



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 09:57 AM EDT

PDB ID : 2E9W
Title : Crystal structure of the extracellular domain of Kit in complex with stem cell factor (SCF)
Authors : Yuzawa, S.; Opatowsky, Y.; Zhang, Z.; Mandiyan, V.; Lax, I.; Schlessinger, J.
Deposited on : 2007-01-27
Resolution : 3.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

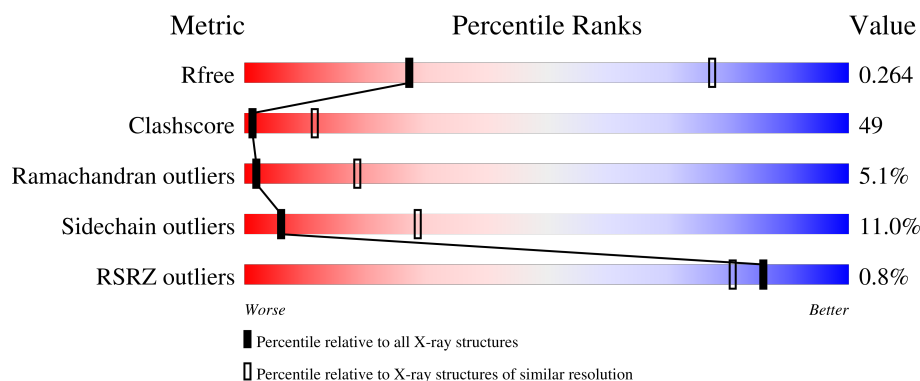
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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

Mol	Chain	Length	Quality of chain
1	A	489	
1	B	489	
2	C	141	
2	D	141	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9168 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 Mast/stem cell growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	468	Total	C	N	O	S	0	0	0
			3548	2244	598	692	14			
1	B	469	Total	C	N	O	S	0	0	0
			3514	2220	594	687	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	130	SER	ASN	engineered mutation	UNP P10721
A	145	SER	ASN	engineered mutation	UNP P10721
B	130	SER	ASN	engineered mutation	UNP P10721
B	145	SER	ASN	engineered mutation	UNP P10721

- Molecule 2 is a protein called Kit ligand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	132	Total	C	N	O	S	0	0	0
			1018	650	165	196	7			
2	D	128	Total	C	N	O	S	0	0	0
			1004	644	163	191	6			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

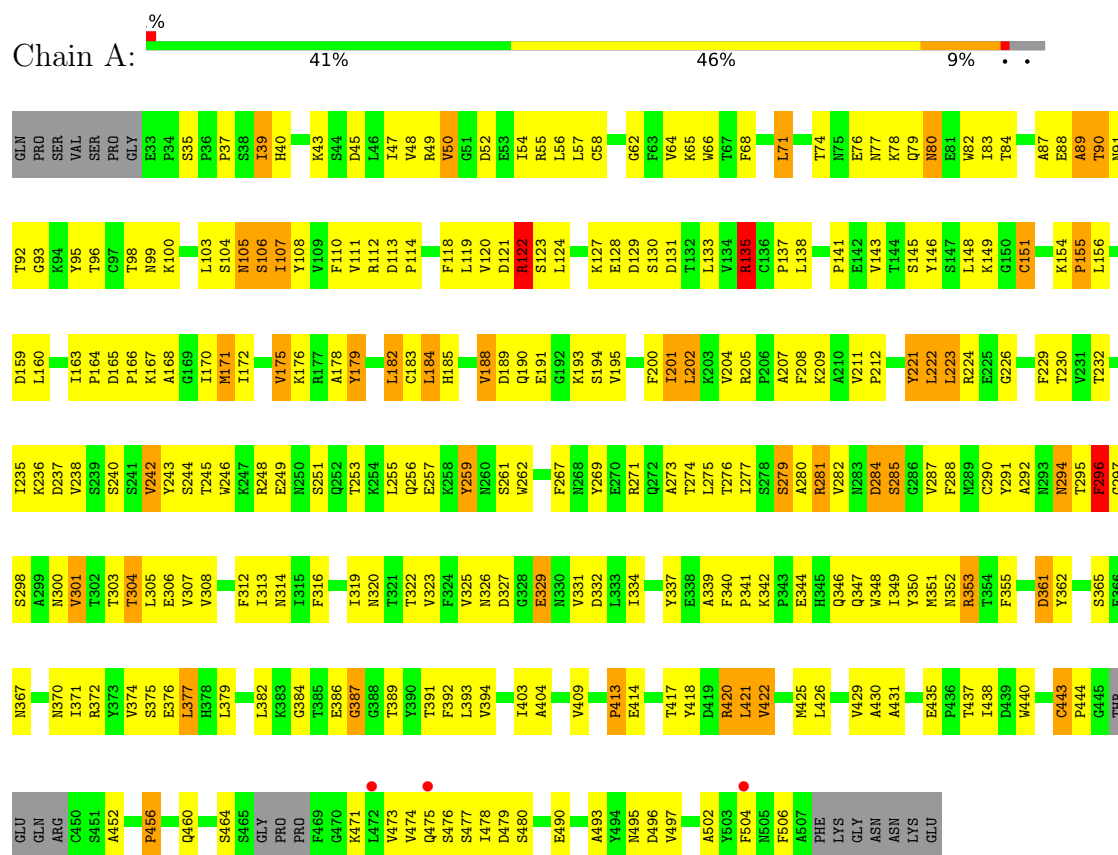


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

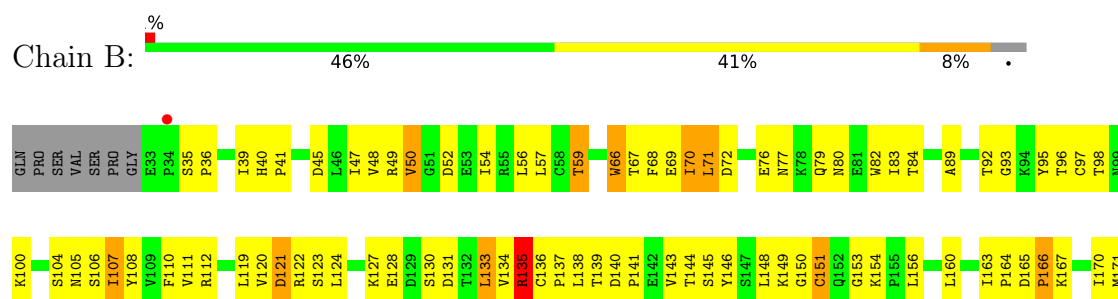
3 Residue-property plots

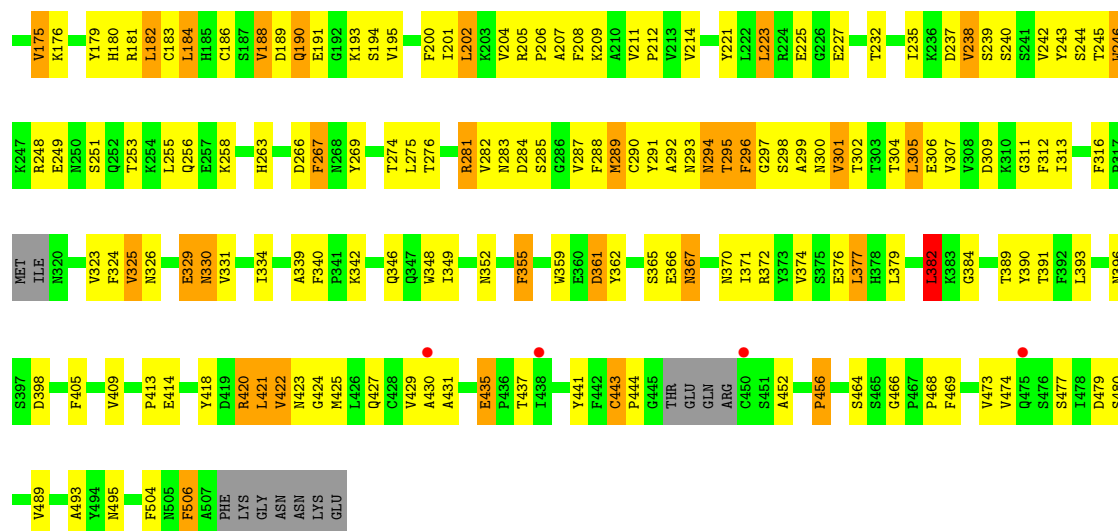
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Mast/stem cell growth factor receptor

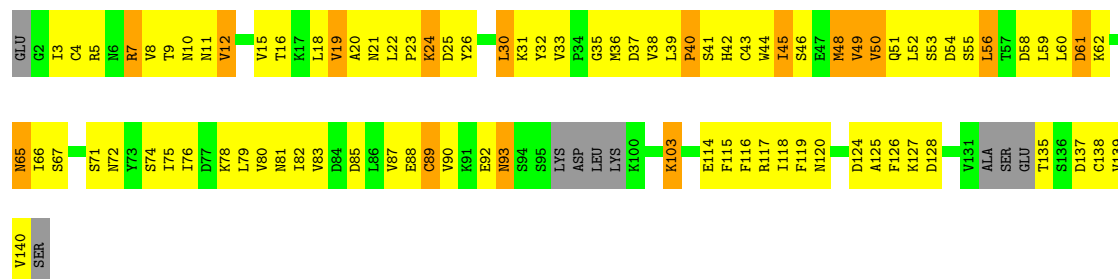


- Molecule 1: Mast/stem cell growth factor receptor

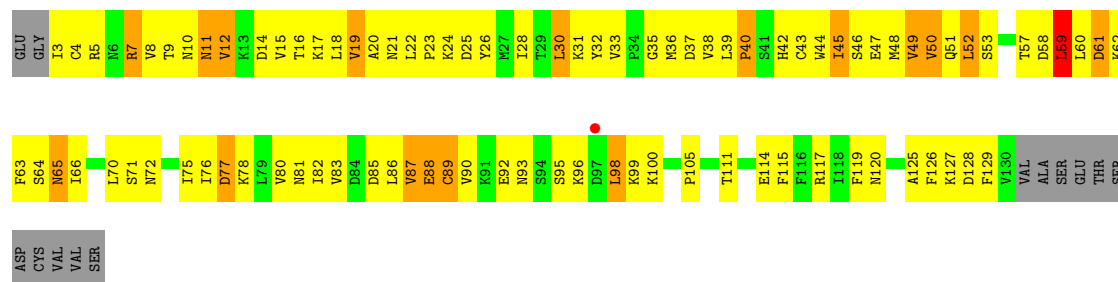




• Molecule 2: Kit ligand



• Molecule 2: Kit ligand



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	269.48Å 52.07Å 189.79Å 90.00° 108.00° 90.00°	Depositor
Resolution (Å)	38.96 – 3.50 38.96 – 3.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (38.96-3.50) 98.1 (38.96-3.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.34 (at 3.48Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.245 , 0.294 0.221 , 0.264	Depositor DCC
R_{free} test set	1595 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	79.7	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 107.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9168	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.52	0/3626	0.82	3/4943 (0.1%)
1	B	0.46	0/3591	0.77	4/4902 (0.1%)
2	C	0.52	0/1034	0.79	1/1403 (0.1%)
2	D	0.51	0/1022	0.78	1/1387 (0.1%)
All	All	0.50	0/9273	0.80	9/12635 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	456	PRO	N-CA-CB	6.25	110.80	103.30
1	A	151	CYS	CA-CB-SG	6.19	125.14	114.00
1	B	121	ASP	N-CA-C	-6.03	94.71	111.00
1	A	456	PRO	N-CA-CB	5.89	110.37	103.30
2	C	48	MET	CG-SD-CE	-5.56	91.30	100.20
1	B	444	PRO	N-CA-CB	5.47	109.87	103.30
1	A	444	PRO	N-CA-CB	5.40	109.78	103.30
2	D	59	LEU	CA-CB-CG	5.09	127.01	115.30
1	B	151	CYS	CA-CB-SG	5.05	123.09	114.00

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	3548	0	3291	328	0
1	B	3514	0	3233	290	0
2	C	1018	0	987	133	0
2	D	1004	0	993	127	0
3	A	42	0	39	2	0
3	B	42	0	39	4	0
All	All	9168	0	8582	866	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 49.

All (866) 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:D:49:VAL:HG13	2:D:87:VAL:HG22	1.22	1.16
1:B:160:LEU:HB2	1:B:179:TYR:HE1	1.10	1.12
2:C:7:ARG:HH21	2:C:89:CYS:HB2	1.03	1.11
1:B:160:LEU:HB2	1:B:179:TYR:CE1	1.86	1.09
1:A:211:VAL:HG22	1:A:297:GLY:HA3	1.36	1.07
1:A:135:ARG:HH11	1:A:135:ARG:HB3	1.16	1.07
2:C:45:ILE:HD11	2:C:126:PHE:CE1	1.90	1.06
2:C:45:ILE:HD11	2:C:126:PHE:HE1	1.19	1.04
1:B:135:ARG:NH1	1:B:135:ARG:HB3	1.74	1.03
2:C:23:PRO:HG2	2:C:26:TYR:HB2	1.40	1.03
2:C:7:ARG:NH2	2:C:89:CYS:HB2	1.75	1.01
1:A:305:LEU:HD23	1:A:306:GLU:N	1.76	1.00
1:B:325:VAL:HG12	1:B:326:ASN:H	1.27	0.99
1:A:319:ILE:HG12	1:A:320:ASN:H	1.27	0.98
1:B:143:VAL:HG11	1:B:188:VAL:HG22	1.45	0.98
2:D:45:ILE:HD11	2:D:126:PHE:HE1	1.25	0.97
1:B:131:ASP:HB3	1:B:171:MET:HE1	1.46	0.97
1:A:135:ARG:HB3	1:A:135:ARG:NH1	1.80	0.96
1:B:290:CYS:HB3	1:B:301:VAL:HG23	1.48	0.96
1:B:135:ARG:HB3	1:B:135:ARG:HH11	1.26	0.96
1:B:182:LEU:HD21	1:B:184:LEU:HD13	1.46	0.96
2:C:7:ARG:HH21	2:C:89:CYS:CB	1.78	0.96
1:A:98:THR:HG22	1:A:104:SER:HB3	1.45	0.95
1:A:138:LEU:HD21	1:A:146:TYR:CE1	2.01	0.94
1:A:259:TYR:HB3	1:A:273:ALA:HA	1.49	0.93
1:B:96:THR:HA	1:B:106:SER:HB3	1.49	0.93
1:A:325:VAL:HG12	1:A:326:ASN:H	1.34	0.92
1:B:124:LEU:HD22	1:B:202:LEU:HA	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:THR:HG23	1:A:274:THR:HB	1.50	0.91
1:B:422:VAL:HG13	1:B:423:ASN:H	1.33	0.90
2:C:59:LEU:HD13	2:C:76:ILE:HD13	1.53	0.90
1:A:124:LEU:HD22	1:A:202:LEU:HB2	1.52	0.90
1:A:124:LEU:CD2	1:A:202:LEU:HB2	2.02	0.90
1:B:348:TRP:CE3	1:B:377:LEU:HD12	2.08	0.89
2:D:45:ILE:HD11	2:D:126:PHE:CE1	2.07	0.89
1:B:294:ASN:ND2	1:B:297:GLY:H	1.71	0.89
1:A:160:LEU:HB2	1:A:179:TYR:CE1	2.07	0.88
1:B:182:LEU:HD21	1:B:184:LEU:CD1	2.02	0.88
1:A:148:LEU:O	1:A:156:LEU:HD11	1.73	0.88
1:A:182:LEU:CD2	1:A:184:LEU:HD13	2.03	0.88
1:A:89:ALA:HA	1:A:111:VAL:HG13	1.54	0.88
1:A:39:ILE:HD12	1:A:40:HIS:H	1.39	0.88
2:C:9:THR:CG2	2:C:11:ASN:HD22	1.88	0.87
2:C:9:THR:HG22	2:C:82:ILE:HD11	1.56	0.87
1:B:290:CYS:HB3	1:B:301:VAL:CG2	2.05	0.86
1:B:182:LEU:HD23	1:B:183:CYS:N	1.90	0.86
1:A:421:LEU:HD22	1:A:425:MET:HG2	1.58	0.85
1:B:131:ASP:HB3	1:B:171:MET:CE	2.05	0.85
1:A:290:CYS:HB3	1:A:301:VAL:HG23	1.59	0.85
1:A:425:MET:HB3	1:A:479:ASP:HA	1.58	0.85
1:B:211:VAL:HG22	1:B:297:GLY:HA3	1.56	0.85
1:A:211:VAL:CG2	1:A:297:GLY:HA3	2.06	0.84
1:A:349:ILE:HD12	1:A:349:ILE:O	1.76	0.84
1:B:293:ASN:OD1	3:B:850:NAG:H62	1.76	0.84
1:B:176:LYS:HD3	1:B:179:TYR:HE2	1.43	0.84
2:D:23:PRO:HG2	2:D:26:TYR:HB2	1.59	0.84
2:D:86:LEU:C	2:D:88:GLU:H	1.82	0.83
1:A:182:LEU:HD22	1:A:184:LEU:HD13	1.59	0.83
1:A:160:LEU:HB2	1:A:179:TYR:HE1	1.42	0.83
2:D:59:LEU:HD13	2:D:76:ILE:HD13	1.60	0.83
1:A:189:ASP:HA	1:A:194:SER:HA	1.62	0.82
1:B:349:ILE:HD11	1:B:391:THR:HB	1.63	0.81
1:B:160:LEU:CB	1:B:179:TYR:HE1	1.92	0.81
1:B:138:LEU:HD21	1:B:146:TYR:CE1	2.16	0.81
1:A:77:ASN:HD21	1:A:79:GLN:HB2	1.46	0.80
1:B:425:MET:HB3	1:B:479:ASP:HA	1.63	0.80
2:C:9:THR:CG2	2:C:82:ILE:HD11	2.11	0.80
2:C:60:LEU:HG	2:C:60:LEU:O	1.80	0.80
1:B:108:TYR:CE2	1:B:167:LYS:HG2	2.17	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ILE:N	1:A:235:ILE:HD12	1.97	0.78
2:C:9:THR:HG21	2:C:11:ASN:HD22	1.49	0.78
1:B:480:SER:HB3	1:B:506:PHE:HZ	1.48	0.78
2:C:16:THR:O	2:C:19:VAL:HG12	1.82	0.78
1:B:244:SER:HA	1:B:291:TYR:O	1.84	0.78
1:A:480:SER:HB3	1:A:506:PHE:CE1	2.17	0.78
2:D:10:ASN:C	2:D:12:VAL:H	1.86	0.77
1:B:246:TRP:O	1:B:255:LEU:HD13	1.84	0.77
1:A:312:PHE:O	1:A:313:ILE:HD13	1.84	0.77
1:A:39:ILE:HD12	1:A:40:HIS:N	2.00	0.77
1:B:182:LEU:CD2	1:B:184:LEU:HD13	2.14	0.77
1:A:182:LEU:HD23	1:A:183:CYS:N	2.01	0.76
1:B:49:ARG:HB2	1:B:52:ASP:OD2	1.85	0.76
1:B:89:ALA:HA	1:B:111:VAL:HG13	1.67	0.76
1:A:201:ILE:HG12	1:A:201:ILE:O	1.84	0.76
1:B:146:TYR:HD2	1:B:164:PRO:HB2	1.51	0.76
2:C:7:ARG:CG	2:C:85:ASP:HB3	2.16	0.76
1:B:145:SER:O	1:B:188:VAL:HA	1.86	0.76
1:A:232:THR:CG2	1:A:274:THR:HB	2.16	0.76
1:B:246:TRP:CD1	1:B:275:LEU:HB2	2.21	0.76
1:B:235:ILE:HD12	1:B:235:ILE:N	2.01	0.75
1:B:349:ILE:HD12	1:B:349:ILE:O	1.87	0.75
2:D:52:LEU:HD11	2:D:119:PHE:HA	1.68	0.75
1:A:420:ARG:H	1:A:420:ARG:HD3	1.52	0.75
1:A:353:ARG:HB2	1:A:353:ARG:HH21	1.52	0.75
1:B:156:LEU:HD22	1:B:184:LEU:HD12	1.69	0.75
1:B:295:THR:HG22	1:B:295:THR:O	1.86	0.74
1:B:68:PHE:HZ	1:B:70:ILE:HD11	1.51	0.74
2:D:18:LEU:HB2	2:D:75:ILE:HG21	1.67	0.74
1:B:176:LYS:HD3	1:B:179:TYR:CE2	2.22	0.74
1:B:312:PHE:O	1:B:313:ILE:HD13	1.87	0.74
1:A:143:VAL:HG11	1:A:188:VAL:HG13	1.68	0.74
1:A:211:VAL:HG22	1:A:297:GLY:CA	2.16	0.74
1:A:176:LYS:HB2	1:A:179:TYR:CE2	2.23	0.74
1:A:138:LEU:HD21	1:A:146:TYR:HE1	1.52	0.74
1:A:138:LEU:HD11	1:A:146:TYR:CD1	2.23	0.73
1:A:295:THR:HG22	1:A:295:THR:O	1.86	0.73
1:B:420:ARG:H	1:B:420:ARG:HD3	1.54	0.73
1:B:98:THR:HG22	1:B:104:SER:HB3	1.71	0.73
1:B:143:VAL:HG11	1:B:188:VAL:CG2	2.17	0.73
1:A:124:LEU:HD22	1:A:202:LEU:CB	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:ASN:ND2	1:A:79:GLN:HB2	2.03	0.73
2:D:7:ARG:NH2	2:D:89:CYS:HB2	2.03	0.73
1:B:146:TYR:CD2	1:B:164:PRO:HB2	2.23	0.72
1:A:281:ARG:O	1:A:284:ASP:HB2	1.90	0.72
1:B:150:GLY:HA2	1:B:156:LEU:HD23	1.71	0.72
2:C:72:ASN:O	2:C:76:ILE:HG13	1.88	0.72
1:B:480:SER:HB3	1:B:506:PHE:CZ	2.24	0.72
1:A:370:ASN:ND2	1:A:372:ARG:H	1.86	0.72
1:B:124:LEU:HD22	1:B:202:LEU:CA	2.20	0.72
2:D:9:THR:CG2	2:D:11:ASN:HD22	2.03	0.72
1:B:133:LEU:HD23	1:B:171:MET:HG2	1.70	0.72
1:B:294:ASN:O	1:B:296:PHE:N	2.22	0.71
1:B:421:LEU:HG	1:B:422:VAL:H	1.55	0.71
1:B:292:ALA:HB3	1:B:299:ALA:HB3	1.73	0.71
1:B:384:GLY:HA2	1:B:409:VAL:HG21	1.72	0.71
2:D:3:ILE:CG2	2:D:129:PHE:HB3	2.21	0.71
1:B:182:LEU:CD2	1:B:184:LEU:CD1	2.69	0.70
1:A:124:LEU:HD22	1:A:202:LEU:CA	2.22	0.70
2:D:89:CYS:O	2:D:93:ASN:HB2	1.91	0.70
1:A:211:VAL:HG13	1:A:212:PRO:HD2	1.72	0.70
1:A:118:PHE:O	1:A:119:LEU:HD23	1.92	0.70
1:B:422:VAL:HG13	1:B:423:ASN:N	2.07	0.70
2:C:18:LEU:HB2	2:C:75:ILE:HG21	1.74	0.70
1:A:351:MET:O	1:A:353:ARG:HG2	1.91	0.70
1:B:396:ASN:HD21	1:B:398:ASP:HB2	1.56	0.70
1:A:351:MET:SD	1:A:389:THR:HG22	2.31	0.70
1:A:108:TYR:CE2	1:A:167:LYS:HG2	2.27	0.70
1:A:480:SER:HB3	1:A:506:PHE:HE1	1.57	0.70
1:B:349:ILE:CD1	1:B:391:THR:HB	2.21	0.70
2:C:38:VAL:HG12	2:C:39:LEU:HD22	1.73	0.70
1:A:319:ILE:HG12	1:A:320:ASN:N	2.04	0.69
1:B:59:THR:HG22	1:B:59:THR:O	1.90	0.69
2:C:23:PRO:HG2	2:C:26:TYR:CB	2.21	0.69
2:C:39:LEU:HB2	2:C:40:PRO:HA	1.73	0.69
2:D:40:PRO:HG3	2:D:43:CYS:SG	2.33	0.69
2:D:9:THR:HG21	2:D:11:ASN:HD22	1.59	0.69
1:A:89:ALA:O	1:A:119:LEU:HD11	1.93	0.68
2:C:9:THR:HG22	2:C:82:ILE:CD1	2.23	0.68
1:A:176:LYS:HD3	1:A:179:TYR:HE2	1.58	0.68
2:D:33:VAL:HG23	2:D:48:MET:SD	2.34	0.68
1:A:89:ALA:HA	1:A:111:VAL:CG1	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:LEU:HD21	1:A:184:LEU:HD13	1.76	0.68
2:C:89:CYS:SG	2:C:90:VAL:N	2.67	0.68
1:A:229:PHE:HB3	1:A:277:ILE:HB	1.75	0.67
1:A:379:LEU:HB3	1:A:382:LEU:HD11	1.75	0.67
2:D:49:VAL:CG1	2:D:87:VAL:HG22	2.13	0.67
1:B:362:TYR:CE1	1:B:374:VAL:HG13	2.29	0.67
2:D:61:ASP:OD1	2:D:62:LYS:HD3	1.93	0.67
1:B:223:LEU:HD12	1:B:227:GLU:HB2	1.76	0.67
1:A:71:LEU:HD23	1:A:135:ARG:HH12	1.59	0.67
1:A:176:LYS:HD3	1:A:179:TYR:CE2	2.29	0.67
2:C:45:ILE:HG23	2:C:46:SER:N	2.08	0.67
2:C:83:VAL:O	2:C:87:VAL:HG23	1.93	0.67
1:B:211:VAL:HG13	1:B:212:PRO:HD2	1.76	0.67
1:A:246:TRP:O	1:A:255:LEU:HD13	1.95	0.67
2:D:9:THR:O	2:D:12:VAL:HG22	1.94	0.67
2:D:126:PHE:C	2:D:128:ASP:H	1.98	0.67
1:A:124:LEU:HD22	1:A:202:LEU:HA	1.76	0.67
1:B:325:VAL:HG12	1:B:326:ASN:N	2.07	0.67
2:D:7:ARG:HH21	2:D:89:CYS:HB2	1.59	0.67
1:B:148:LEU:O	1:B:156:LEU:HD11	1.95	0.66
1:A:160:LEU:CB	1:A:179:TYR:HE1	2.08	0.66
1:B:128:GLU:HB3	1:B:207:ALA:HB2	1.77	0.66
1:A:305:LEU:HD23	1:A:306:GLU:H	1.61	0.66
1:B:275:LEU:HD12	1:B:276:THR:N	2.11	0.66
1:B:300:ASN:HB2	3:B:900:NAG:C7	2.26	0.66
1:A:48:VAL:CG1	1:A:52:ASP:HB2	2.25	0.66
1:B:163:ILE:HG13	1:B:163:ILE:O	1.96	0.66
1:A:47:ILE:HG12	1:A:110:PHE:HB2	1.77	0.66
1:A:146:TYR:HD2	1:A:164:PRO:HB2	1.59	0.66
1:A:325:VAL:HG12	1:A:326:ASN:N	2.09	0.66
2:D:4:CYS:HB2	2:D:126:PHE:HD2	1.61	0.66
2:D:28:ILE:HG21	2:D:115:PHE:CD1	2.31	0.66
2:C:9:THR:HG21	2:C:11:ASN:ND2	2.11	0.66
1:B:237:ASP:HB3	1:B:242:VAL:HG11	1.76	0.65
1:B:135:ARG:HH11	1:B:135:ARG:CB	2.06	0.65
1:A:223:LEU:N	1:A:223:LEU:HD23	2.10	0.65
1:B:422:VAL:HG22	1:B:423:ASN:N	2.12	0.65
1:B:108:TYR:CD2	1:B:167:LYS:HE2	2.31	0.65
2:D:49:VAL:HG13	2:D:87:VAL:CG2	2.14	0.65
1:A:326:ASN:O	1:A:329:GLU:HB2	1.96	0.65
2:D:7:ARG:HH21	2:D:89:CYS:CB	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:32:TYR:CE1	2:D:36:MET:SD	2.89	0.65
2:D:52:LEU:HD13	2:D:119:PHE:HD1	1.62	0.65
2:D:86:LEU:C	2:D:88:GLU:N	2.51	0.65
1:B:331:VAL:HG13	1:B:379:LEU:HD12	1.77	0.65
1:B:396:ASN:ND2	1:B:398:ASP:H	1.95	0.65
1:A:222:LEU:HG	1:A:340:PHE:CE1	2.32	0.64
1:B:294:ASN:HD21	1:B:297:GLY:N	1.94	0.64
1:A:281:ARG:N	1:A:281:ARG:HD2	2.12	0.64
1:A:66:TRP:HB2	1:A:77:ASN:HB3	1.79	0.64
1:B:68:PHE:HE1	1:B:93:GLY:HA3	1.63	0.64
1:B:182:LEU:HD23	1:B:182:LEU:C	2.17	0.64
1:B:326:ASN:HB2	1:B:329:GLU:OE1	1.97	0.64
1:A:111:VAL:HG13	1:A:111:VAL:O	1.98	0.64
1:B:56:LEU:HB2	1:B:82:TRP:HB3	1.79	0.64
1:A:149:LYS:C	1:A:156:LEU:HD21	2.17	0.64
1:B:56:LEU:CD1	1:B:107:ILE:HD11	2.28	0.64
1:B:294:ASN:HD21	1:B:297:GLY:H	1.44	0.64
1:B:431:ALA:HB2	1:B:473:VAL:HG12	1.79	0.64
1:A:438:ILE:HG21	1:A:476:SER:OG	1.98	0.64
1:B:143:VAL:CG1	1:B:188:VAL:HG22	2.24	0.64
2:D:77:ASP:OD1	2:D:78:LYS:HD2	1.96	0.64
1:A:226:GLY:O	1:A:279:SER:HA	1.98	0.63
1:B:292:ALA:O	1:B:298:SER:HA	1.98	0.63
2:C:9:THR:HG23	2:C:11:ASN:H	1.63	0.63
2:C:45:ILE:HD13	2:C:125:ALA:HB3	1.78	0.63
1:B:92:THR:OG1	1:B:111:VAL:HG12	1.98	0.63
1:B:294:ASN:ND2	1:B:297:GLY:N	2.45	0.63
2:D:10:ASN:C	2:D:12:VAL:N	2.51	0.63
1:B:119:LEU:O	1:B:137:PRO:HD2	1.99	0.63
1:A:414:GLU:O	1:A:430:ALA:HA	1.98	0.63
1:B:67:THR:HB	1:B:96:THR:HB	1.80	0.63
1:A:78:LYS:O	1:A:79:GLN:HG2	1.99	0.63
2:D:36:MET:HA	2:D:44:TRP:NE1	2.13	0.63
1:A:222:LEU:C	1:A:222:LEU:HD12	2.18	0.63
1:B:160:LEU:HD12	1:B:179:TYR:CE1	2.34	0.62
2:D:32:TYR:HE1	2:D:36:MET:SD	2.22	0.62
2:D:39:LEU:HB2	2:D:40:PRO:HA	1.80	0.62
1:A:232:THR:HG23	1:A:274:THR:CB	2.26	0.62
1:B:68:PHE:CZ	1:B:70:ILE:HD11	2.31	0.62
1:B:334:ILE:HG22	1:B:376:GLU:HG2	1.81	0.62
1:A:305:LEU:HD21	1:A:307:VAL:HG23	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:LEU:HD11	1:B:146:TYR:CD1	2.34	0.62
1:A:326:ASN:HB2	1:A:329:GLU:OE1	2.00	0.62
1:B:305:LEU:HD22	1:B:306:GLU:N	2.14	0.62
3:A:750:NAG:H82	3:A:750:NAG:C1	2.29	0.62
2:C:126:PHE:C	2:C:128:ASP:H	2.01	0.62
2:D:50:VAL:HG23	2:D:87:VAL:HG11	1.81	0.62
2:D:5:ARG:O	2:D:8:VAL:HG12	1.99	0.62
1:B:175:VAL:CG1	1:B:204:VAL:HG22	2.30	0.62
1:B:289:MET:HB2	1:B:302:THR:HG22	1.81	0.61
1:A:151:CYS:HA	1:A:185:HIS:HD2	1.65	0.61
1:B:190:GLN:HG3	1:B:190:GLN:O	2.00	0.61
2:C:49:VAL:HG13	2:C:87:VAL:HG22	1.83	0.61
2:D:50:VAL:CG1	2:D:51:GLN:N	2.64	0.61
1:A:55:ARG:HG2	1:A:83:ILE:HG22	1.81	0.61
1:A:229:PHE:HD2	1:A:277:ILE:HG12	1.65	0.61
1:B:384:GLY:HA2	1:B:409:VAL:CG2	2.30	0.61
1:B:79:GLN:HE21	1:B:79:GLN:HA	1.66	0.61
1:A:294:ASN:ND2	1:A:297:GLY:H	1.98	0.61
1:B:50:VAL:HG12	1:B:112:ARG:O	2.01	0.61
1:A:35:SER:C	1:A:103:LEU:HD12	2.21	0.60
2:C:92:GLU:O	2:C:92:GLU:HG2	1.99	0.60
2:C:126:PHE:O	2:C:127:LYS:HB2	2.00	0.60
2:C:32:TYR:CE1	2:C:36:MET:SD	2.95	0.60
1:A:238:VAL:HG13	1:A:267:PHE:HB3	1.84	0.60
1:A:296:PHE:CD1	1:A:296:PHE:O	2.55	0.60
1:A:135:ARG:HH11	1:A:135:ARG:CB	2.03	0.60
1:B:120:VAL:CG1	1:B:200:PHE:HZ	2.15	0.60
1:B:138:LEU:HD21	1:B:146:TYR:HE1	1.65	0.60
2:C:33:VAL:HG23	2:C:48:MET:SD	2.42	0.60
2:D:23:PRO:HG2	2:D:26:TYR:CB	2.31	0.60
2:D:92:GLU:O	2:D:92:GLU:HG2	2.00	0.60
2:D:59:LEU:HD13	2:D:76:ILE:CD1	2.31	0.60
1:A:305:LEU:CD2	1:A:307:VAL:HG23	2.32	0.60
1:A:426:LEU:O	1:A:477:SER:HB3	2.01	0.60
2:D:111:THR:OG1	2:D:114:GLU:HG3	2.01	0.60
1:B:72:ASP:O	2:D:99:LYS:HD2	2.01	0.59
1:A:143:VAL:HG11	1:A:188:VAL:HG22	1.84	0.59
2:C:40:PRO:CD	2:C:43:CYS:SG	2.90	0.59
2:C:89:CYS:O	2:C:93:ASN:HB2	2.03	0.59
1:B:39:ILE:HD13	1:B:66:TRP:CH2	2.37	0.59
1:A:133:LEU:HD12	1:A:135:ARG:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:LEU:HD11	1:B:107:ILE:HD11	1.85	0.59
2:D:12:VAL:O	2:D:15:VAL:HG23	2.03	0.59
2:D:83:VAL:O	2:D:87:VAL:HG23	2.03	0.59
1:A:138:LEU:HD11	1:A:146:TYR:CE1	2.37	0.59
2:D:89:CYS:SG	2:D:90:VAL:N	2.76	0.59
1:A:68:PHE:HE1	1:A:93:GLY:HA3	1.67	0.59
1:A:143:VAL:HG11	1:A:188:VAL:CG1	2.33	0.59
1:B:362:TYR:CE1	1:B:374:VAL:CG1	2.85	0.59
2:D:86:LEU:O	2:D:88:GLU:N	2.34	0.59
1:B:160:LEU:HD12	1:B:179:TYR:CD1	2.37	0.58
2:D:66:ILE:HB	2:D:71:SER:HB3	1.85	0.58
1:A:146:TYR:CD2	1:A:164:PRO:HB2	2.37	0.58
1:B:156:LEU:CD2	1:B:184:LEU:HD12	2.33	0.58
2:C:139:VAL:O	2:C:140:VAL:HB	2.04	0.58
1:A:222:LEU:HD12	1:A:223:LEU:N	2.18	0.58
1:B:128:GLU:HB3	1:B:207:ALA:CB	2.33	0.58
1:A:64:VAL:O	1:A:65:LYS:HB3	2.02	0.58
1:A:403:ILE:HD12	1:A:404:ALA:H	1.68	0.58
1:B:108:TYR:CG	1:B:167:LYS:HE2	2.39	0.58
1:A:211:VAL:HG11	1:A:298:SER:O	2.03	0.58
1:B:340:PHE:HB2	1:B:371:ILE:HD11	1.86	0.58
1:A:389:THR:HG23	1:A:389:THR:O	2.03	0.58
2:D:17:LYS:NZ	2:D:70:LEU:HD12	2.19	0.58
1:B:150:GLY:HA2	1:B:156:LEU:CD2	2.34	0.58
2:D:8:VAL:HG13	2:D:8:VAL:O	2.04	0.58
1:A:47:ILE:HD11	1:A:141:PRO:HG3	1.85	0.57
1:B:393:LEU:N	1:B:393:LEU:HD12	2.18	0.57
2:C:45:ILE:HD13	2:C:125:ALA:CB	2.34	0.57
1:A:413:PRO:HD3	1:A:495:ASN:HB3	1.86	0.57
1:B:127:LYS:HG3	1:B:128:GLU:N	2.19	0.57
1:A:350:TYR:CE1	1:A:351:MET:HG2	2.39	0.57
1:A:296:PHE:CD1	1:A:296:PHE:C	2.78	0.57
1:A:334:ILE:HG22	1:A:376:GLU:HG2	1.86	0.57
2:D:60:LEU:HD13	2:D:77:ASP:N	2.19	0.57
1:A:205:ARG:NH1	2:C:88:GLU:HG3	2.20	0.56
1:A:237:ASP:OD2	1:A:238:VAL:N	2.39	0.56
1:B:89:ALA:HA	1:B:111:VAL:CG1	2.35	0.56
1:B:291:TYR:CE1	1:B:298:SER:HB3	2.41	0.56
1:A:108:TYR:CD2	1:A:167:LYS:HE2	2.40	0.56
1:B:429:VAL:HG13	1:B:474:VAL:O	2.04	0.56
2:C:3:ILE:HG12	2:C:93:ASN:ND2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:18:LEU:O	2:C:22:LEU:HG	2.05	0.56
2:D:7:ARG:NH2	2:D:89:CYS:CB	2.66	0.56
1:A:138:LEU:HD12	1:A:166:PRO:HB3	1.87	0.56
1:A:431:ALA:HB2	1:A:473:VAL:HG12	1.87	0.56
1:B:131:ASP:CB	1:B:171:MET:HE1	2.29	0.56
1:B:182:LEU:HD21	1:B:184:LEU:HD11	1.87	0.56
1:B:421:LEU:HD22	1:B:425:MET:CG	2.35	0.56
2:D:90:VAL:C	2:D:92:GLU:H	2.08	0.56
2:C:38:VAL:O	2:C:39:LEU:HB3	2.04	0.56
2:D:50:VAL:HG12	2:D:51:GLN:N	2.20	0.56
1:A:120:VAL:HB	1:A:200:PHE:CZ	2.41	0.56
1:A:151:CYS:CB	1:A:183:CYS:O	2.53	0.56
1:A:305:LEU:CD2	1:A:306:GLU:N	2.61	0.56
2:C:7:ARG:HG2	2:C:85:ASP:HB3	1.87	0.56
2:C:65:ASN:HD22	2:C:66:ILE:H	1.54	0.56
2:D:9:THR:CG2	2:D:82:ILE:HD11	2.36	0.56
1:A:151:CYS:HB2	1:A:183:CYS:O	2.05	0.56
2:D:10:ASN:HA	2:D:12:VAL:HG23	1.88	0.56
1:A:201:ILE:O	1:A:201:ILE:CG1	2.53	0.55
1:A:340:PHE:HB2	1:A:371:ILE:HD11	1.89	0.55
1:B:214:VAL:HG21	1:B:301:VAL:HG21	1.88	0.55
1:B:289:MET:HG3	1:B:302:THR:HG23	1.87	0.55
1:A:235:ILE:HD12	1:A:235:ILE:H	1.71	0.55
1:B:111:VAL:O	1:B:139:THR:HG22	2.07	0.55
1:B:275:LEU:HD12	1:B:276:THR:H	1.70	0.55
2:C:44:TRP:O	2:C:45:ILE:C	2.44	0.55
2:C:45:ILE:HG23	2:C:46:SER:H	1.70	0.55
2:D:16:THR:O	2:D:19:VAL:HG12	2.06	0.55
1:A:56:LEU:CD1	1:A:107:ILE:HD11	2.35	0.55
1:A:149:LYS:O	1:A:156:LEU:HD21	2.05	0.55
1:A:349:ILE:HD11	1:A:391:THR:HB	1.88	0.55
1:B:176:LYS:HB2	1:B:179:TYR:CE2	2.42	0.55
1:A:365:SER:C	1:A:367:ASN:H	2.10	0.55
2:C:58:ASP:O	2:C:59:LEU:C	2.44	0.55
1:A:62:GLY:O	1:A:64:VAL:HG23	2.07	0.55
1:A:64:VAL:HG21	1:A:100:LYS:HA	1.89	0.55
1:A:235:ILE:N	1:A:235:ILE:CD1	2.65	0.55
1:A:294:ASN:C	1:A:294:ASN:HD22	2.10	0.55
1:A:418:TYR:HB2	1:A:504:PHE:CE1	2.42	0.55
1:B:296:PHE:O	1:B:296:PHE:CD1	2.59	0.55
2:C:65:ASN:HD22	2:C:66:ILE:N	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:ASN:ND2	1:B:294:ASN:C	2.60	0.54
1:B:365:SER:C	1:B:367:ASN:H	2.10	0.54
2:C:38:VAL:HG12	2:C:39:LEU:CD2	2.37	0.54
1:A:49:ARG:HB2	1:A:52:ASP:OD2	2.06	0.54
1:A:349:ILE:CD1	1:A:391:THR:HB	2.37	0.54
1:B:182:LEU:CD2	1:B:182:LEU:C	2.75	0.54
2:C:40:PRO:HG3	2:C:42:HIS:CE1	2.43	0.54
2:C:61:ASP:OD1	2:C:62:LYS:HD3	2.07	0.54
1:A:71:LEU:HD23	1:A:135:ARG:NH1	2.23	0.54
1:A:145:SER:O	1:A:188:VAL:HA	2.08	0.54
2:D:98:LEU:HD23	2:D:98:LEU:H	1.72	0.54
1:A:282:VAL:HA	1:A:307:VAL:CG1	2.37	0.54
1:B:110:PHE:CZ	1:B:141:PRO:HB3	2.43	0.54
1:B:180:HIS:C	1:B:182:LEU:H	2.11	0.54
1:B:205:ARG:NH1	2:D:88:GLU:HG2	2.22	0.54
1:B:311:GLY:N	1:B:398:ASP:OD1	2.38	0.54
2:C:7:ARG:HE	2:C:89:CYS:HB3	1.73	0.54
1:B:305:LEU:HD11	1:B:307:VAL:HG23	1.90	0.54
2:C:10:ASN:HA	2:C:12:VAL:HG23	1.89	0.54
2:D:18:LEU:O	2:D:22:LEU:HG	2.08	0.54
1:A:56:LEU:HD13	1:A:107:ILE:HD11	1.90	0.53
1:A:420:ARG:HG2	1:A:420:ARG:O	2.09	0.53
1:B:71:LEU:HD23	1:B:135:ARG:HH12	1.73	0.53
2:C:76:ILE:O	2:C:80:VAL:HG23	2.08	0.53
1:A:87:ALA:HB1	1:A:111:VAL:HG21	1.91	0.53
1:A:208:PHE:CD2	1:A:294:ASN:HB2	2.44	0.53
1:B:225:GLU:OE2	1:B:282:VAL:HG23	2.08	0.53
2:C:32:TYR:HE1	2:C:36:MET:SD	2.31	0.53
2:C:137:ASP:O	2:C:139:VAL:N	2.41	0.53
2:D:10:ASN:O	2:D:12:VAL:N	2.41	0.53
1:A:124:LEU:HD21	1:A:202:LEU:HB2	1.89	0.53
1:B:160:LEU:HD23	1:B:160:LEU:C	2.29	0.53
1:B:190:GLN:O	1:B:191:GLU:HB2	2.09	0.53
1:B:214:VAL:CG2	1:B:301:VAL:HG21	2.38	0.53
1:A:108:TYR:CG	1:A:167:LYS:HE2	2.44	0.53
1:B:413:PRO:HD3	1:B:495:ASN:HB3	1.91	0.53
2:C:78:LYS:CD	2:C:78:LYS:N	2.71	0.53
1:A:176:LYS:HB2	1:A:179:TYR:HE2	1.70	0.53
1:B:96:THR:HA	1:B:106:SER:CB	2.29	0.53
1:B:214:VAL:HG13	1:B:214:VAL:O	2.07	0.53
2:C:66:ILE:HD11	2:D:20:ALA:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:THR:CG2	1:A:104:SER:HB3	2.30	0.53
2:D:53:SER:HA	2:D:83:VAL:HG21	1.91	0.53
1:A:420:ARG:HD3	1:A:420:ARG:N	2.22	0.53
1:B:293:ASN:OD1	3:B:850:NAG:C6	2.52	0.53
2:C:49:VAL:CG1	2:C:87:VAL:HG22	2.39	0.53
2:D:17:LYS:HZ1	2:D:70:LEU:HD12	1.73	0.53
1:A:294:ASN:ND2	1:A:294:ASN:C	2.62	0.52
1:B:418:TYR:HB2	1:B:504:PHE:CE1	2.43	0.52
2:C:135:THR:HA	2:C:138:CYS:SG	2.49	0.52
2:D:7:ARG:CG	2:D:85:ASP:HB3	2.39	0.52
1:A:88:GLU:O	1:A:90:THR:N	2.42	0.52
2:D:45:ILE:HG23	2:D:46:SER:N	2.24	0.52
1:B:221:TYR:HB2	1:B:305:LEU:HD23	1.92	0.52
1:B:237:ASP:HB3	1:B:242:VAL:CG1	2.40	0.52
2:C:40:PRO:HD2	2:C:43:CYS:SG	2.49	0.52
1:B:112:ARG:NE	1:B:140:ASP:OD2	2.42	0.52
2:C:59:LEU:CD1	2:C:76:ILE:HD13	2.32	0.52
2:C:78:LYS:N	2:C:78:LYS:HD2	2.24	0.52
2:C:103:LYS:NZ	2:C:103:LYS:HB3	2.24	0.52
1:B:235:ILE:N	1:B:235:ILE:CD1	2.71	0.52
1:B:138:LEU:HD12	1:B:166:PRO:HB3	1.92	0.52
1:A:96:THR:HG23	1:A:106:SER:HB3	1.92	0.52
1:A:312:PHE:CD1	1:A:312:PHE:N	2.77	0.52
1:B:71:LEU:HD22	1:B:121:ASP:HB2	1.92	0.52
1:B:120:VAL:HG12	1:B:136:CYS:HA	1.91	0.52
1:B:207:ALA:O	1:B:209:LYS:HG3	2.10	0.52
1:B:294:ASN:ND2	1:B:294:ASN:O	2.42	0.52
1:B:110:PHE:CE2	1:B:141:PRO:HB3	2.45	0.52
2:D:51:GLN:OE1	2:D:51:GLN:HA	2.09	0.52
1:A:137:PRO:HD3	1:A:168:ALA:O	2.10	0.52
1:B:420:ARG:HD3	1:B:420:ARG:N	2.23	0.52
1:A:243:TYR:O	1:A:292:ALA:HA	2.10	0.51
1:B:79:GLN:HA	1:B:79:GLN:NE2	2.25	0.51
1:B:346:GLN:HA	1:B:393:LEU:O	2.10	0.51
2:C:30:LEU:HD11	2:C:52:LEU:CD2	2.40	0.51
2:D:87:VAL:HG12	2:D:87:VAL:O	2.10	0.51
1:B:211:VAL:CG1	1:B:212:PRO:HD2	2.38	0.51
2:C:18:LEU:HD12	2:C:75:ILE:CG2	2.41	0.51
2:D:3:ILE:HG12	2:D:93:ASN:ND2	2.25	0.51
1:A:261:SER:O	2:C:10:ASN:OD1	2.28	0.51
1:A:340:PHE:C	1:A:340:PHE:CD2	2.84	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:TRP:HA	1:B:246:TRP:CE3	2.44	0.51
1:B:422:VAL:CG1	1:B:423:ASN:H	2.08	0.51
2:D:36:MET:HA	2:D:44:TRP:CD1	2.46	0.51
1:B:47:ILE:HG12	1:B:110:PHE:HB2	1.93	0.51
1:B:121:ASP:C	1:B:123:SER:H	2.14	0.51
1:A:182:LEU:CD2	1:A:182:LEU:C	2.79	0.51
1:B:127:LYS:HA	1:B:205:ARG:HB3	1.93	0.51
1:B:251:SER:OG	1:B:253:THR:HG22	2.09	0.51
1:A:133:LEU:CD1	1:A:135:ARG:HD2	2.39	0.51
1:B:66:TRP:CZ3	1:B:97:CYS:HB2	2.46	0.51
1:B:288:PHE:O	1:B:302:THR:HA	2.11	0.51
2:C:9:THR:HG23	2:C:11:ASN:HD22	1.70	0.51
2:D:80:VAL:O	2:D:81:ASN:C	2.47	0.51
1:A:230:THR:HG23	1:A:230:THR:O	2.11	0.51
1:A:248:ARG:NH2	1:A:285:SER:O	2.44	0.51
2:D:30:LEU:HD22	2:D:31:LYS:N	2.25	0.50
1:A:344:GLU:O	1:A:346:GLN:HG3	2.11	0.50
1:B:175:VAL:HG11	1:B:204:VAL:HG22	1.93	0.50
1:B:294:ASN:HD22	1:B:297:GLY:H	1.56	0.50
2:C:78:LYS:CD	2:C:78:LYS:H	2.23	0.50
1:A:131:ASP:HB3	1:A:171:MET:CE	2.42	0.50
1:A:418:TYR:HB2	1:A:504:PHE:HE1	1.77	0.50
1:B:281:ARG:O	1:B:284:ASP:HB2	2.11	0.50
2:C:18:LEU:C	2:C:18:LEU:HD23	2.32	0.50
2:D:3:ILE:HG22	2:D:129:PHE:HB3	1.92	0.50
1:B:281:ARG:HD2	1:B:281:ARG:N	2.25	0.50
2:C:44:TRP:O	2:C:46:SER:N	2.45	0.50
2:C:52:LEU:HD11	2:C:119:PHE:HA	1.92	0.50
2:D:38:VAL:HG12	2:D:39:LEU:HD22	1.94	0.50
1:A:112:ARG:O	1:A:112:ARG:HG3	2.11	0.50
1:B:237:ASP:CB	1:B:242:VAL:HG11	2.40	0.50
2:C:24:LYS:HG3	2:D:62:LYS:O	2.12	0.50
1:A:48:VAL:HG12	1:A:52:ASP:HB2	1.94	0.50
1:A:138:LEU:CD2	1:A:146:TYR:CE1	2.85	0.50
2:C:12:VAL:O	2:C:15:VAL:HG23	2.11	0.50
2:C:50:VAL:CG1	2:C:51:GLN:N	2.74	0.50
2:C:59:LEU:HD13	2:C:76:ILE:CD1	2.36	0.50
2:C:41:SER:HA	2:C:44:TRP:CZ2	2.47	0.50
2:D:40:PRO:CG	2:D:43:CYS:SG	2.99	0.50
1:A:66:TRP:O	1:A:76:GLU:HA	2.12	0.49
1:A:127:LYS:HG3	1:A:128:GLU:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:TYR:HE1	1:A:298:SER:HB3	1.77	0.49
1:A:348:TRP:CG	1:A:377:LEU:HG	2.46	0.49
1:B:443:CYS:CB	1:B:452:ALA:HB3	2.42	0.49
1:A:290:CYS:HB3	1:A:301:VAL:CG2	2.38	0.49
1:B:121:ASP:HB3	1:B:135:ARG:CB	2.42	0.49
1:B:291:TYR:HE1	1:B:298:SER:HB3	1.76	0.49
1:B:294:ASN:C	1:B:294:ASN:HD22	2.16	0.49
2:C:49:VAL:HG13	2:C:87:VAL:CG2	2.41	0.49
1:A:413:PRO:HD3	1:A:495:ASN:CB	2.42	0.49
1:A:490:GLU:HG2	1:A:502:ALA:O	2.12	0.49
2:D:60:LEU:O	2:D:60:LEU:HG	2.12	0.49
1:B:98:THR:HA	1:B:104:SER:HB3	1.93	0.49
1:B:370:ASN:ND2	1:B:372:ARG:H	2.10	0.49
1:A:92:THR:OG1	1:A:111:VAL:HG12	2.12	0.49
1:A:127:LYS:HB3	1:A:130:SER:OG	2.13	0.49
1:A:443:CYS:CB	1:A:452:ALA:HB3	2.43	0.49
1:B:40:HIS:HA	1:B:41:PRO:C	2.33	0.49
1:B:296:PHE:CD1	1:B:296:PHE:C	2.85	0.49
2:D:31:LYS:HB2	2:D:51:GLN:NE2	2.28	0.49
2:D:44:TRP:O	2:D:45:ILE:C	2.50	0.49
1:A:240:SER:HA	1:A:269:TYR:CE2	2.48	0.49
2:C:7:ARG:NH2	2:C:89:CYS:CB	2.55	0.49
2:C:30:LEU:HD22	2:C:31:LYS:N	2.28	0.49
1:A:255:LEU:HD12	1:A:255:LEU:N	2.28	0.49
1:A:287:VAL:HG22	1:A:304:THR:HB	1.94	0.49
1:B:323:VAL:HG12	1:B:324:PHE:N	2.27	0.49
1:A:82:TRP:CD1	1:A:82:TRP:C	2.86	0.48
1:A:351:MET:O	1:A:353:ARG:N	2.46	0.48
2:D:126:PHE:O	2:D:127:LYS:HB2	2.13	0.48
1:A:207:ALA:O	1:A:209:LYS:HG3	2.13	0.48
1:B:305:LEU:CD1	1:B:307:VAL:HG23	2.42	0.48
2:C:126:PHE:C	2:C:128:ASP:N	2.66	0.48
2:D:9:THR:HG22	2:D:82:ILE:HD11	1.95	0.48
1:A:83:ILE:HD12	1:A:83:ILE:O	2.14	0.48
1:A:259:TYR:CD2	1:A:259:TYR:N	2.80	0.48
1:B:180:HIS:ND1	1:B:181:ARG:N	2.60	0.48
2:D:50:VAL:HG23	2:D:87:VAL:CG1	2.43	0.48
1:A:232:THR:HA	1:A:274:THR:HA	1.95	0.48
1:A:361:ASP:OD1	1:A:375:SER:HB2	2.13	0.48
1:B:414:GLU:O	1:B:430:ALA:HA	2.13	0.48
1:A:205:ARG:HH11	2:C:88:GLU:HG3	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:ILE:HG12	1:B:201:ILE:O	2.14	0.48
1:A:238:VAL:HG12	1:A:238:VAL:O	2.12	0.48
1:A:313:ILE:HD13	1:A:339:ALA:HA	1.96	0.48
1:B:239:SER:O	1:B:242:VAL:HG13	2.13	0.48
2:D:126:PHE:C	2:D:128:ASP:N	2.65	0.48
1:A:49:ARG:HG2	1:A:49:ARG:HH11	1.79	0.48
1:A:202:LEU:HD11	1:A:204:VAL:HG22	1.94	0.48
1:B:240:SER:HA	1:B:269:TYR:CE2	2.49	0.48
2:C:30:LEU:HD22	2:C:31:LYS:H	1.78	0.48
2:C:50:VAL:O	2:C:53:SER:HB3	2.14	0.48
2:D:58:ASP:O	2:D:59:LEU:C	2.51	0.48
1:A:176:LYS:HB2	1:A:179:TYR:CD2	2.48	0.48
1:A:325:VAL:CG1	1:A:329:GLU:HB3	2.44	0.48
2:C:7:ARG:HG3	2:C:85:ASP:HB3	1.93	0.48
1:A:57:LEU:HD12	1:A:80:ASN:O	2.14	0.48
1:A:244:SER:HA	1:A:291:TYR:O	2.13	0.48
1:A:348:TRP:CZ3	1:A:392:PHE:HB2	2.48	0.48
1:B:290:CYS:HB3	1:B:301:VAL:HG21	1.92	0.48
1:B:290:CYS:CB	1:B:301:VAL:HG23	2.33	0.48
2:C:3:ILE:O	2:C:4:CYS:HB2	2.14	0.48
1:A:362:TYR:CE1	1:A:374:VAL:CG1	2.97	0.48
1:A:391:THR:HG22	1:A:392:PHE:N	2.29	0.48
1:A:49:ARG:HG2	1:A:49:ARG:NH1	2.29	0.47
1:A:291:TYR:CE1	1:A:298:SER:HB3	2.49	0.47
1:B:287:VAL:CG1	1:B:288:PHE:N	2.77	0.47
1:A:143:VAL:CG1	1:A:188:VAL:HG22	2.45	0.47
1:A:261:SER:OG	2:C:9:THR:HA	2.14	0.47
1:A:54:ILE:O	1:A:83:ILE:HA	2.15	0.47
1:A:121:ASP:C	1:A:123:SER:H	2.16	0.47
1:A:127:LYS:HG3	1:A:128:GLU:H	1.80	0.47
1:A:240:SER:HA	1:A:269:TYR:CZ	2.50	0.47
1:A:313:ILE:HD12	1:A:339:ALA:HB1	1.96	0.47
1:B:39:ILE:HD13	1:B:66:TRP:CZ2	2.50	0.47
1:B:389:THR:HA	1:B:405:PHE:O	2.13	0.47
1:A:222:LEU:C	1:A:223:LEU:HD23	2.33	0.47
1:B:77:ASN:HD21	1:B:79:GLN:HB2	1.79	0.47
1:B:191:GLU:C	1:B:193:LYS:H	2.17	0.47
1:B:441:TYR:O	1:B:489:VAL:HG13	2.13	0.47
1:A:417:THR:HG23	1:A:417:THR:O	2.14	0.47
2:D:18:LEU:HD11	2:D:76:ILE:CG1	2.45	0.47
1:A:65:LYS:HE3	1:A:76:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:ILE:CG1	1:A:320:ASN:H	2.13	0.47
1:B:188:VAL:HG12	1:B:195:VAL:CG2	2.45	0.47
2:D:18:LEU:HD21	2:D:22:LEU:HD11	1.97	0.47
2:D:23:PRO:O	2:D:25:ASP:N	2.48	0.47
1:A:78:LYS:O	1:A:79:GLN:CG	2.61	0.47
1:A:425:MET:HB2	1:A:478:ILE:O	2.14	0.47
1:B:98:THR:CG2	1:B:104:SER:HB3	2.44	0.47
1:A:240:SER:O	1:A:271:ARG:NH2	2.47	0.47
1:A:460:GLN:HA	1:A:475:GLN:O	2.15	0.47
1:B:138:LEU:HD11	1:B:146:TYR:CE1	2.50	0.47
1:B:208:PHE:HD1	1:B:208:PHE:H	1.62	0.47
2:C:39:LEU:HA	2:C:40:PRO:O	2.14	0.47
2:C:126:PHE:CD1	2:C:126:PHE:N	2.82	0.47
2:D:18:LEU:C	2:D:18:LEU:HD23	2.35	0.47
1:A:188:VAL:HG12	1:A:195:VAL:CG2	2.45	0.47
1:A:353:ARG:HB2	1:A:353:ARG:NH2	2.24	0.47
1:B:248:ARG:O	1:B:249:GLU:C	2.52	0.47
1:B:420:ARG:N	1:B:420:ARG:CD	2.78	0.47
2:D:31:LYS:CB	2:D:51:GLN:NE2	2.78	0.47
2:D:47:GLU:OE1	2:D:47:GLU:HA	2.15	0.47
1:A:259:TYR:HB3	1:A:273:ALA:CA	2.33	0.47
1:B:182:LEU:CD2	1:B:184:LEU:HD11	2.44	0.47
1:B:184:LEU:HD22	1:B:184:LEU:N	2.30	0.47
2:D:21:ASN:HB3	2:D:72:ASN:HD21	1.80	0.47
1:B:95:TYR:O	1:B:106:SER:HB2	2.15	0.46
1:A:143:VAL:HG11	1:A:188:VAL:CG2	2.44	0.46
1:A:164:PRO:HA	1:A:170:ILE:HA	1.98	0.46
1:A:248:ARG:O	1:A:249:GLU:C	2.53	0.46
1:B:48:VAL:O	1:B:111:VAL:HA	2.14	0.46
1:A:120:VAL:HB	1:A:200:PHE:HZ	1.78	0.46
1:A:386:GLU:HG3	1:A:386:GLU:O	2.15	0.46
1:B:427:GLN:HG3	1:B:477:SER:OG	2.15	0.46
2:C:8:VAL:HG22	2:C:8:VAL:O	2.16	0.46
2:D:3:ILE:HG23	2:D:129:PHE:HB3	1.97	0.46
1:A:88:GLU:C	1:A:90:THR:N	2.69	0.46
1:A:182:LEU:HD22	1:A:184:LEU:CD1	2.36	0.46
1:A:246:TRP:HB2	1:A:257:GLU:OE1	2.15	0.46
1:A:295:THR:O	1:A:295:THR:CG2	2.57	0.46
1:A:440:TRP:HZ3	1:A:504:PHE:HE2	1.64	0.46
1:B:149:LYS:C	1:B:156:LEU:HD21	2.36	0.46
1:B:56:LEU:HD13	1:B:107:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:VAL:HG13	1:B:111:VAL:O	2.15	0.46
1:A:138:LEU:HD11	1:A:146:TYR:CG	2.51	0.46
2:C:49:VAL:HG12	2:C:50:VAL:N	2.30	0.46
1:A:68:PHE:CE1	1:A:93:GLY:HA3	2.49	0.46
1:A:121:ASP:O	1:A:123:SER:N	2.49	0.46
1:B:124:LEU:HD22	1:B:202:LEU:CB	2.45	0.46
2:D:28:ILE:CG2	2:D:115:PHE:CD1	2.97	0.46
2:D:33:VAL:HG11	2:D:44:TRP:HB3	1.98	0.46
1:A:37:PRO:HB2	1:A:58:CYS:SG	2.56	0.46
1:A:88:GLU:O	1:A:111:VAL:HG11	2.15	0.46
1:A:221:TYR:CD2	1:A:221:TYR:N	2.84	0.46
1:A:245:THR:HG23	1:A:291:TYR:HB3	1.97	0.46
1:A:287:VAL:CG1	1:A:288:PHE:N	2.79	0.46
2:D:23:PRO:C	2:D:25:ASP:H	2.19	0.46
2:D:36:MET:HB2	2:D:44:TRP:CE2	2.51	0.46
1:A:182:LEU:HD23	1:A:182:LEU:C	2.35	0.46
1:A:183:CYS:HA	1:A:201:ILE:HA	1.98	0.46
1:A:340:PHE:HA	1:A:341:PRO:C	2.35	0.46
1:A:437:THR:O	1:A:493:ALA:HA	2.16	0.46
1:A:480:SER:HB3	1:A:506:PHE:CZ	2.51	0.46
1:A:74:THR:O	1:A:74:THR:HG23	2.16	0.46
1:B:179:TYR:O	1:B:182:LEU:HB3	2.15	0.46
1:A:280:ALA:C	1:A:281:ARG:HD2	2.36	0.45
2:C:115:PHE:HD2	2:C:116:PHE:CD1	2.34	0.45
1:A:135:ARG:H	1:A:135:ARG:HG2	1.41	0.45
1:A:236:LYS:NZ	1:A:236:LYS:HB3	2.31	0.45
1:B:263:HIS:N	2:D:11:ASN:HD21	2.15	0.45
1:B:365:SER:O	1:B:366:GLU:HB2	2.15	0.45
2:C:33:VAL:HG21	2:C:48:MET:HG2	1.98	0.45
2:C:40:PRO:CG	2:C:43:CYS:SG	3.04	0.45
1:A:39:ILE:CD1	1:A:40:HIS:N	2.75	0.45
1:A:122:ARG:HG3	1:A:122:ARG:HH11	1.82	0.45
1:A:224:ARG:HB2	1:A:340:PHE:HE2	1.81	0.45
1:A:326:ASN:O	1:A:327:ASP:C	2.55	0.45
1:B:245:THR:HG22	1:B:291:TYR:HB3	1.98	0.45
2:C:9:THR:O	2:C:12:VAL:HG22	2.16	0.45
2:D:9:THR:HG23	2:D:82:ILE:HD11	1.98	0.45
1:A:47:ILE:HD11	1:A:141:PRO:CG	2.46	0.45
1:B:124:LEU:CD2	1:B:202:LEU:HB2	2.47	0.45
2:C:30:LEU:CD2	2:C:31:LYS:H	2.30	0.45
1:A:95:TYR:N	1:A:95:TYR:CD2	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:LEU:HD13	1:A:184:LEU:HD11	1.99	0.45
1:B:68:PHE:CD1	1:B:69:GLU:N	2.85	0.45
1:B:202:LEU:HD11	1:B:204:VAL:HG22	1.98	0.45
2:C:45:ILE:CG2	2:C:46:SER:N	2.77	0.45
2:C:139:VAL:O	2:C:140:VAL:CB	2.64	0.45
2:D:63:PHE:N	2:D:63:PHE:CD1	2.84	0.45
1:A:113:ASP:OD2	1:A:114:PRO:HD2	2.16	0.45
1:A:175:VAL:HG11	1:A:204:VAL:HG22	1.99	0.45
1:A:222:LEU:HG	1:A:340:PHE:CD1	2.51	0.45
1:B:160:LEU:HD12	1:B:179:TYR:HE1	1.81	0.45
1:B:237:ASP:O	1:B:239:SER:N	2.49	0.45
1:A:251:SER:OG	1:A:253:THR:HG22	2.17	0.45
2:C:33:VAL:CG2	2:C:48:MET:HG2	2.46	0.45
2:D:51:GLN:O	2:D:52:LEU:C	2.54	0.45
1:A:232:THR:HG23	1:A:274:THR:CA	2.47	0.45
1:A:305:LEU:HD23	1:A:305:LEU:C	2.36	0.45
1:B:124:LEU:HD22	1:B:202:LEU:HB2	1.98	0.45
2:C:51:GLN:O	2:C:52:LEU:C	2.55	0.45
2:C:58:ASP:O	2:C:60:LEU:N	2.50	0.45
1:A:332:ASP:HA	1:A:377:LEU:O	2.17	0.45
1:B:79:GLN:HE21	1:B:79:GLN:CA	2.25	0.45
1:B:182:LEU:HD22	1:B:184:LEU:CD2	2.46	0.45
1:A:50:VAL:HG12	1:A:112:ARG:O	2.17	0.45
1:A:384:GLY:C	1:A:386:GLU:H	2.19	0.45
1:B:135:ARG:H	1:B:135:ARG:HG2	1.32	0.45
2:C:118:ILE:O	2:C:119:PHE:C	2.55	0.45
2:D:45:ILE:HD13	2:D:125:ALA:HB3	1.98	0.45
2:D:60:LEU:CD1	2:D:76:ILE:HB	2.47	0.45
2:C:10:ASN:C	2:C:12:VAL:H	2.21	0.44
2:C:20:ALA:HB3	2:D:66:ILE:HD11	1.99	0.44
1:A:143:VAL:CG1	1:A:188:VAL:HG13	2.45	0.44
1:B:67:THR:N	1:B:96:THR:O	2.46	0.44
1:B:82:TRP:CZ2	1:B:95:TYR:HE1	2.35	0.44
1:B:93:GLY:O	1:B:108:TYR:CD1	2.70	0.44
1:B:421:LEU:HD22	1:B:425:MET:HG3	1.99	0.44
1:A:54:ILE:HB	1:A:84:THR:OG1	2.18	0.44
1:A:182:LEU:CD2	1:A:183:CYS:N	2.78	0.44
1:A:348:TRP:CE2	1:A:392:PHE:HD2	2.35	0.44
1:A:403:ILE:HD12	1:A:404:ALA:N	2.32	0.44
1:B:165:ASP:O	1:B:167:LYS:N	2.51	0.44
1:B:424:GLY:O	1:B:480:SER:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:103:LYS:HD2	2:C:103:LYS:C	2.37	0.44
2:D:52:LEU:HD13	2:D:119:PHE:CD1	2.48	0.44
3:A:750:NAG:C1	3:A:750:NAG:C8	2.93	0.44
1:B:263:HIS:H	2:D:11:ASN:HD21	1.65	0.44
1:A:236:LYS:HB3	1:A:236:LYS:HZ2	1.82	0.44
1:A:296:PHE:C	1:A:296:PHE:HD1	2.19	0.44
1:B:283:ASN:C	1:B:285:SER:H	2.21	0.44
1:B:413:PRO:HD3	1:B:495:ASN:CB	2.47	0.44
2:C:10:ASN:C	2:C:12:VAL:N	2.71	0.44
1:A:182:LEU:CD2	1:A:184:LEU:CD1	2.87	0.44
1:B:164:PRO:HB3	1:B:170:ILE:HG13	1.99	0.44
2:D:3:ILE:HD12	2:D:4:CYS:H	1.82	0.44
1:A:495:ASN:O	1:A:497:VAL:N	2.51	0.44
1:B:100:LYS:O	1:B:100:LYS:HG2	2.18	0.44
1:B:339:ALA:O	1:B:371:ILE:HD11	2.18	0.44
2:D:60:LEU:HD12	2:D:76:ILE:HB	2.00	0.44
1:A:99:ASN:HB2	1:A:103:LEU:HB2	1.99	0.44
1:B:255:LEU:N	1:B:255:LEU:HD12	2.32	0.44
2:C:45:ILE:CD1	2:C:126:PHE:CE1	2.82	0.44
1:A:88:GLU:C	1:A:90:THR:H	2.20	0.43
1:A:105:ASN:O	1:A:106:SER:HB3	2.18	0.43
1:A:188:VAL:O	1:A:195:VAL:HG22	2.18	0.43
1:A:190:GLN:O	1:A:191:GLU:HB2	2.18	0.43
1:A:249:GLU:HB2	1:A:287:VAL:HG12	1.99	0.43
1:A:294:ASN:HD22	1:A:294:ASN:N	2.16	0.43
1:A:429:VAL:HG13	1:A:474:VAL:O	2.18	0.43
1:B:149:LYS:C	1:B:150:GLY:O	2.54	0.43
1:B:289:MET:HE2	1:B:289:MET:HB3	1.93	0.43
2:C:23:PRO:CG	2:C:26:TYR:HB2	2.30	0.43
1:A:431:ALA:CB	1:A:473:VAL:HG12	2.47	0.43
1:B:110:PHE:CG	1:B:141:PRO:HD3	2.53	0.43
1:B:164:PRO:HA	1:B:170:ILE:HA	1.99	0.43
2:C:88:GLU:O	2:C:89:CYS:C	2.57	0.43
1:A:235:ILE:H	1:A:235:ILE:CD1	2.28	0.43
1:B:180:HIS:C	1:B:182:LEU:N	2.71	0.43
1:B:323:VAL:C	1:B:324:PHE:HD2	2.22	0.43
2:C:18:LEU:HD11	2:C:76:ILE:HG12	2.00	0.43
2:D:126:PHE:O	2:D:128:ASP:N	2.52	0.43
1:A:175:VAL:CG1	1:A:204:VAL:HG22	2.48	0.43
1:A:331:VAL:HG13	1:A:379:LEU:HD12	2.00	0.43
2:D:65:ASN:HD22	2:D:66:ILE:H	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ARG:O	1:A:50:VAL:C	2.53	0.43
1:A:160:LEU:HD12	1:A:179:TYR:CD1	2.54	0.43
1:A:300:ASN:O	1:A:301:VAL:HG13	2.19	0.43
1:A:386:GLU:O	1:A:387:GLY:O	2.36	0.43
1:B:54:ILE:O	1:B:83:ILE:HA	2.19	0.43
2:C:126:PHE:O	2:C:127:LYS:CB	2.66	0.43
1:A:184:LEU:N	1:A:184:LEU:HD22	2.34	0.43
1:A:346:GLN:HG2	1:A:394:VAL:HG23	2.01	0.43
2:D:98:LEU:HD23	2:D:98:LEU:N	2.33	0.43
1:B:66:TRP:O	1:B:76:GLU:HA	2.19	0.43
1:B:176:LYS:HB2	1:B:179:TYR:CD2	2.54	0.43
3:B:950:NAG:O3	3:B:950:NAG:C7	2.66	0.43
2:C:33:VAL:O	2:C:36:MET:HG2	2.18	0.43
2:C:44:TRP:CE3	2:C:45:ILE:N	2.87	0.43
2:D:4:CYS:HB2	2:D:126:PHE:CD2	2.46	0.43
1:A:346:GLN:O	1:A:347:GLN:HB3	2.18	0.43
1:B:35:SER:OG	1:B:36:PRO:HD2	2.19	0.43
1:B:66:TRP:HB2	1:B:77:ASN:HB3	2.00	0.43
1:B:223:LEU:HA	1:B:340:PHE:HZ	1.84	0.43
2:C:30:LEU:HD11	2:C:52:LEU:HD23	2.01	0.43
2:D:3:ILE:C	2:D:5:ARG:H	2.22	0.43
1:A:221:TYR:N	1:A:221:TYR:HD2	2.17	0.43
1:A:334:ILE:HG22	1:A:376:GLU:CG	2.49	0.43
2:D:90:VAL:C	2:D:92:GLU:N	2.71	0.43
1:A:275:LEU:HD12	1:A:276:THR:N	2.33	0.42
1:B:68:PHE:CZ	1:B:70:ILE:CG1	3.02	0.42
1:B:124:LEU:HD11	1:B:134:VAL:HG22	2.02	0.42
2:C:24:LYS:NZ	2:D:64:SER:OG	2.52	0.42
2:C:58:ASP:O	2:C:61:ASP:N	2.44	0.42
2:D:89:CYS:SG	2:D:90:VAL:HG23	2.58	0.42
2:D:96:LYS:HG3	2:D:98:LEU:HD21	2.00	0.42
1:A:164:PRO:HB3	1:A:170:ILE:HG13	2.00	0.42
1:B:153:GLY:O	1:B:154:LYS:C	2.58	0.42
1:B:313:ILE:HD11	1:B:396:ASN:CG	2.40	0.42
1:B:334:ILE:HG22	1:B:376:GLU:CG	2.48	0.42
1:A:365:SER:C	1:A:367:ASN:N	2.72	0.42
2:C:5:ARG:O	2:C:8:VAL:HG12	2.19	0.42
2:C:56:LEU:CD1	2:C:79:LEU:HB3	2.49	0.42
1:A:146:TYR:CE2	1:A:170:ILE:HD12	2.54	0.42
1:A:163:ILE:HA	1:A:164:PRO:HD2	1.92	0.42
1:B:289:MET:CB	1:B:302:THR:HG22	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:58:ASP:C	2:C:60:LEU:N	2.71	0.42
1:B:136:CYS:HB3	1:B:200:PHE:CZ	2.54	0.42
1:B:390:TYR:CD1	1:B:390:TYR:N	2.87	0.42
1:A:121:ASP:HB3	1:A:135:ARG:HB2	2.00	0.42
2:C:53:SER:O	2:C:54:ASP:C	2.55	0.42
2:C:114:GLU:O	2:C:117:ARG:HB3	2.19	0.42
1:A:165:ASP:HA	1:A:166:PRO:HD2	1.86	0.42
1:A:305:LEU:CD2	1:A:305:LEU:C	2.88	0.42
1:B:245:THR:CG2	1:B:291:TYR:HB3	2.50	0.42
1:A:237:ASP:OD1	1:A:242:VAL:HG12	2.20	0.42
1:A:355:PHE:N	1:A:355:PHE:CD1	2.87	0.42
1:A:384:GLY:O	1:A:409:VAL:HG11	2.19	0.42
1:B:92:THR:OG1	1:B:111:VAL:CG1	2.67	0.42
1:B:334:ILE:HG13	1:B:334:ILE:O	2.20	0.42
1:B:435:GLU:O	1:B:435:GLU:HG2	2.20	0.42
1:A:43:LYS:O	1:A:107:ILE:HG22	2.20	0.42
1:A:105:ASN:HD22	1:A:105:ASN:HA	1.54	0.42
1:A:346:GLN:HA	1:A:393:LEU:O	2.20	0.42
1:B:202:LEU:HD11	1:B:204:VAL:CG2	2.50	0.42
2:C:23:PRO:O	2:C:25:ASP:N	2.53	0.42
2:D:25:ASP:N	2:D:25:ASP:OD1	2.51	0.42
1:A:224:ARG:HA	1:A:308:VAL:HG22	2.02	0.42
1:B:240:SER:HA	1:B:269:TYR:CD2	2.55	0.42
2:D:17:LYS:O	2:D:20:ALA:N	2.53	0.42
1:A:96:THR:HA	1:A:106:SER:HB3	2.02	0.41
1:A:160:LEU:C	1:A:160:LEU:HD23	2.41	0.41
1:A:281:ARG:N	1:A:281:ARG:CD	2.81	0.41
1:B:221:TYR:CB	1:B:305:LEU:HD23	2.49	0.41
1:A:350:TYR:O	1:A:351:MET:C	2.58	0.41
1:A:421:LEU:HD23	1:A:422:VAL:O	2.19	0.41
1:A:108:TYR:CD2	1:A:167:LYS:HG2	2.54	0.41
1:B:295:THR:O	1:B:295:THR:CG2	2.58	0.41
2:D:52:LEU:O	2:D:53:SER:C	2.58	0.41
1:A:262:TRP:HA	2:C:9:THR:OG1	2.21	0.41
1:A:294:ASN:HD22	1:A:294:ASN:H	1.67	0.41
1:A:296:PHE:O	1:A:296:PHE:HD1	2.01	0.41
1:B:112:ARG:O	1:B:112:ARG:HG3	2.19	0.41
1:B:128:GLU:C	1:B:130:SER:H	2.24	0.41
1:B:144:THR:HB	1:B:189:ASP:HB2	2.02	0.41
2:C:51:GLN:O	2:C:54:ASP:N	2.54	0.41
1:B:54:ILE:HB	1:B:84:THR:OG1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:PRO:HB2	1:B:238:VAL:HG11	2.01	0.41
1:B:355:PHE:N	1:B:355:PHE:CD1	2.88	0.41
1:B:382:LEU:HD12	1:B:382:LEU:HA	1.75	0.41
1:B:437:THR:O	1:B:493:ALA:HA	2.20	0.41
2:C:48:MET:HE2	2:C:48:MET:HB3	1.74	0.41
2:D:31:LYS:HD3	2:D:51:GLN:HE22	1.85	0.41
1:A:190:GLN:N	1:A:193:LYS:O	2.53	0.41
1:A:294:ASN:HD21	1:A:297:GLY:H	1.65	0.41
2:C:54:ASP:O	2:C:55:SER:C	2.58	0.41
1:A:128:GLU:O	1:A:129:ASP:HB2	2.20	0.41
1:A:393:LEU:HD12	1:A:393:LEU:N	2.36	0.41
1:B:66:TRP:NE1	1:B:82:TRP:HB2	2.36	0.41
1:B:211:VAL:CG1	1:B:212:PRO:CD	2.98	0.41
1:B:330:ASN:OD1	1:B:330:ASN:N	2.54	0.41
2:C:78:LYS:H	2:C:78:LYS:HD3	1.84	0.41
1:A:121:ASP:C	1:A:123:SER:N	2.73	0.41
1:B:243:TYR:O	1:B:292:ALA:HA	2.21	0.41
1:B:258:LYS:O	1:B:274:THR:HG22	2.21	0.41
2:D:32:TYR:OH	2:D:36:MET:HG3	2.21	0.41
1:A:151:CYS:HB3	1:A:183:CYS:O	2.19	0.41
1:A:236:LYS:O	1:A:237:ASP:HB2	2.21	0.41
1:A:314:ASN:O	1:A:337:TYR:HB2	2.21	0.41
1:A:320:ASN:C	1:A:322:THR:H	2.24	0.41
1:A:348:TRP:CE2	1:A:377:LEU:HB2	2.55	0.41
1:B:151:CYS:HB3	1:B:183:CYS:O	2.20	0.41
1:B:205:ARG:HH11	2:D:88:GLU:HG2	1.84	0.41
1:B:232:THR:HG23	1:B:274:THR:HB	2.03	0.41
1:B:237:ASP:OD2	1:B:238:VAL:N	2.54	0.41
2:C:36:MET:HG3	2:C:37:ASP:H	1.86	0.41
2:D:47:GLU:O	2:D:48:MET:C	2.58	0.41
2:D:82:ILE:O	2:D:83:VAL:C	2.59	0.41
1:A:88:GLU:O	1:A:91:ASN:N	2.53	0.41
1:A:323:VAL:HG11	1:A:331:VAL:HG21	2.03	0.41
1:B:238:VAL:O	1:B:238:VAL:HG12	2.20	0.41
1:B:266:ASP:O	1:B:267:PHE:C	2.59	0.41
1:B:371:ILE:HD12	1:B:371:ILE:HA	1.95	0.41
2:C:90:VAL:C	2:C:92:GLU:H	2.24	0.41
1:B:57:LEU:HA	1:B:57:LEU:HD12	1.86	0.40
1:B:313:ILE:HD12	1:B:339:ALA:HB1	2.03	0.40
2:C:25:ASP:N	2:C:25:ASP:OD1	2.54	0.40
1:B:89:ALA:O	1:B:119:LEU:HD11	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:359:TRP:HZ3	1:B:361:ASP:OD2	2.03	0.40
2:C:50:VAL:HG12	2:C:51:GLN:N	2.36	0.40
2:C:80:VAL:O	2:C:81:ASN:C	2.58	0.40
2:D:58:ASP:O	2:D:61:ASP:N	2.45	0.40
2:C:124:ASP:C	2:C:126:PHE:N	2.73	0.40
1:A:171:MET:O	1:A:172:ILE:C	2.60	0.40
1:A:334:ILE:HG13	1:A:334:ILE:O	2.22	0.40
1:A:348:TRP:CE3	1:A:377:LEU:HD12	2.56	0.40
1:B:237:ASP:O	1:B:269:TYR:HB3	2.21	0.40
1:B:431:ALA:CB	1:B:473:VAL:HG12	2.47	0.40
2:D:32:TYR:OH	2:D:37:ASP:HB3	2.21	0.40
2:D:45:ILE:HD13	2:D:125:ALA:CB	2.51	0.40
1:A:413:PRO:CG	1:A:495:ASN:HB2	2.51	0.40
1:B:72:ASP:HB3	2:D:99:LYS:HD2	2.03	0.40
1:B:223:LEU:HD21	1:B:305:LEU:HD21	2.04	0.40
2:C:66:ILE:HB	2:C:71:SER:HB3	2.02	0.40
2:C:74:SER:O	2:C:78:LYS:HD3	2.22	0.40
2:D:70:LEU:HA	2:D:70:LEU:HD23	1.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	462/489 (94%)	368 (80%)	72 (16%)	22 (5%)	2	20
1	B	463/489 (95%)	378 (82%)	63 (14%)	22 (5%)	2	20
2	C	126/141 (89%)	88 (70%)	33 (26%)	5 (4%)	3	24
2	D	126/141 (89%)	86 (68%)	29 (23%)	11 (9%)	1	9
All	All	1177/1260 (93%)	920 (78%)	197 (17%)	60 (5%)	2	19

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	352	ASN
1	A	422	VAL
1	A	456	PRO
1	B	135	ARG
1	B	295	THR
1	B	422	VAL
1	B	456	PRO
1	B	466	GLY
1	B	469	PHE
2	C	40	PRO
2	C	45	ILE
2	D	40	PRO
1	A	122	ARG
1	A	175	VAL
1	A	242	VAL
1	A	296	PHE
1	A	464	SER
1	A	496	ASP
1	B	238	VAL
1	B	267	PHE
1	B	296	PHE
1	B	352	ASN
1	B	382	LEU
1	B	421	LEU
1	B	464	SER
2	C	35	GLY
2	C	67	SER
2	D	24	LYS
2	D	35	GLY
2	D	42	HIS
2	D	87	VAL
2	D	95	SER
1	A	89	ALA
1	A	155	PRO
1	A	387	GLY
1	A	471	LYS
1	B	70	ILE
2	C	24	LYS
2	D	105	PRO
1	A	106	SER
1	A	135	ARG
1	A	154	LYS
1	B	166	PRO

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Mol	Chain	Res	Type
1	B	202	LEU
1	B	325	VAL
1	B	468	PRO
2	D	11	ASN
2	D	14	ASP
1	A	178	ALA
1	A	279	SER
1	A	285	SER
1	A	413	PRO
1	A	421	LEU
1	B	122	ARG
1	B	367	ASN
2	D	100	LYS
1	B	175	VAL
2	D	45	ILE
1	A	443	CYS
1	B	443	CYS

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	372/438 (85%)	333 (90%)	39 (10%)	7	31
1	B	364/438 (83%)	327 (90%)	37 (10%)	7	32
2	C	117/135 (87%)	103 (88%)	14 (12%)	5	24
2	D	116/135 (86%)	99 (85%)	17 (15%)	3	18
All	All	969/1146 (85%)	862 (89%)	107 (11%)	6	29

All (107) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ILE
1	A	45	ASP
1	A	50	VAL
1	A	71	LEU

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Mol	Chain	Res	Type
1	A	80	ASN
1	A	90	THR
1	A	105	ASN
1	A	107	ILE
1	A	122	ARG
1	A	135	ARG
1	A	155	PRO
1	A	159	ASP
1	A	171	MET
1	A	179	TYR
1	A	182	LEU
1	A	184	LEU
1	A	188	VAL
1	A	201	ILE
1	A	202	LEU
1	A	221	TYR
1	A	222	LEU
1	A	223	LEU
1	A	256	GLN
1	A	259	TYR
1	A	281	ARG
1	A	284	ASP
1	A	294	ASN
1	A	296	PHE
1	A	301	VAL
1	A	303	THR
1	A	304	THR
1	A	316	PHE
1	A	329	GLU
1	A	342	LYS
1	A	353	ARG
1	A	361	ASP
1	A	377	LEU
1	A	420	ARG
1	A	435	GLU
1	B	45	ASP
1	B	50	VAL
1	B	59	THR
1	B	66	TRP
1	B	71	LEU
1	B	80	ASN
1	B	105	ASN

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Mol	Chain	Res	Type
1	B	107	ILE
1	B	133	LEU
1	B	135	ARG
1	B	182	LEU
1	B	184	LEU
1	B	186	CYS
1	B	188	VAL
1	B	190	GLN
1	B	194	SER
1	B	223	LEU
1	B	246	TRP
1	B	256	GLN
1	B	281	ARG
1	B	289	MET
1	B	294	ASN
1	B	301	VAL
1	B	304	THR
1	B	305	LEU
1	B	309	ASP
1	B	316	PHE
1	B	329	GLU
1	B	330	ASN
1	B	342	LYS
1	B	355	PHE
1	B	361	ASP
1	B	377	LEU
1	B	382	LEU
1	B	420	ARG
1	B	435	GLU
1	B	506	PHE
2	C	7	ARG
2	C	12	VAL
2	C	19	VAL
2	C	21	ASN
2	C	30	LEU
2	C	49	VAL
2	C	50	VAL
2	C	56	LEU
2	C	61	ASP
2	C	65	ASN
2	C	89	CYS
2	C	93	ASN

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Mol	Chain	Res	Type
2	C	103	LYS
2	C	120	ASN
2	D	7	ARG
2	D	12	VAL
2	D	19	VAL
2	D	30	LEU
2	D	49	VAL
2	D	50	VAL
2	D	52	LEU
2	D	57	THR
2	D	59	LEU
2	D	61	ASP
2	D	65	ASN
2	D	77	ASP
2	D	88	GLU
2	D	89	CYS
2	D	98	LEU
2	D	117	ARG
2	D	120	ASN

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

Mol	Chain	Res	Type
1	A	77	ASN
1	A	79	GLN
1	A	105	ASN
1	A	185	HIS
1	A	294	ASN
1	A	320	ASN
1	A	370	ASN
1	A	410	ASN
1	A	427	GLN
1	A	475	GLN
1	B	77	ASN
1	B	79	GLN
1	B	105	ASN
1	B	190	GLN
1	B	294	ASN
1	B	320	ASN
1	B	396	ASN
1	B	410	ASN
1	B	427	GLN

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Mol	Chain	Res	Type
1	B	475	GLN
2	C	11	ASN
2	C	21	ASN
2	C	65	ASN
2	C	93	ASN
2	C	120	ASN
2	D	11	ASN
2	D	21	ASN
2	D	51	GLN
2	D	65	ASN
2	D	93	ASN
2	D	120	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	A	750	1	14,14,15	0.76	0	17,19,21	1.12	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	850	1	14,14,15	0.96	1 (7%)	17,19,21	0.98	1 (5%)
3	NAG	A	800	1	14,14,15	0.58	0	17,19,21	0.72	1 (5%)
3	NAG	B	900	1	14,14,15	0.63	0	17,19,21	0.67	0
3	NAG	B	950	1	14,14,15	0.55	0	17,19,21	0.71	1 (5%)
3	NAG	A	700	1	14,14,15	0.58	0	17,19,21	0.68	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
3	NAG	A	750	1	-	6/6/23/26	0/1/1/1
3	NAG	B	850	1	-	6/6/23/26	0/1/1/1
3	NAG	A	800	1	-	4/6/23/26	0/1/1/1
3	NAG	B	900	1	-	3/6/23/26	0/1/1/1
3	NAG	B	950	1	-	6/6/23/26	0/1/1/1
3	NAG	A	700	1	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	850	NAG	C1-C2	2.63	1.56	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	750	NAG	C2-N2-C7	-2.57	119.25	122.90
3	B	850	NAG	C1-O5-C5	2.56	115.66	112.19
3	B	950	NAG	C2-N2-C7	-2.21	119.76	122.90
3	A	750	NAG	C3-C4-C5	-2.14	106.42	110.24
3	A	800	NAG	C2-N2-C7	-2.09	119.93	122.90

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	750	NAG	C3-C2-N2-C7
3	A	750	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	A	750	NAG	O7-C7-N2-C2
3	B	850	NAG	C3-C2-N2-C7
3	B	850	NAG	C8-C7-N2-C2
3	B	850	NAG	O7-C7-N2-C2
3	B	900	NAG	C8-C7-N2-C2
3	B	900	NAG	O7-C7-N2-C2
3	B	950	NAG	C8-C7-N2-C2
3	B	950	NAG	O7-C7-N2-C2
3	A	700	NAG	O5-C5-C6-O6
3	B	950	NAG	O5-C5-C6-O6
3	A	700	NAG	C8-C7-N2-C2
3	B	850	NAG	C4-C5-C6-O6
3	B	950	NAG	C4-C5-C6-O6
3	A	700	NAG	O7-C7-N2-C2
3	A	750	NAG	O5-C5-C6-O6
3	A	700	NAG	C4-C5-C6-O6
3	B	950	NAG	C1-C2-N2-C7
3	B	850	NAG	O5-C5-C6-O6
3	A	750	NAG	C4-C5-C6-O6
3	A	800	NAG	C4-C5-C6-O6
3	A	800	NAG	O5-C5-C6-O6
3	B	900	NAG	O5-C5-C6-O6
3	B	950	NAG	C3-C2-N2-C7
3	A	800	NAG	C8-C7-N2-C2
3	A	800	NAG	O7-C7-N2-C2
3	B	850	NAG	C1-C2-N2-C7
3	A	750	NAG	C1-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	750	NAG	2	0
3	B	850	NAG	2	0
3	B	900	NAG	1	0
3	B	950	NAG	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	468/489 (95%)	-0.48	3 (0%) 89 86	7, 62, 160, 197	0
1	B	469/489 (95%)	-0.37	5 (1%) 80 75	7, 89, 169, 213	0
2	C	132/141 (93%)	-0.65	0 100 100	5, 40, 168, 197	0
2	D	128/141 (90%)	-0.63	1 (0%) 86 81	5, 50, 163, 214	0
All	All	1197/1260 (95%)	-0.47	9 (0%) 86 81	5, 71, 167, 214	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	475	GLN	3.4
1	B	450	CYS	3.1
1	A	475	GLN	3.0
1	B	34	PRO	2.6
1	A	504	PHE	2.5
2	D	97	ASP	2.5
1	B	430	ALA	2.2
1	A	472	LEU	2.1
1	B	438	ILE	2.1

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 monosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	B	850	14/15	0.73	0.23	135,148,160,162	0
3	NAG	A	800	14/15	0.79	0.17	155,168,177,178	0
3	NAG	A	750	14/15	0.82	0.21	81,128,137,154	0
3	NAG	B	900	14/15	0.82	0.18	117,129,151,154	0
3	NAG	A	700	14/15	0.89	0.13	118,134,144,145	0
3	NAG	B	950	14/15	0.90	0.16	154,161,175,183	0

6.5 Other polymers [i](#)

There are no such residues in this entry.