.20	0.42
3:D:48:TYR:O	3:D:49:ASP:HB2	2.19	0.42
2:E:178:LEU:HD12	2:E:182:LEU:O	2.19	0.42
1:B:161:MET:O	1:B:161:MET:HG2	2.19	0.42
1:B:222:VAL:O	1:B:225:SER:HB3	2.18	0.42
1:A:270:ASN:OD1	1:A:444:LEU:HB2	2.19	0.42
3:F:183:ASP:O	3:F:185:TYR:N	2.51	0.42
1:A:28:ARG:HE	1:B:443:PRO:HG2	1.84	0.42
1:A:430:LEU:CD1	1:B:219:PHE:HB3	2.49	0.42
1:B:403:ARG:HD2	1:B:433:THR:HG23	2.02	0.42
1:A:35:ILE:HG21	1:A:176:THR:HG21	2.01	0.42
1:A:456:GLN:C	1:A:458:ALA:H	2.21	0.42
1:B:279:LEU:HD23	1:B:279:LEU:C	2.40	0.42
2:C:153:TYR:CE1	2:C:158:VAL:HG13	2.55	0.42
2:C:47:TRP:CE2	3:D:95:GLN:NE2	2.87	0.42
3:D:4:LEU:HD11	3:D:89:GLN:HG2	2.02	0.42
2:E:20:LEU:HD13	2:E:115:THR:CG2	2.50	0.42
1:B:163:LEU:CD2	1:B:174:ARG:HA	2.49	0.42
3:F:15:PRO:HD3	3:F:105:ILE:CG2	2.49	0.42
2:E:111:TRP:N	2:E:111:TRP:CD1	2.87	0.42
3:D:210:ARG:HH11	3:D:210:ARG:HG2	1.84	0.42
2:E:31:ARG:NH1	2:E:31:ARG:CG	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:116:ILE:HD12	3:F:193:CYS:CB	2.47	0.42
2:C:212:THR:CG2	2:C:213:LYS:N	2.82	0.42
2:C:106:TRP:CD1	2:C:106:TRP:N	2.79	0.42
3:D:147:TRP:O	3:D:154:ARG:HB3	2.19	0.42
1:A:244:LEU:N	1:A:418:ASN:HD21	2.04	0.42
1:B:72:ALA:HA	1:B:78:LEU:HD21	2.02	0.42
1:B:136:LEU:H	1:B:136:LEU:CD1	2.32	0.42
1:A:417:ASP:O	1:A:417:ASP:OD1	2.37	0.42
3:D:90:TRP:CE3	3:D:95:GLN:OE1	2.73	0.42
3:F:88:GLN:HG2	3:F:89:GLN:H	1.81	0.42
1:B:380:PRO:HG2	3:F:93:HIS:HB3	2.02	0.42
2:E:91:THR:O	2:E:91:THR:HG22	2.20	0.42
2:E:76:LYS:O	2:E:77:ASP:HB2	2.20	0.42
1:B:109:ILE:HD13	1:B:445:TYR:HE2	1.84	0.42
3:F:65:GLY:O	3:F:66:SER:CB	2.67	0.42
2:E:98:ARG:O	2:E:109:ASP:HB3	2.20	0.42
1:A:108:GLY:HA3	1:A:153:GLN:HE21	1.84	0.42
2:C:41:PRO:HD3	2:C:92:ALA:HA	2.01	0.42
1:A:293:LEU:C	1:A:295:GLY:N	2.72	0.42
1:B:451:ARG:C	1:B:453:LEU:N	2.73	0.42
3:D:74:ILE:HG22	3:D:77:MET:N	2.35	0.42
1:B:60:LEU:O	1:B:64:ARG:HG3	2.20	0.42
1:B:128:LEU:HD23	1:B:128:LEU:HA	1.88	0.42
3:D:139:TYR:CA	3:D:140:PRO:O	2.66	0.42
3:D:47:ILE:HD12	3:D:47:ILE:N	2.35	0.42
1:A:224:MET:O	1:A:228:MET:HG2	2.20	0.42
3:D:117:PHE:HA	3:D:118:PRO:HD3	1.95	0.41
3:D:183:ASP:OD2	3:D:187:ARG:NH2	2.53	0.41
3:F:7:SER:HB2	3:F:22:THR:CA	2.49	0.41
1:A:127:VAL:O	1:A:128:LEU:C	2.58	0.41
1:A:403:ARG:HD2	1:A:433:THR:HG23	2.01	0.41
2:E:150:VAL:HB	2:E:185:LEU:HD12	2.02	0.41
1:A:187:ALA:O	1:A:191:ASN:N	2.53	0.41
3:F:85:TYR:CD1	3:F:85:TYR:N	2.88	0.41
1:B:313:SER:OG	1:B:314:GLY:N	2.53	0.41
2:E:40:ALA:HA	2:E:92:ALA:HB2	2.02	0.41
1:B:31:THR:HB	1:B:36:LEU:HD21	2.02	0.41
3:D:78:GLU:N	3:D:78:GLU:OE2	2.53	0.41
1:A:348:PHE:CD2	1:A:356:ILE:HD12	2.55	0.41
1:B:146:GLY:HA3	1:B:148:GLU:OE2	2.20	0.41
1:A:57:VAL:O	1:A:57:VAL:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:185:TYR:C	3:D:187:ARG:N	2.74	0.41
1:A:28:ARG:NH2	1:B:443:PRO:HB3	2.35	0.41
1:A:235:GLU:O	1:A:236:VAL:CG2	2.69	0.41
2:C:87:ARG:HB3	2:C:89:GLU:OE1	2.20	0.41
1:A:150:PRO:CG	1:A:354:GLY:HA2	2.50	0.41
2:C:141:ALA:O	2:C:193:SER:HB2	2.21	0.41
1:B:184:ALA:HB1	1:B:225:SER:HB2	2.01	0.41
1:A:279:LEU:C	1:A:279:LEU:HD23	2.40	0.41
3:D:131:VAL:O	3:D:147:TRP:CH2	2.73	0.41
1:B:383:HIS:HD2	2:E:33:TRP:CE3	2.38	0.41
1:A:223:ILE:CD1	1:B:426:ILE:HG22	2.49	0.41
1:B:197:ILE:HD13	1:B:219:PHE:CE1	2.55	0.41
1:B:293:LEU:C	1:B:295:GLY:N	2.73	0.41
1:A:274:LEU:CA	1:A:277:GLN:HE21	2.24	0.41
3:D:119:PRO:HG3	3:D:131:VAL:HG22	2.00	0.41
1:A:430:LEU:HD22	1:B:223:ILE:CD1	2.51	0.41
1:A:109:ILE:N	1:A:110:PRO:CD	2.83	0.41
1:B:148:GLU:OE1	1:B:357:PHE:HB3	2.21	0.41
1:B:57:VAL:CG1	1:B:139:LEU:HB3	2.50	0.41
3:D:48:TYR:CD1	3:D:48:TYR:O	2.73	0.41
1:A:358:ALA:HA	1:A:361:LEU:HD12	2.02	0.41
1:B:91:MET:HG3	1:B:296:GLY:CA	2.50	0.41
1:A:95:PHE:O	1:A:97:VAL:N	2.54	0.41
1:A:113:GLU:HG3	1:A:204:MET:HA	2.02	0.41
3:D:42:SER:HA	3:D:43:PRO:HD3	1.85	0.41
3:D:110:ALA:C	3:D:199:THR:HG21	2.40	0.41
3:F:147:TRP:CG	3:F:178:LEU:HD22	2.56	0.41
1:B:107:SER:HB2	1:B:348:PHE:CZ	2.55	0.41
1:A:197:ILE:HD13	1:A:219:PHE:CZ	2.56	0.41
3:D:95:GLN:H	3:D:95:GLN:HG2	1.59	0.41
2:E:91:THR:OG1	2:E:119:VAL:CG2	2.58	0.41
1:A:28:ARG:HH21	1:B:443:PRO:HB3	1.85	0.41
3:D:202:SER:HB3	3:D:203:PRO:CD	2.40	0.41
1:B:143:MET:HB3	1:B:347:CYS:SG	2.60	0.41
1:B:187:ALA:O	1:B:191:ASN:N	2.54	0.41
1:B:92:PHE:CZ	1:B:96:LEU:HD11	2.56	0.41
1:B:20:GLN:O	1:B:23:ARG:HB3	2.20	0.41
3:F:38:LYS:H	3:F:41:THR:HG23	1.84	0.41
3:D:86:TYR:CE2	3:D:100:GLY:HA3	2.56	0.41
3:F:180:LEU:HD22	3:F:184:GLU:CG	2.51	0.41
3:D:89:GLN:C	3:D:89:GLN:CD	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:ILE:O	1:B:410:ILE:HG22	2.21	0.41
1:A:176:THR:HG22	1:A:177:LEU:N	2.35	0.41
1:B:57:VAL:HG12	1:B:57:VAL:O	2.21	0.41
2:C:73:ASP:C	2:C:75:ALA:N	2.74	0.41
3:F:22:THR:HG22	3:F:23:CYS:N	2.36	0.41
2:C:108:PHE:CZ	3:D:95:GLN:OE1	2.74	0.41
3:D:112:PRO:HG2	3:D:204:ILE:CD1	2.39	0.41
1:B:235:GLU:O	1:B:236:VAL:CG2	2.69	0.41
1:A:72:ALA:HA	1:A:78:LEU:HD21	2.03	0.41
1:A:200:ILE:HD13	1:A:204:MET:HG3	2.03	0.41
1:B:144:VAL:HG21	1:B:343:THR:HB	2.02	0.41
2:E:12:VAL:HG11	2:E:18:LEU:HB2	2.03	0.41
3:F:117:PHE:HA	3:F:118:PRO:HD3	1.78	0.41
2:E:27:PHE:N	2:E:27:PHE:CD1	2.89	0.41
3:D:210:ARG:HG3	3:D:210:ARG:H	1.63	0.40
3:D:197:HIS:O	3:D:199:THR:N	2.55	0.40
3:F:181:THR:O	3:F:182:LYS:C	2.59	0.40
2:E:107:TYR:C	2:E:107:TYR:CD1	2.95	0.40
3:F:90:TRP:CD2	3:F:95:GLN:HB3	2.56	0.40
2:C:6:GLU:OE2	2:C:96:CYS:SG	2.79	0.40
2:E:201:VAL:HG13	2:E:201:VAL:O	2.21	0.40
3:D:134:PHE:C	3:D:135:LEU:HD22	2.42	0.40
1:B:423:LEU:HD12	1:B:423:LEU:HA	1.94	0.40
2:E:20:LEU:HD11	2:E:94:TYR:CD2	2.56	0.40
3:F:121:SER:HA	3:F:124:LEU:CD1	2.42	0.40
3:F:37:GLN:HE21	3:F:86:TYR:HE1	1.68	0.40
1:B:108:GLY:HA3	1:B:153:GLN:HE21	1.86	0.40
1:B:201:ILE:O	1:B:201:ILE:HG13	2.21	0.40
3:D:185:TYR:HA	3:D:191:TYR:OH	2.21	0.40
1:A:270:ASN:O	1:A:273:VAL:CG1	2.70	0.40
1:A:21:LEU:HD23	1:B:119:GLN:HG3	2.03	0.40
1:A:171:ASP:HB3	1:A:175:HIS:CD2	2.56	0.40
2:C:185:LEU:HD12	2:C:185:LEU:O	2.22	0.40
2:E:134:PRO:HD3	2:E:146:LEU:HD22	2.02	0.40
1:A:348:PHE:CZ	4:A:466:SEK:SE	3.24	0.40
2:E:127:PRO:CA	2:E:153:TYR:HB3	2.52	0.40
1:A:281:HIS:ND1	1:A:284:HIS:CE1	2.82	0.40
1:A:166:PHE:O	1:A:167:ARG:O	2.39	0.40
1:B:148:GLU:O	1:B:152:VAL:HG23	2.21	0.40
1:A:20:GLN:O	1:A:23:ARG:HB3	2.21	0.40
1:A:375:ALA:O	1:A:377:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:101:TYR:CD2	2:C:101:TYR:N	2.89	0.40
2:C:38:ARG:NH1	2:C:68:PHE:HZ	2.20	0.40
1:B:281:HIS:ND1	1:B:284:HIS:CE1	2.82	0.40
1:B:100:TYR:N	1:B:100:TYR:CD2	2.89	0.40
1:B:24:GLN:O	1:B:25:LEU:C	2.59	0.40
1:B:172:GLU:O	1:B:173:ALA:C	2.59	0.40
2:C:28:ASP:C	2:C:28:ASP:OD1	2.60	0.40
3:D:185:TYR:C	3:D:210:ARG:HH12	2.24	0.40
3:D:22:THR:HG22	3:D:23:CYS:H	1.87	0.40
1:B:284:HIS:HA	1:B:290:LYS:HB3	2.04	0.40
1:A:167:ARG:O	1:A:168:LEU:HG	2.21	0.40
1:A:133:PHE:HA	1:A:136:LEU:HD13	2.04	0.40
1:A:375:ALA:C	1:A:377:GLU:H	2.24	0.40
3:D:116:ILE:HG23	3:D:116:ILE:O	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	442/465 (95%)	344 (78%)	80 (18%)	18 (4%)	3	20
1	B	439/465 (94%)	336 (76%)	85 (19%)	18 (4%)	3	20
2	C	219/221 (99%)	187 (85%)	22 (10%)	10 (5%)	3	17
2	E	219/221 (99%)	184 (84%)	24 (11%)	11 (5%)	3	16
3	D	209/211 (99%)	153 (73%)	40 (19%)	16 (8%)	1	6
3	F	209/211 (99%)	168 (80%)	28 (13%)	13 (6%)	2	10
All	All	1737/1794 (97%)	1372 (79%)	279 (16%)	86 (5%)	3	16

All (86) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	ILE
1	A	283	VAL
1	B	201	ILE
1	B	283	VAL
2	C	53	PRO
2	C	65	LYS
2	C	199	GLU
3	D	7	SER
3	D	126	SER
3	D	137	ASN
3	D	152	SER
3	D	165	GLN
3	D	169	ASP
3	D	198	LYS
2	E	41	PRO
2	E	51	ILE
2	E	66	ASP
2	E	122	ALA
2	E	189	VAL
3	F	7	SER
3	F	66	SER
3	F	90	TRP
3	F	92	SER
3	F	198	LYS
3	F	210	ARG
1	A	72	ALA
1	A	165	ILE
1	A	167	ARG
1	A	318	ASN
1	B	96	LEU
1	B	165	ILE
1	B	318	ASN
2	C	31	ARG
2	C	54	VAL
2	C	135	GLY
2	C	198	SER
3	D	17	ASP
3	D	67	GLY
3	D	80	GLU
2	E	58	ILE
1	A	132	PHE
1	A	455	LYS
1	B	72	ALA

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Mol	Chain	Res	Type
1	B	132	PHE
1	B	167	ARG
1	B	310	PRO
1	B	351	GLY
2	C	109	ASP
3	D	11	MET
2	E	62	PRO
2	E	140	ALA
3	F	137	ASN
1	A	96	LEU
1	A	282	ARG
1	A	386	ALA
1	B	19	ARG
1	B	95	PHE
1	B	176	THR
1	B	282	ARG
2	C	142	SER
3	D	167	SER
3	D	186	GLU
2	E	138	ALA
3	F	182	LYS
3	F	184	GLU
1	A	95	PHE
1	A	176	THR
1	A	310	PRO
2	C	220	PRO
3	D	27	SER
3	D	83	ALA
2	E	53	PRO
3	F	93	HIS
3	F	170	SER
1	A	376	VAL
1	A	454	ALA
3	F	39	SER
1	A	351	GLY
1	B	200	ILE
3	D	59	VAL
1	A	200	ILE
2	E	69	ILE
3	F	203	PRO
1	B	206	PRO
1	B	376	VAL

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Mol	Chain	Res	Type
1	B	443	PRO

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	335/353 (95%)	328 (98%)	7 (2%)	61	86
1	B	332/353 (94%)	323 (97%)	9 (3%)	52	82
2	C	181/181 (100%)	172 (95%)	9 (5%)	30	67
2	E	181/181 (100%)	165 (91%)	16 (9%)	12	43
3	D	185/185 (100%)	168 (91%)	17 (9%)	11	40
3	F	185/185 (100%)	168 (91%)	17 (9%)	11	40
All	All	1399/1438 (97%)	1324 (95%)	75 (5%)	27	64

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	LEU
1	A	85	CYS
1	A	103	GLU
1	A	138	THR
1	A	233	ASN
1	A	246	ASP
1	A	453	LEU
1	B	65	MET
1	B	85	CYS
1	B	103	GLU
1	B	138	THR
1	B	208	PHE
1	B	233	ASN
1	B	246	ASP
1	B	277	GLN
1	B	330	MET
2	C	18	LEU

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Mol	Chain	Res	Type
2	C	30	SER
2	C	149	LEU
2	C	157	PRO
2	C	167	LEU
2	C	178	LEU
2	C	185	LEU
2	C	188	SER
2	C	203	CYS
3	D	1	ASP
3	D	22	THR
3	D	46	TRP
3	D	48	TYR
3	D	77	MET
3	D	78	GLU
3	D	89	GLN
3	D	94	PRO
3	D	96	THR
3	D	106	LEU
3	D	117	PHE
3	D	138	PHE
3	D	163	THR
3	D	169	ASP
3	D	183	ASP
3	D	192	THR
3	D	208	PHE
2	E	27	PHE
2	E	41	PRO
2	E	43	LYS
2	E	52	ASN
2	E	53	PRO
2	E	54	VAL
2	E	59	ASN
2	E	77	ASP
2	E	86	VAL
2	E	107	TYR
2	E	116	THR
2	E	157	PRO
2	E	185	LEU
2	E	188	SER
2	E	203	CYS
2	E	204	ASN
3	F	1	ASP

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Mol	Chain	Res	Type
3	F	15	PRO
3	F	21	MET
3	F	68	THR
3	F	77	MET
3	F	88	GLN
3	F	90	TRP
3	F	119	PRO
3	F	143	ILE
3	F	153	GLU
3	F	160	ASN
3	F	161	SER
3	F	162	TRP
3	F	173	SER
3	F	174	MET
3	F	175	SER
3	F	179	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	153	GLN
1	A	157	ASN
1	A	175	HIS
1	A	207	GLN
1	A	277	GLN
1	A	284	HIS
1	A	287	ASN
1	A	327	ASN
1	A	383	HIS
1	A	418	ASN
1	A	437	GLN
1	B	119	GLN
1	B	153	GLN
1	B	157	ASN
1	B	207	GLN
1	B	277	GLN
1	B	284	HIS
1	B	287	ASN
1	B	327	ASN
1	B	418	ASN
1	B	437	GLN

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Mol	Chain	Res	Type
2	C	163	ASN
2	C	172	HIS
3	D	6	GLN
3	D	89	GLN
3	D	137	ASN
2	E	39	GLN
2	E	163	ASN
3	F	6	GLN
3	F	33	HIS

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](#)

Of 8 ligands modelled in this entry, 8 are modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	444/465 (95%)	-0.16	7 (1%) 74 55	77, 77, 77, 77	0
1	B	441/465 (94%)	-0.04	7 (1%) 74 55	77, 77, 77, 77	0
2	C	221/221 (100%)	-0.13	4 (1%) 71 50	77, 77, 77, 77	0
2	E	221/221 (100%)	-0.14	1 (0%) 91 83	77, 77, 77, 77	0
3	D	211/211 (100%)	-0.11	1 (0%) 91 83	77, 77, 77, 77	0
3	F	211/211 (100%)	-0.06	4 (1%) 70 48	77, 77, 77, 77	0
All	All	1749/1794 (97%)	-0.11	24 (1%) 78 60	77, 77, 77, 77	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	72	ALA	3.8
3	F	27	SER	3.3
3	F	190	SER	3.3
2	C	136	SER	3.0
1	A	168	LEU	2.9
2	C	139	ALA	2.8
2	E	222	ALA	2.8
1	B	75	TYR	2.8
2	C	135	GLY	2.7
3	F	149	ILE	2.7
1	A	235	GLU	2.7
1	B	358	ALA	2.5
1	B	76	PRO	2.4
1	A	71	THR	2.4
1	B	359	PRO	2.4
1	A	31	THR	2.2
2	C	138	ALA	2.2
1	B	356	ILE	2.2
3	D	58	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	73	ASP	2.2
1	B	108	GLY	2.1
1	B	79	LEU	2.1
3	F	154	ARG	2.0
1	A	167	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	SEK	A	466	1/3	0.73	0.30	2.13	76,76,76,76	0
4	SEK	B	466	1/3	0.77	0.41	1.64	76,76,76,76	0
4	SEK	A	468	1/3	-	-	-	76,76,76,76	1
4	SEK	B	468	1/3	-	-	-	76,76,76,76	1
4	SEK	B	467	1/3	-	-	-	76,76,76,76	1
4	SEK	A	467	1/3	-	-	-	76,76,76,76	1
4	SEK	A	469	1/3	-	-	-	76,76,76,76	1
4	SEK	B	469	1/3	-	-	-	76,76,76,76	1

6.5 Other polymers [i](#)

There are no such residues in this entry.