



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 02:14 PM BST

PDB ID : 3TWJ
Title : Rho-associated protein kinase 1 (ROCK 1) IN COMPLEX WITH RKI1447
Authors : Martin, M.P.; Zhu, J.-Y.; Schonbrunn, E.
Deposited on : 2011-09-21
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
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) : 2.13.1

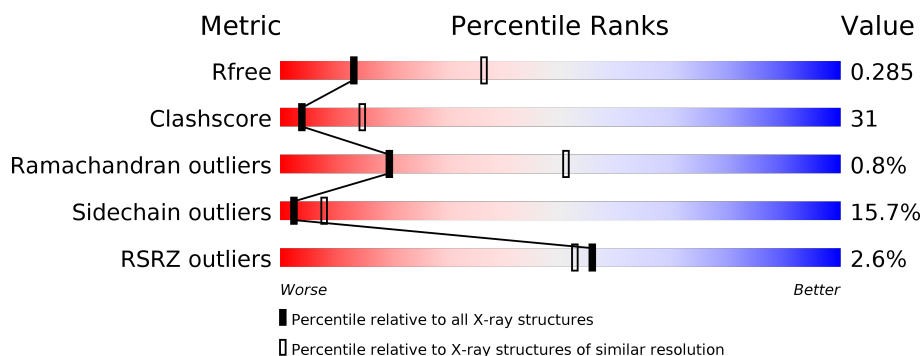
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	410	<div> <div>2%</div> <div>44%</div> <div>45%</div> <div>7%</div> <div>.</div> </div>
1	B	410	<div> <div>2%</div> <div>44%</div> <div>41%</div> <div>11%</div> <div>..</div> </div>
1	C	410	<div> <div>5%</div> <div>46%</div> <div>40%</div> <div>11%</div> <div>.</div> </div>
1	D	410	<div> <div>%</div> <div>47%</div> <div>41%</div> <div>8%</div> <div>..</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	07R	A	1	-	-	X	-
2	07R	C	2	-	-	X	-

2 Entry composition [i](#)

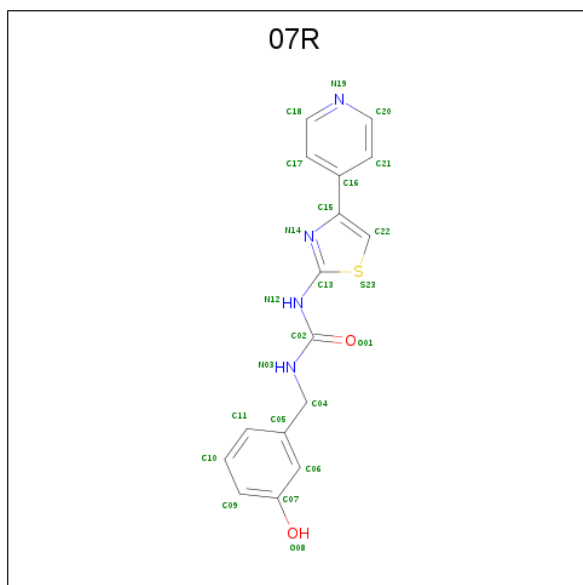
There are 4 unique types of molecules in this entry. The entry contains 12964 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Rho-associated protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3222	2059	532	610	21			
1	B	395	Total	C	N	O	S	0	0	0
			3211	2050	531	609	21			
1	C	396	Total	C	N	O	S	0	0	0
			3222	2059	532	610	21			
1	D	395	Total	C	N	O	S	70	0	0
			3211	2050	531	609	21			

- Molecule 2 is 1-[(3-hydroxyphenyl)methyl]-3-(4-pyridin-4-yl-1,3-thiazol-2-yl)urea (three-letter code: 07R) (formula: C₁₆H₁₄N₄O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			23	16	4	2	1		
2	C	1	Total	C	N	O	S	0	0
			23	16	4	2	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

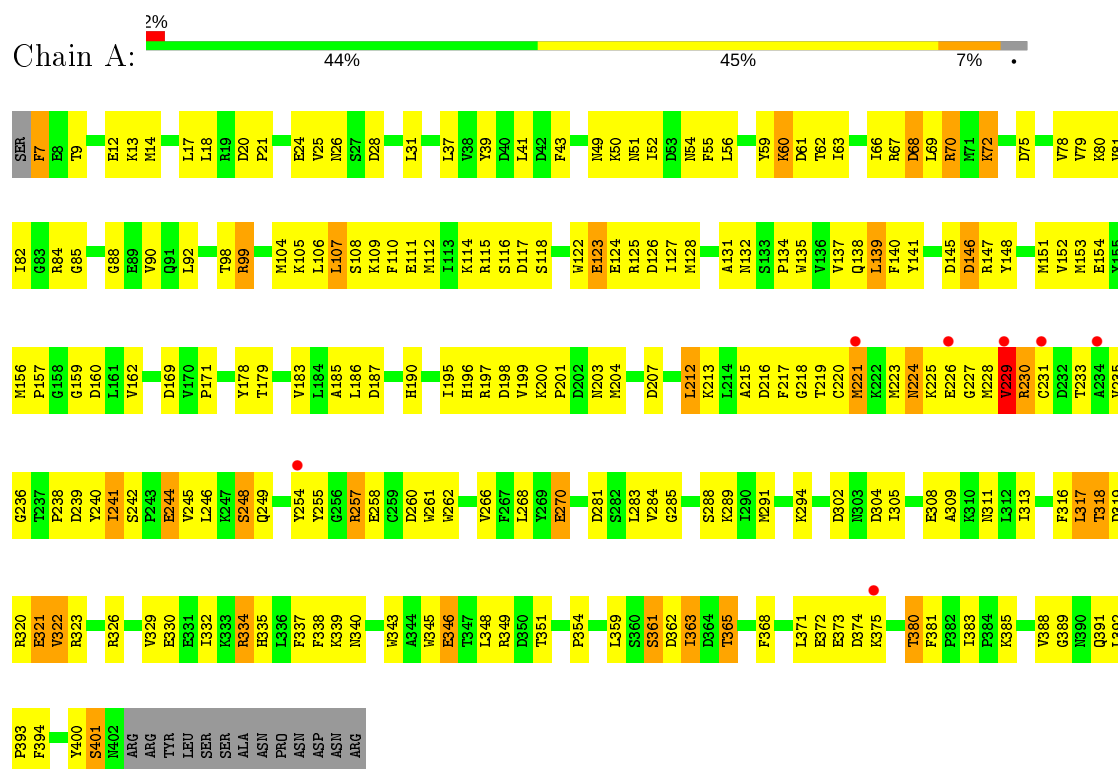
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	O	0	0
			5	5		
4	B	16	Total	O	0	0
			16	16		
4	C	5	Total	O	0	0
			5	5		
4	D	14	Total	O	0	0
			14	14		

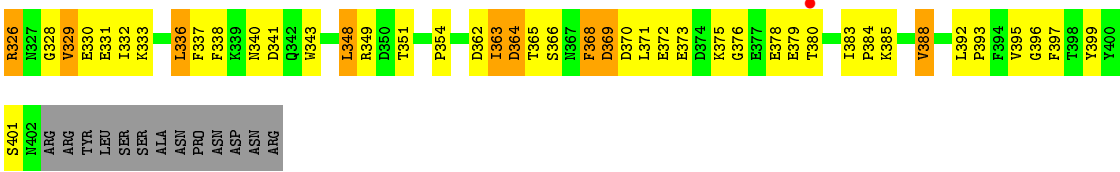
3 Residue-property plots

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: Rho-associated protein kinase 1







4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	145.67Å 150.92Å 205.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.74 – 2.90 19.74 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.74-2.90) 89.6 (19.74-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 2.88Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.224 , 0.289 0.218 , 0.285	Depositor DCC
R_{free} test set	1048 reflections (2.10%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.119 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12964	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 07R, EDO

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	0.55	0/3299	0.67	1/4457 (0.0%)
1	B	0.63	0/3287	0.79	0/4441
1	C	0.55	0/3299	0.73	3/4457 (0.1%)
1	D	0.60	0/3287	0.74	2/4441 (0.0%)
All	All	0.58	0/13172	0.73	6/17796 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	12
1	C	0	7
1	D	0	10
All	All	0	30

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	253	GLY	N-CA-C	6.20	128.60	113.10
1	D	302	ASP	CB-CG-OD1	5.68	123.41	118.30
1	A	302	ASP	CB-CG-OD2	5.21	122.99	118.30
1	C	302	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	251	GLY	N-CA-C	5.09	125.82	113.10
1	D	106	LEU	CA-CB-CG	5.09	127.00	115.30

There are no chirality outliers.

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	7	PHE	Peptide
1	B	114	LYS	Peptide
1	B	115	ARG	Peptide
1	B	118	SER	Peptide
1	B	148	TYR	Peptide
1	B	218	GLY	Peptide
1	B	220	CYS	Peptide
1	B	227	GLY	Peptide
1	B	250	GLY	Peptide
1	B	302	ASP	Peptide
1	B	363	ILE	Peptide
1	B	375	LYS	Peptide
1	B	9	THR	Peptide
1	C	217	PHE	Peptide
1	C	219	THR	Peptide
1	C	236	GLY	Peptide
1	C	252	ASP	Peptide
1	C	303	ASN	Peptide
1	C	360	SER	Peptide
1	C	361	SER	Peptide
1	D	116	SER	Peptide
1	D	19	ARG	Peptide
1	D	21	PRO	Peptide
1	D	220	CYS	Peptide
1	D	229	VAL	Peptide
1	D	232	ASP	Peptide
1	D	233	THR	Peptide
1	D	363	ILE	Peptide
1	D	369	ASP	Peptide
1	D	9	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3222	0	3120	194	0
1	B	3211	0	3111	192	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3222	0	3120	225	0
1	D	3211	0	3111	175	0
2	A	23	0	14	16	0
2	C	23	0	14	14	0
3	A	4	0	6	0	0
3	B	4	0	6	2	0
3	D	4	0	6	3	0
4	A	5	0	0	1	0
4	B	16	0	0	4	0
4	C	5	0	0	1	0
4	D	14	0	0	1	0
All	All	12964	0	12508	775	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 31.

All (775) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:ASP:HA	1:B:302:ASP:HB3	1.23	1.10
1:A:372:GLU:OE2	1:A:375:LYS:HE3	1.48	1.10
1:B:80:LYS:HE2	1:B:370:ASP:HA	1.21	1.10
1:B:222:LYS:HB3	1:B:229:VAL:HG21	1.34	1.08
1:D:233:THR:HG22	1:D:234:ALA:H	1.01	1.08
1:A:156:MET:HE1	1:A:213:LYS:HD2	1.39	1.05
1:B:225:LYS:HB2	1:B:228:MET:CE	1.86	1.05
1:D:84:ARG:HH21	1:D:371:LEU:HD12	1.23	1.01
1:A:216:ASP:HB2	2:A:1:07R:N12	1.75	0.99
1:B:113:ILE:HD11	1:B:393:PRO:HG2	1.45	0.99
1:B:225:LYS:HB2	1:B:228:MET:HE3	1.43	0.98
1:C:230:ARG:HH21	1:C:251:GLY:HA2	1.27	0.97
1:C:195:ILE:HD12	1:C:221:MET:HE3	1.44	0.96
1:D:233:THR:HG22	1:D:234:ALA:N	1.80	0.92
1:C:162:VAL:HG23	1:C:201:PRO:HB2	1.53	0.91
1:B:301:ASP:CA	1:B:302:ASP:HB3	2.01	0.91
1:C:9:THR:HG22	1:C:11:PHE:H	1.38	0.88
1:C:183:VAL:HG22	1:C:261:TRP:HZ3	1.39	0.88
1:B:223:MET:SD	1:B:224:ASN:ND2	2.47	0.87
1:A:153:MET:SD	2:A:1:07R:H14	2.14	0.86
1:D:204:MET:HB3	1:D:212:LEU:HD11	1.56	0.86
1:A:37:LEU:O	1:A:41:LEU:HB2	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:LYS:HA	1:B:228:MET:SD	2.18	0.84
1:C:211:HIS:CD2	1:C:349:ARG:HA	2.13	0.84
1:A:361:SER:HB2	1:A:363:ILE:H	1.43	0.83
1:A:235:VAL:HG12	1:A:236:GLY:H	1.44	0.82
1:A:41:LEU:HD13	1:A:52:ILE:HG23	1.60	0.81
1:C:230:ARG:HH21	1:C:251:GLY:CA	1.92	0.81
1:C:230:ARG:NH2	1:C:251:GLY:HA2	1.95	0.81
1:B:333:LYS:HB3	1:B:345:TRP:NE1	1.96	0.81
1:C:205:LEU:O	1:C:206:LEU:HD23	1.81	0.81
1:C:308:GLU:HG2	1:C:336:LEU:HB2	1.64	0.80
1:C:183:VAL:HG22	1:C:261:TRP:CZ3	2.16	0.79
1:C:197:ARG:CZ	1:C:219:THR:CG2	2.60	0.79
1:B:227:GLY:O	1:B:229:VAL:HG13	1.82	0.79
1:C:135:TRP:CH2	1:C:349:ARG:HG3	2.18	0.78
1:B:370:ASP:O	1:B:371:LEU:HD23	1.83	0.78
1:A:156:MET:HE1	1:A:213:LYS:CD	2.14	0.78
1:A:230:ARG:HB3	1:A:254:TYR:CD2	2.19	0.77
1:A:153:MET:SD	2:A:1:07R:C22	2.71	0.77
1:D:131:ALA:HA	1:D:192:MET:HE1	1.66	0.77
1:B:223:MET:HB2	1:B:224:ASN:ND2	2.00	0.76
1:A:393:PRO:HG2	1:A:394:PHE:CE1	2.20	0.75
1:A:105:LYS:HE2	1:A:107:LEU:HD21	1.69	0.75
1:C:85:GLY:HA3	2:C:2:07R:C07	2.17	0.75
1:B:333:LYS:HD2	1:B:345:TRP:CD2	2.21	0.74
1:B:300:PRO:O	1:B:302:ASP:HB3	1.87	0.74
1:B:80:LYS:HE2	1:B:370:ASP:CA	2.12	0.74
1:A:372:GLU:CD	1:A:375:LYS:HE3	2.06	0.74
1:B:225:LYS:CA	1:B:228:MET:SD	2.75	0.74
1:C:197:ARG:HD2	1:C:255:TYR:OH	1.87	0.74
1:A:124:GLU:HB2	1:A:218:GLY:HA2	1.69	0.74
1:D:233:THR:CG2	1:D:234:ALA:H	1.87	0.73
1:A:372:GLU:OE2	1:A:375:LYS:CE	2.35	0.73
1:A:348:LEU:O	1:A:351:THR:HG22	1.88	0.73
1:A:154:GLU:O	2:A:1:07R:H12	1.88	0.73
1:B:221:MET:HG2	1:B:229:VAL:HB	1.70	0.72
1:B:378:GLU:HG3	1:B:379:GLU:H	1.52	0.72
1:C:238:PRO:HG3	1:C:283:LEU:CD1	2.19	0.72
1:C:199:VAL:HG21	1:C:260:ASP:HB3	1.70	0.72
1:B:223:MET:HG3	1:B:224:ASN:OD1	1.90	0.72
1:C:368:PHE:CZ	2:C:2:07R:H11	2.24	0.72
1:C:43:PHE:CE2	1:C:384:PRO:HG2	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LYS:HE3	1:A:365:THR:HG21	1.71	0.71
1:B:333:LYS:HB3	1:B:345:TRP:CE2	2.25	0.71
1:C:194:PHE:HB3	1:C:217:PHE:HZ	1.54	0.71
1:C:194:PHE:HB3	1:C:217:PHE:CZ	2.25	0.71
1:B:314:CYS:O	1:B:318:THR:HG23	1.90	0.71
1:D:308:GLU:CD	1:D:308:GLU:H	1.93	0.71
1:A:238:PRO:HG3	1:A:283:LEU:CD1	2.21	0.70
1:D:105:LYS:HE2	1:D:107:LEU:HD21	1.72	0.70
1:A:230:ARG:HB3	1:A:254:TYR:HD2	1.55	0.70
1:C:216:ASP:OD2	2:C:2:07R:C02	2.39	0.70
1:D:321:GLU:H	1:D:321:GLU:CD	1.91	0.70
1:B:141:TYR:OH	3:B:2:EDO:H11	1.91	0.70
1:D:80:LYS:HD3	1:D:365:THR:HG23	1.73	0.70
1:B:257:ARG:H	1:B:257:ARG:NE	1.89	0.70
1:D:286:THR:O	1:D:290:ILE:HG13	1.91	0.70
1:C:230:ARG:HG3	1:C:230:ARG:NH1	2.07	0.70
1:B:74:GLU:O	1:B:96:LYS:HE3	1.92	0.70
1:A:49:ASN:HD22	1:A:52:ILE:HG13	1.57	0.69
1:C:221:MET:CE	1:C:229:VAL:HG13	2.22	0.69
1:D:211:HIS:CE1	1:D:349:ARG:HA	2.28	0.69
1:B:359:LEU:HG	1:B:360:SER:N	2.07	0.68
1:B:220:CYS:SG	1:B:221:MET:N	2.66	0.68
1:C:185:ALA:O	1:C:189:ILE:HG13	1.93	0.68
1:B:181:GLU:OE1	1:B:211:HIS:HD2	1.75	0.68
1:A:216:ASP:HB2	2:A:1:07R:H9	1.59	0.68
1:A:313:ILE:HG23	1:A:317:LEU:HD22	1.74	0.68
1:C:127:ILE:HD13	1:C:192:MET:CE	2.24	0.68
1:A:169:ASP:O	1:A:171:PRO:HD3	1.94	0.68
1:C:197:ARG:NE	1:C:219:THR:CG2	2.57	0.67
1:C:230:ARG:HG3	1:C:230:ARG:HH11	1.60	0.67
1:A:362:ASP:OD1	1:A:363:ILE:HG12	1.95	0.67
1:D:83:GLY:HA2	1:D:371:LEU:HG	1.75	0.67
1:B:249:GLN:N	1:B:250:GLY:HA3	2.08	0.67
1:C:127:ILE:HD13	1:C:192:MET:HE2	1.76	0.67
1:D:19:ARG:HH21	1:D:21:PRO:HG3	1.59	0.67
1:B:221:MET:HG2	1:B:229:VAL:CG1	2.25	0.67
1:C:230:ARG:NH2	1:C:232:ASP:OD2	2.27	0.67
1:A:17:LEU:HG	1:A:25:VAL:CG2	2.24	0.67
1:C:162:VAL:CG2	1:C:201:PRO:HB2	2.25	0.67
1:B:301:ASP:HA	1:B:302:ASP:CB	2.12	0.67
1:C:46:LEU:H	1:C:46:LEU:HD23	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:ASP:OD2	1:B:237:THR:HG23	1.95	0.66
1:A:156:MET:CE	1:A:213:LYS:HD2	2.22	0.66
1:A:7:PHE:N	4:A:416:HOH:O	2.29	0.66
1:A:212:LEU:HG	1:A:213:LYS:N	2.09	0.66
1:C:72:LYS:HB3	1:C:74:GLU:OE1	1.95	0.66
1:A:238:PRO:HA	1:A:241:ILE:HG13	1.76	0.65
1:B:221:MET:HG3	1:B:222:LYS:HB2	1.78	0.65
1:D:160:ASP:CG	1:D:162:VAL:HG13	2.17	0.65
1:A:204:MET:HB3	1:A:212:LEU:HD11	1.79	0.65
1:D:276:THR:HG23	1:D:277:PRO:HD2	1.78	0.65
1:A:90:VAL:HG23	2:A:1:07R:H8	1.78	0.65
1:D:135:TRP:CH2	1:D:349:ARG:HB2	2.31	0.65
1:A:85:GLY:H	2:A:1:07R:C10	2.10	0.64
1:C:248:SER:HB2	1:C:253:GLY:HA2	1.79	0.64
1:D:195:ILE:HG22	1:D:197:ARG:HG3	1.79	0.64
1:C:87:PHE:HB2	2:C:2:07R:H6	1.79	0.64
1:A:56:LEU:O	1:A:60:LYS:HB2	1.98	0.64
1:B:257:ARG:H	1:B:257:ARG:HE	1.45	0.64
1:D:200:LYS:HD3	1:D:237:THR:OG1	1.97	0.64
1:D:216:ASP:O	1:D:217:PHE:HD2	1.82	0.64
1:A:221:MET:HG2	1:A:229:VAL:HG11	1.79	0.63
1:A:388:VAL:HG23	1:A:389:GLY:H	1.63	0.63
1:A:137:VAL:HG21	1:A:215:ALA:HB2	1.80	0.63
1:D:248:SER:C	1:D:250:GLY:H	2.01	0.63
1:C:197:ARG:NE	1:C:219:THR:HG21	2.13	0.63
1:D:156:MET:HA	1:D:156:MET:HE2	1.79	0.63
1:D:293:HIS:HA	1:D:296:SER:HB3	1.80	0.63
1:B:224:ASN:O	1:B:225:LYS:HG2	1.98	0.63
1:D:239:ASP:HB3	1:D:276:THR:HG21	1.79	0.63
1:B:316:PHE:O	1:B:323:ARG:HD3	1.99	0.63
1:C:221:MET:HE3	1:C:229:VAL:HG13	1.81	0.62
1:C:74:GLU:O	1:C:96:LYS:HE3	1.99	0.62
1:A:190:HIS:CE1	1:A:257:ARG:HB2	2.33	0.62
1:C:217:PHE:CD2	1:C:220:CYS:SG	2.92	0.62
1:A:107:LEU:HD11	1:A:151:MET:HE2	1.80	0.62
1:C:178:TYR:O	1:C:182:VAL:HG23	1.99	0.62
1:C:110:PHE:O	1:C:113:ILE:HG13	2.00	0.62
1:C:83:GLY:HA2	1:C:371:LEU:HD11	1.81	0.62
1:D:112:MET:HG2	1:D:120:PHE:CZ	2.35	0.62
1:B:74:GLU:N	1:B:74:GLU:CD	2.53	0.62
1:C:85:GLY:HA3	2:C:2:07R:C06	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:GLU:HG2	1:A:320:ARG:HD2	1.81	0.62
1:C:221:MET:CE	1:C:255:TYR:CE1	2.83	0.62
1:A:235:VAL:HG12	1:A:236:GLY:N	2.14	0.62
1:C:353:ALA:HB1	1:C:354:PRO:HD2	1.82	0.62
1:B:225:LYS:HB2	1:B:228:MET:SD	2.40	0.62
1:B:84:ARG:HH22	1:B:372:GLU:HB3	1.65	0.61
1:C:110:PHE:CE2	1:C:379:GLU:HB3	2.35	0.61
1:C:261:TRP:O	1:C:264:VAL:HG23	2.00	0.61
1:D:19:ARG:HD2	1:D:21:PRO:HD3	1.82	0.61
1:C:109:LYS:HD2	1:C:146:ASP:O	2.01	0.61
1:A:123:GLU:HG3	1:A:220:CYS:O	1.99	0.61
1:B:266:VAL:HG13	1:B:277:PRO:HD2	1.82	0.61
1:D:19:ARG:HD2	1:D:21:PRO:CG	2.31	0.61
1:A:105:LYS:HD2	2:A:1:07R:O01	2.01	0.61
1:A:200:LYS:HB2	1:A:201:PRO:HD2	1.82	0.61
1:B:333:LYS:HD2	1:B:345:TRP:CE2	2.36	0.61
1:C:195:ILE:HD12	1:C:221:MET:CE	2.24	0.60
1:D:110:PHE:CD2	1:D:380:THR:HA	2.36	0.60
1:B:300:PRO:O	1:B:302:ASP:CB	2.49	0.60
1:A:224:ASN:N	1:A:224:ASN:OD1	2.33	0.60
1:C:196:HIS:CD2	1:C:214:LEU:HD23	2.37	0.60
1:C:217:PHE:CD2	1:C:220:CYS:CB	2.85	0.60
1:C:217:PHE:HD2	1:C:220:CYS:SG	2.24	0.60
1:C:197:ARG:HD2	1:C:255:TYR:CZ	2.37	0.60
1:C:38:VAL:HG21	1:C:63:ILE:HD13	1.84	0.60
1:C:197:ARG:CZ	1:C:219:THR:HG22	2.30	0.60
1:C:126:ASP:HA	1:C:130:PHE:CE1	2.37	0.60
1:C:197:ARG:HD2	1:C:255:TYR:CE1	2.36	0.60
1:D:95:HIS:CD2	3:D:1:EDO:H11	2.37	0.60
1:B:361:SER:OG	1:B:363:ILE:HG22	2.01	0.59
1:D:336:LEU:HD12	1:D:336:LEU:H	1.67	0.59
1:C:178:TYR:OH	1:C:354:PRO:HG2	2.02	0.59
1:C:196:HIS:CE1	1:C:198:ASP:O	2.55	0.59
1:C:223:MET:HG2	1:C:227:GLY:HA2	1.82	0.59
1:A:68:ASP:O	1:A:72:LYS:HE2	2.02	0.59
1:B:249:GLN:HG3	4:B:430:HOH:O	2.01	0.59
1:D:98:THR:HG21	3:D:1:EDO:O2	2.01	0.59
1:C:238:PRO:HG3	1:C:283:LEU:HD11	1.84	0.59
1:D:323:ARG:O	1:D:326:ARG:HB3	2.02	0.59
1:D:98:THR:O	1:D:99:ARG:HB2	2.01	0.59
1:C:359:LEU:HD22	1:C:364:ASP:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:323:ARG:O	1:D:326:ARG:HD3	2.02	0.59
1:B:147:ARG:NH2	1:B:380:THR:HG22	2.17	0.59
1:C:268:LEU:HD12	1:C:312:LEU:HD23	1.85	0.59
1:D:123:GLU:O	1:D:127:ILE:HG13	2.02	0.59
1:D:102:TYR:HE1	1:D:140:PHE:CD1	2.21	0.59
1:D:343:TRP:HB3	1:D:351:THR:HG21	1.83	0.59
1:D:160:ASP:OD1	1:D:162:VAL:HG13	2.02	0.59
1:C:127:ILE:HD12	1:C:189:ILE:HG23	1.84	0.59
1:C:181:GLU:HB3	1:C:212:LEU:HD22	1.85	0.59
1:A:85:GLY:HA3	2:A:1:07R:C07	2.33	0.58
1:B:222:LYS:CB	1:B:229:VAL:HG21	2.22	0.58
1:C:392:LEU:N	1:C:393:PRO:HD2	2.18	0.58
1:B:321:GLU:CD	1:B:321:GLU:H	2.07	0.58
1:B:374:ASP:C	1:B:375:LYS:HG2	2.24	0.58
1:A:187:ASP:OD2	1:A:329:VAL:HG11	2.03	0.58
1:A:228:MET:O	1:A:229:VAL:HG13	2.03	0.58
1:A:316:PHE:O	1:A:323:ARG:HD2	2.02	0.58
1:B:81:VAL:HG22	1:B:91:GLN:HG2	1.85	0.58
1:A:82:ILE:O	1:A:82:ILE:HG22	2.03	0.58
1:D:155:TYR:O	1:D:156:MET:HE3	2.03	0.58
1:A:17:LEU:HG	1:A:25:VAL:HG21	1.86	0.58
1:C:232:ASP:O	1:C:233:THR:OG1	2.22	0.58
1:C:347:THR:O	1:C:347:THR:HG23	2.03	0.58
1:B:196:HIS:CE1	1:B:198:ASP:O	2.56	0.58
1:C:38:VAL:HG11	1:C:63:ILE:CD1	2.34	0.58
1:C:109:LYS:HE3	1:C:145:ASP:O	2.04	0.57
1:C:200:LYS:HE3	1:C:202:ASP:HB2	1.85	0.57
1:B:134:PRO:O	1:B:213:LYS:HE3	2.03	0.57
1:D:230:ARG:HB3	1:D:283:LEU:HG	1.86	0.57
1:D:244:GLU:HG2	1:D:245:VAL:N	2.19	0.57
1:C:195:ILE:HG23	1:C:257:ARG:HA	1.86	0.57
1:C:308:GLU:CG	1:C:336:LEU:HB2	2.33	0.57
1:D:80:LYS:HZ2	1:D:368:PHE:HB3	1.69	0.57
1:C:185:ALA:CB	1:C:214:LEU:HD13	2.34	0.57
1:D:160:ASP:HB3	1:D:205:LEU:HD13	1.85	0.57
1:A:135:TRP:HB3	1:A:185:ALA:HA	1.87	0.57
1:A:248:SER:HG	1:A:255:TYR:HE1	1.53	0.57
1:D:125:ARG:NH1	1:D:397:PHE:O	2.37	0.57
1:A:197:ARG:O	1:A:198:ASP:HB3	2.04	0.57
1:C:244:GLU:HG3	1:C:255:TYR:HB2	1.86	0.57
1:D:134:PRO:O	1:D:213:LYS:HE3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:GLN:OE1	1:B:106:LEU:HD11	2.04	0.57
1:B:362:ASP:OD1	1:B:363:ILE:N	2.38	0.57
1:D:363:ILE:O	1:D:364:ASP:C	2.44	0.57
1:A:85:GLY:HA3	2:A:1:07R:C09	2.35	0.56
1:A:178:TYR:OH	1:A:354:PRO:HG2	2.05	0.56
1:A:261:TRP:HB3	1:A:316:PHE:CE2	2.41	0.56
1:B:121:PHE:CE1	1:B:122:TRP:NE1	2.72	0.56
1:D:202:ASP:N	1:D:202:ASP:OD1	2.35	0.56
1:C:221:MET:HE3	1:C:229:VAL:CG1	2.36	0.56
1:C:186:LEU:HD12	1:C:261:TRP:CZ3	2.40	0.56
1:D:117:ASP:CG	1:D:118:SER:H	2.09	0.56
1:D:24:GLU:O	1:D:29:CYS:HB2	2.06	0.56
1:D:176:ARG:HA	1:D:337:PHE:HE1	1.71	0.56
1:A:124:GLU:HA	1:A:217:PHE:HB2	1.87	0.56
1:A:9:THR:HG22	1:A:12:GLU:CD	2.26	0.56
1:B:302:ASP:O	1:B:302:ASP:OD1	2.22	0.56
1:A:196:HIS:O	1:A:219:THR:HG23	2.06	0.56
1:D:19:ARG:HD2	1:D:21:PRO:CD	2.35	0.56
1:B:248:SER:OG	1:B:255:TYR:HD2	1.89	0.56
1:B:359:LEU:CG	1:B:360:SER:N	2.68	0.56
1:C:330:GLU:O	1:C:334:ARG:HG3	2.05	0.56
1:C:160:ASP:HB3	1:C:205:LEU:HD13	1.86	0.55
1:C:95:HIS:CE1	1:C:97:SER:HB2	2.40	0.55
1:B:221:MET:HG2	1:B:229:VAL:CB	2.33	0.55
1:B:95:HIS:HB3	1:B:98:THR:OG1	2.06	0.55
1:C:176:ARG:HD3	1:C:338:PHE:O	2.06	0.55
1:A:305:ILE:HG22	1:A:309:ALA:HB3	1.87	0.55
1:B:221:MET:CG	1:B:229:VAL:HB	2.36	0.55
1:C:155:TYR:CE2	1:C:157:PRO:HB3	2.41	0.55
1:A:109:LYS:HB2	1:A:147:ARG:O	2.06	0.55
1:D:110:PHE:O	1:D:113:ILE:HG13	2.06	0.55
1:D:80:LYS:CD	1:D:365:THR:HG23	2.35	0.55
1:A:216:ASP:HB2	2:A:1:07R:C02	2.36	0.55
1:C:126:ASP:HA	1:C:130:PHE:CD1	2.42	0.55
1:C:153:MET:SD	2:C:2:07R:H14	2.46	0.55
1:A:160:ASP:OD2	1:A:162:VAL:N	2.39	0.55
1:C:221:MET:HE2	1:C:255:TYR:CE1	2.40	0.55
1:A:231:CYS:HB3	1:A:233:THR:HG23	1.89	0.55
1:A:242:SER:O	1:A:246:LEU:HG	2.06	0.55
1:B:311:ASN:ND2	4:B:418:HOH:O	2.39	0.55
1:C:204:MET:HB3	1:C:212:LEU:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:273:VAL:HG13	1:C:300:PRO:HG2	1.89	0.55
1:B:287:TYR:O	1:B:291:MET:HG2	2.07	0.55
1:A:128:MET:HG3	1:A:217:PHE:HD2	1.72	0.54
1:A:98:THR:O	1:A:99:ARG:HB2	2.07	0.54
1:D:216:ASP:C	1:D:217:PHE:HD2	2.10	0.54
1:B:39:TYR:CE1	1:B:146:ASP:HB3	2.41	0.54
1:C:155:TYR:CZ	1:C:157:PRO:HB3	2.43	0.54
1:B:359:LEU:HD23	1:B:360:SER:H	1.71	0.54
1:A:13:LYS:O	1:A:17:LEU:HB2	2.08	0.54
1:B:39:TYR:CD1	1:B:146:ASP:HB3	2.42	0.54
1:D:19:ARG:CD	1:D:21:PRO:HD3	2.38	0.54
1:D:34:LEU:O	1:D:38:VAL:HG23	2.07	0.54
1:D:81:VAL:O	1:D:371:LEU:HB2	2.06	0.54
1:C:216:ASP:OD2	2:C:2:07R:N03	2.40	0.54
1:C:221:MET:HE1	1:C:255:TYR:CE1	2.42	0.54
1:A:20:ASP:OD2	1:A:21:PRO:HD2	2.07	0.54
1:B:348:LEU:O	1:B:351:THR:HG23	2.07	0.54
1:C:156:MET:HG3	1:C:205:LEU:HB3	1.89	0.54
1:C:318:THR:HG21	1:C:323:ARG:HA	1.89	0.54
1:A:255:TYR:HA	1:A:320:ARG:HH22	1.72	0.54
1:C:85:GLY:HA3	2:C:2:07R:C09	2.38	0.54
1:B:84:ARG:O	1:B:219:THR:O	2.25	0.54
1:B:231:CYS:HA	1:B:238:PRO:HG2	1.90	0.54
1:B:372:GLU:HG2	1:B:374:ASP:HB2	1.91	0.53
1:A:41:LEU:HD21	1:B:387:PHE:CE1	2.43	0.53
1:B:231:CYS:SG	1:B:232:ASP:N	2.81	0.53
1:C:146:ASP:OD1	1:C:146:ASP:N	2.40	0.53
1:C:198:ASP:OD1	1:C:200:LYS:HE2	2.07	0.53
1:D:164:LEU:O	1:D:164:LEU:HD23	2.08	0.53
1:D:19:ARG:HD2	1:D:21:PRO:HB3	1.91	0.53
1:B:200:LYS:HE2	1:B:202:ASP:HB2	1.90	0.53
1:C:241:ILE:HG21	1:C:246:LEU:CD2	2.37	0.53
1:D:392:LEU:N	1:D:393:PRO:HD2	2.24	0.53
1:A:18:LEU:HA	1:A:26:ASN:HA	1.91	0.53
1:C:181:GLU:CB	1:C:212:LEU:HD22	2.38	0.53
1:C:312:LEU:HD22	1:C:337:PHE:CD1	2.43	0.53
1:B:98:THR:HG21	3:B:2:EDO:H22	1.90	0.53
1:C:329:VAL:HA	1:C:332:ILE:HD12	1.89	0.53
1:A:116:SER:O	1:A:117:ASP:C	2.47	0.53
1:A:392:LEU:N	1:A:393:PRO:HD2	2.24	0.53
1:B:198:ASP:HB2	1:B:236:GLY:HA2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:370:ASP:O	1:C:371:LEU:HD23	2.09	0.53
1:D:287:TYR:O	1:D:291:MET:HG2	2.09	0.53
1:A:69:LEU:CD2	1:B:13:LYS:HB3	2.39	0.53
1:A:49:ASN:HD22	1:A:52:ILE:CG1	2.21	0.53
1:B:361:SER:C	4:B:420:HOH:O	2.47	0.53
1:A:14:MET:CE	1:B:69:LEU:HB2	2.39	0.53
1:C:302:ASP:O	1:C:302:ASP:OD1	2.27	0.53
1:C:60:LYS:O	1:C:63:ILE:HG13	2.09	0.53
1:A:138:GLN:HG2	1:A:140:PHE:CE2	2.44	0.53
1:A:186:LEU:HD13	1:A:260:ASP:HB3	1.91	0.53
1:A:85:GLY:N	2:A:1:07R:C10	2.72	0.53
1:C:109:LYS:HD3	1:C:394:PHE:CD1	2.44	0.53
1:C:230:ARG:CG	1:C:230:ARG:HH11	2.22	0.53
1:A:196:HIS:HA	1:A:220:CYS:SG	2.48	0.53
1:B:17:LEU:HB3	1:B:25:VAL:CG2	2.39	0.52
1:A:108:SER:HA	1:A:148:TYR:HD1	1.74	0.52
1:A:104:MET:HA	1:A:151:MET:O	2.09	0.52
1:A:128:MET:HG3	1:A:217:PHE:CD2	2.44	0.52
1:C:282:SER:OG	1:C:284:VAL:HG12	2.10	0.52
1:C:248:SER:O	1:C:249:GLN:NE2	2.42	0.52
1:C:66:ILE:HD11	1:D:17:LEU:HD13	1.90	0.52
1:B:228:MET:HG3	1:B:230:ARG:CD	2.39	0.52
1:A:104:MET:HG2	1:A:104:MET:O	2.09	0.52
1:B:291:MET:HA	1:B:291:MET:HE3	1.91	0.52
1:B:302:ASP:OD1	1:B:305:ILE:HB	2.10	0.52
1:B:149:LEU:HB3	1:B:397:PHE:CE1	2.45	0.52
1:C:359:LEU:HD21	1:C:366:SER:OG	2.09	0.52
1:C:309:ALA:O	1:C:313:ILE:HG13	2.10	0.52
1:D:110:PHE:HE2	1:D:379:GLU:HG3	1.74	0.52
1:B:46:LEU:HD21	1:B:386:ALA:C	2.30	0.52
1:D:315:ALA:HB1	1:D:324:LEU:HD22	1.92	0.52
1:B:108:SER:O	1:B:112:MET:HB2	2.11	0.51
1:D:305:ILE:O	1:D:310:LYS:HE3	2.10	0.51
1:A:66:ILE:HG22	1:A:67:ARG:N	2.23	0.51
1:B:149:LEU:HD22	1:B:397:PHE:CD1	2.45	0.51
1:B:160:ASP:HA	1:B:204:MET:O	2.11	0.51
1:A:242:SER:OG	1:A:245:VAL:HG23	2.09	0.51
1:A:361:SER:CB	1:A:363:ILE:HG13	2.40	0.51
1:B:338:PHE:O	1:B:340:ASN:ND2	2.43	0.51
1:C:110:PHE:CE1	1:C:381:PHE:HA	2.45	0.51
1:B:324:LEU:HD21	1:B:332:ILE:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:LEU:HD13	1:C:287:TYR:CD1	2.46	0.51
1:C:381:PHE:HD2	1:C:381:PHE:H	1.59	0.51
1:A:285:GLY:O	1:A:289:LYS:HB2	2.10	0.51
1:D:102:TYR:CE1	1:D:140:PHE:CD1	2.99	0.51
1:D:84:ARG:NH2	1:D:371:LEU:HD12	2.07	0.51
1:A:122:TRP:O	1:A:126:ASP:HB2	2.11	0.51
1:A:318:THR:O	1:A:323:ARG:NH1	2.42	0.51
1:C:223:MET:CG	1:C:227:GLY:HA2	2.40	0.51
1:A:361:SER:HB2	1:A:363:ILE:HG13	1.93	0.51
1:C:110:PHE:HE1	1:C:381:PHE:HA	1.75	0.51
1:D:325:GLY:HA2	1:D:328:GLY:O	2.11	0.51
1:D:87:PHE:HZ	1:D:116:SER:HB3	1.76	0.51
1:B:228:MET:HG3	1:B:230:ARG:HD3	1.93	0.50
1:D:372:GLU:O	1:D:372:GLU:HG3	2.10	0.50
1:B:110:PHE:O	1:B:114:LYS:HB3	2.12	0.50
1:A:14:MET:HE2	1:B:69:LEU:HB2	1.93	0.50
1:C:15:ASP:O	1:C:19:ARG:HG3	2.11	0.50
1:D:270:GLU:HG3	1:D:270:GLU:O	2.10	0.50
1:D:29:CYS:SG	1:D:396:GLY:HA2	2.51	0.50
1:B:123:GLU:O	1:B:127:ILE:HG13	2.11	0.50
1:B:277:PRO:HB2	1:B:278:PHE:CD2	2.47	0.50
1:C:359:LEU:HD22	1:C:364:ASP:CB	2.41	0.50
1:D:95:HIS:HB3	1:D:98:THR:OG1	2.12	0.50
1:B:222:LYS:HB3	1:B:229:VAL:CG2	2.23	0.50
1:C:109:LYS:HE2	1:C:149:LEU:HD23	1.93	0.50
1:C:60:LYS:HA	1:C:63:ILE:HD11	1.92	0.50
1:B:156:MET:HE2	1:B:213:LYS:HB2	1.93	0.50
1:D:131:ALA:HA	1:D:192:MET:CE	2.39	0.50
1:C:63:ILE:HA	1:C:66:ILE:HB	1.92	0.50
1:B:169:ASP:O	1:B:171:PRO:HD3	2.11	0.49
1:D:170:VAL:HG13	1:D:174:TRP:HB2	1.93	0.49
1:A:308:GLU:OE1	1:A:308:GLU:N	2.42	0.49
1:A:321:GLU:CD	1:A:321:GLU:H	2.15	0.49
1:B:359:LEU:HG	1:B:360:SER:O	2.11	0.49
1:D:19:ARG:HD2	1:D:21:PRO:CB	2.42	0.49
1:D:176:ARG:HA	1:D:337:PHE:CE1	2.48	0.49
1:D:265:GLY:HA3	1:D:317:LEU:HD13	1.94	0.49
1:A:60:LYS:O	1:A:63:ILE:HG22	2.13	0.49
1:B:299:PHE:HB3	1:B:300:PRO:HD2	1.94	0.49
1:C:248:SER:HB2	1:C:253:GLY:CA	2.43	0.49
1:D:196:HIS:O	1:D:197:ARG:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:VAL:HA	1:B:332:ILE:HG13	1.95	0.49
1:C:196:HIS:HD2	1:C:214:LEU:HD23	1.77	0.49
1:C:135:TRP:CZ3	1:C:349:ARG:HG3	2.47	0.49
1:D:203:ASN:HB3	1:D:215:ALA:O	2.12	0.49
1:A:50:LYS:HG3	1:A:54:ASN:ND2	2.28	0.49
1:A:66:ILE:O	1:A:70:ARG:HB2	2.12	0.49
1:B:74:GLU:H	1:B:74:GLU:CD	2.16	0.49
1:C:241:ILE:HG21	1:C:246:LEU:HD23	1.95	0.49
1:D:302:ASP:OD2	1:D:304:ASP:N	2.46	0.49
1:C:335:HIS:CE1	1:C:337:PHE:H	2.31	0.49
1:D:257:ARG:HB3	1:D:257:ARG:HH11	1.78	0.49
1:D:370:ASP:O	1:D:371:LEU:HD22	2.13	0.49
1:B:242:SER:HB3	1:B:244:GLU:OE1	2.13	0.49
1:A:41:LEU:HD21	1:B:387:PHE:HE1	1.76	0.49
1:C:172:GLU:OE2	1:C:306:SER:HB3	2.12	0.49
1:C:124:GLU:HG3	1:C:218:GLY:HA2	1.95	0.49
1:C:225:LYS:HE3	1:C:226:GLU:N	2.28	0.49
1:D:95:HIS:NE2	3:D:1:EDO:H11	2.27	0.49
1:B:163:ASN:O	1:B:166:SER:HB2	2.13	0.48
1:B:225:LYS:CB	1:B:228:MET:SD	3.01	0.48
1:C:221:MET:SD	1:C:229:VAL:HG13	2.52	0.48
1:A:109:LYS:NZ	1:A:145:ASP:O	2.44	0.48
1:A:109:LYS:HB3	1:A:381:PHE:HZ	1.78	0.48
1:B:300:PRO:C	1:B:302:ASP:HB3	2.33	0.48
1:B:374:ASP:O	1:B:375:LYS:HG2	2.13	0.48
1:C:73:ALA:HB2	1:C:150:TYR:CZ	2.48	0.48
1:A:90:VAL:HG23	2:A:1:07R:C11	2.44	0.48
1:D:80:LYS:HD2	1:D:369:ASP:O	2.14	0.48
1:A:255:TYR:HA	1:A:320:ARG:NH2	2.28	0.48
1:B:380:THR:O	1:B:381:PHE:C	2.51	0.48
1:C:105:LYS:HB3	1:C:151:MET:HB2	1.96	0.48
1:B:195:ILE:HG22	1:B:197:ARG:HB2	1.96	0.48
1:B:343:TRP:HB3	1:B:351:THR:HG21	1.95	0.48
1:C:105:LYS:H	1:C:153:MET:HE2	1.78	0.48
1:A:146:ASP:OD1	1:A:146:ASP:N	2.45	0.48
1:A:80:LYS:HB3	1:A:82:ILE:HD11	1.96	0.48
1:B:200:LYS:HZ3	1:B:219:THR:HG21	1.79	0.48
1:D:205:LEU:N	1:D:205:LEU:HD22	2.29	0.48
1:C:59:TYR:CE2	1:D:24:GLU:HB3	2.49	0.48
1:A:225:LYS:HG3	1:A:226:GLU:H	1.78	0.48
1:A:373:GLU:HG3	1:A:375:LYS:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:325:GLY:HA2	1:C:332:ILE:HD11	1.96	0.48
1:C:343:TRP:CD2	1:C:348:LEU:HD11	2.49	0.48
1:C:312:LEU:HB2	1:C:335:HIS:CE1	2.48	0.48
1:D:108:SER:O	1:D:112:MET:HE2	2.14	0.48
1:D:114:LYS:C	1:D:116:SER:H	2.17	0.48
1:D:200:LYS:HB2	1:D:201:PRO:HD2	1.96	0.48
1:D:50:LYS:HA	1:D:53:ASP:HB3	1.96	0.48
1:A:88:GLY:HA3	1:A:106:LEU:O	2.14	0.47
1:B:137:VAL:HG23	1:B:214:LEU:O	2.14	0.47
1:B:392:LEU:N	1:B:393:PRO:CD	2.77	0.47
1:D:248:SER:C	1:D:250:GLY:N	2.67	0.47
1:C:273:VAL:O	1:C:273:VAL:HG12	2.12	0.47
1:C:205:LEU:C	1:C:206:LEU:HD23	2.34	0.47
1:C:41:LEU:HD21	1:C:387:PHE:CD2	2.49	0.47
1:D:80:LYS:NZ	1:D:368:PHE:HB3	2.28	0.47
1:B:178:TYR:OH	1:B:355:VAL:HG23	2.15	0.47
1:B:94:ARG:HD2	1:B:99:ARG:HE	1.79	0.47
1:C:244:GLU:OE2	1:C:323:ARG:NH2	2.45	0.47
1:A:308:GLU:HG2	1:A:337:PHE:HA	1.95	0.47
1:D:164:LEU:HD23	1:D:164:LEU:C	2.35	0.47
1:A:319:ASP:HB2	1:A:322:VAL:HG23	1.97	0.47
1:B:155:TYR:O	1:B:157:PRO:HD3	2.15	0.47
1:B:221:MET:HG3	1:B:222:LYS:CB	2.43	0.47
1:B:46:LEU:HD21	1:B:386:ALA:HA	1.95	0.47
1:C:50:LYS:O	1:C:54:ASN:HB2	2.14	0.47
1:A:255:TYR:HA	1:A:320:ARG:HH12	1.79	0.47
1:B:383:ILE:HA	1:B:384:PRO:HD3	1.74	0.47
1:C:268:LEU:HD23	1:C:268:LEU:HA	1.67	0.47
1:D:50:LYS:HD3	1:D:50:LYS:HA	1.64	0.47
1:B:225:LYS:CG	1:B:225:LYS:O	2.63	0.47
1:C:102:TYR:HE1	1:C:140:PHE:CD1	2.32	0.47
1:D:258:GLU:HG2	1:D:259:CYS:N	2.29	0.47
1:D:81:VAL:HG21	1:D:373:GLU:HA	1.97	0.47
1:A:195:ILE:HD11	1:A:229:VAL:HG21	1.96	0.47
1:A:330:GLU:O	1:A:334:ARG:HB3	2.15	0.47
1:A:346:GLU:CD	1:A:346:GLU:N	2.68	0.47
1:A:80:LYS:CE	1:A:365:THR:HG21	2.44	0.47
1:C:160:ASP:HB2	1:C:201:PRO:O	2.15	0.47
1:D:329:VAL:HG23	1:D:333:LYS:HE3	1.97	0.47
1:A:39:TYR:CZ	1:A:67:ARG:CZ	2.98	0.47
1:C:38:VAL:HG11	1:C:63:ILE:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:THR:O	1:A:183:VAL:HG23	2.15	0.46
1:A:215:ALA:HB1	2:A:1:07R:S23	2.55	0.46
1:B:200:LYS:HE3	1:B:237:THR:HG21	1.97	0.46
1:C:269:TYR:CG	1:C:277:PRO:HG3	2.50	0.46
1:C:45:ALA:HB3	1:C:46:LEU:HD23	1.96	0.46
1:A:81:VAL:C	1:A:82:ILE:HD13	2.36	0.46
1:B:279:TYR:C	1:B:279:TYR:CD2	2.88	0.46
1:C:257:ARG:HG3	1:C:257:ARG:H	1.44	0.46
1:D:160:ASP:OD2	1:D:162:VAL:HG13	2.14	0.46
1:A:157:PRO:HD2	1:A:207:ASP:HA	1.98	0.46
1:A:230:ARG:HG3	1:A:231:CYS:N	2.31	0.46
1:A:339:LYS:O	1:A:340:ASN:HB3	2.16	0.46
1:C:135:TRP:HB3	1:C:185:ALA:HB2	1.96	0.46
1:D:244:GLU:HG3	1:D:255:TYR:HB2	1.98	0.46
1:D:248:SER:O	1:D:250:GLY:N	2.48	0.46
1:A:240:TYR:OH	1:A:270:GLU:OE2	2.26	0.46
1:B:109:LYS:HG2	1:B:394:PHE:CE1	2.50	0.46
1:D:9:THR:O	1:D:11:PHE:N	2.49	0.46
1:D:200:LYS:HD2	1:D:202:ASP:CG	2.36	0.46
1:C:167:ASN:C	1:C:168:TYR:CD1	2.88	0.46
1:C:368:PHE:CE2	2:C:2:07R:H11	2.50	0.46
1:B:247:LYS:HD2	1:B:291:MET:HE1	1.98	0.46
1:C:9:THR:HG22	1:C:10:ARG:N	2.30	0.46
1:C:110:PHE:HD1	1:C:381:PHE:CD2	2.33	0.46
1:D:135:TRP:HB3	1:D:185:ALA:HB2	1.98	0.46
1:A:238:PRO:HG3	1:A:283:LEU:HD11	1.97	0.46
1:A:41:LEU:HD23	1:A:41:LEU:HA	1.68	0.46
1:B:266:VAL:HG13	1:B:277:PRO:HG2	1.96	0.46
1:C:46:LEU:N	1:C:46:LEU:HD23	2.27	0.46
1:D:200:LYS:O	1:D:204:MET:HG3	2.16	0.46
1:A:111:GLU:HG3	1:A:115:ARG:HE	1.81	0.46
1:A:49:ASN:HB3	1:A:52:ILE:HD12	1.97	0.46
1:C:392:LEU:N	1:C:393:PRO:CD	2.78	0.46
1:D:72:LYS:HD2	1:D:74:GLU:HB3	1.97	0.46
1:C:122:TRP:HZ3	1:C:125:ARG:NH1	2.14	0.46
1:D:80:LYS:HB3	1:D:80:LYS:HE3	1.35	0.46
1:B:377:GLU:OE2	1:B:377:GLU:HA	2.16	0.45
1:C:286:THR:HG22	1:C:290:ILE:HD12	1.97	0.45
1:D:80:LYS:HD2	1:D:369:ASP:C	2.37	0.45
1:B:266:VAL:HG13	1:B:277:PRO:CD	2.45	0.45
1:B:92:LEU:HA	1:B:92:LEU:HD12	1.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:MET:HA	1:D:156:MET:CE	2.47	0.45
1:D:160:ASP:C	1:D:160:ASP:OD1	2.54	0.45
1:A:49:ASN:ND2	1:A:52:ILE:HG13	2.28	0.45
1:C:127:ILE:HD13	1:C:192:MET:HE1	1.96	0.45
1:C:194:PHE:CZ	1:C:222:LYS:HE3	2.51	0.45
1:C:230:ARG:NE	1:C:253:GLY:H	2.14	0.45
1:C:260:ASP:O	1:C:264:VAL:HG22	2.16	0.45
1:D:261:TRP:HB3	1:D:316:PHE:CE2	2.51	0.45
1:A:115:ARG:O	1:A:116:SER:HB2	2.16	0.45
1:B:223:MET:CG	1:B:224:ASN:OD1	2.63	0.45
1:B:303:ASN:HA	1:B:304:ASP:O	2.16	0.45
1:C:216:ASP:CG	2:C:2:07R:C02	2.85	0.45
1:D:187:ASP:OD1	1:D:329:VAL:HG11	2.16	0.45
1:D:24:GLU:O	1:D:29:CYS:CB	2.65	0.45
1:A:107:LEU:HD11	1:A:151:MET:CE	2.46	0.45
1:B:161:LEU:HD23	1:B:161:LEU:HA	1.64	0.45
1:D:80:LYS:HD2	1:D:369:ASP:HA	1.98	0.45
1:A:137:VAL:CG2	1:A:215:ALA:HB2	2.46	0.45
1:B:205:LEU:O	1:B:212:LEU:HA	2.16	0.45
1:D:11:PHE:O	1:D:15:ASP:N	2.38	0.45
1:D:272:LEU:HA	1:D:272:LEU:HD23	1.77	0.45
1:A:246:LEU:HD12	1:A:291:MET:HE1	1.99	0.45
1:B:348:LEU:HD13	1:B:348:LEU:HA	1.72	0.45
1:D:193:GLY:HA2	1:D:257:ARG:HH22	1.82	0.45
1:A:104:MET:HE2	1:A:152:VAL:HG22	1.99	0.45
1:C:123:GLU:HB3	1:C:194:PHE:CE2	2.52	0.45
1:C:318:THR:CG2	1:C:323:ARG:HA	2.46	0.45
1:D:12:GLU:O	1:D:16:ASN:HB2	2.17	0.45
1:D:365:THR:O	1:D:366:SER:C	2.54	0.45
1:A:123:GLU:CG	1:A:220:CYS:O	2.64	0.45
1:B:117:ASP:CG	1:B:118:SER:H	2.19	0.45
1:C:204:MET:HB3	1:C:212:LEU:CD1	2.46	0.45
1:C:205:LEU:O	1:C:212:LEU:HA	2.17	0.45
1:D:232:ASP:O	1:D:233:THR:C	2.55	0.45
1:D:319:ASP:HB3	1:D:321:GLU:OE2	2.16	0.45
1:A:14:MET:HB2	1:A:14:MET:HE2	1.87	0.45
1:B:118:SER:O	1:B:120:PHE:N	2.50	0.45
1:C:131:ALA:HA	1:C:192:MET:SD	2.57	0.45
1:D:269:TYR:CD1	1:D:277:PRO:HD3	2.51	0.45
1:B:219:THR:O	1:B:220:CYS:SG	2.75	0.44
1:B:80:LYS:NZ	1:B:373:GLU:OE1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:GLU:HG2	1:C:258:GLU:H	1.59	0.44
1:C:30:LEU:HD11	1:D:31:LEU:HD21	1.99	0.44
1:D:321:GLU:HG2	1:D:322:VAL:HG13	1.99	0.44
1:B:277:PRO:HB2	1:B:278:PHE:CE2	2.52	0.44
1:C:245:VAL:HG22	1:C:255:TYR:CD1	2.52	0.44
1:A:262:TRP:O	1:A:266:VAL:HG23	2.17	0.44
1:D:348:LEU:O	1:D:351:THR:HG23	2.17	0.44
1:A:31:LEU:HA	1:A:31:LEU:HD23	1.81	0.44
1:A:37:LEU:HD12	1:A:37:LEU:HA	1.79	0.44
1:B:145:ASP:OD1	1:B:145:ASP:C	2.56	0.44
1:D:185:ALA:HB1	1:D:214:LEU:HD22	1.99	0.44
1:B:265:GLY:HA3	1:B:317:LEU:HD13	2.00	0.44
1:C:340:ASN:HD22	1:C:340:ASN:N	2.15	0.44
1:A:127:ILE:O	1:A:131:ALA:HB2	2.18	0.44
1:A:110:PHE:CE1	1:A:380:THR:O	2.70	0.44
1:B:104:MET:HE1	1:B:150:TYR:HB3	2.00	0.44
1:B:18:LEU:HA	1:B:18:LEU:HD23	1.66	0.44
1:B:344:ALA:HB3	1:B:347:THR:HB	2.00	0.44
1:C:159:GLY:HA2	1:C:368:PHE:CE1	2.53	0.44
1:D:161:LEU:CD2	1:D:212:LEU:HD12	2.48	0.44
1:A:392:LEU:N	1:A:393:PRO:CD	2.80	0.44
1:B:88:GLY:HA3	1:B:106:LEU:O	2.17	0.44
1:C:214:LEU:HD12	1:C:214:LEU:N	2.32	0.44
1:D:112:MET:HG2	1:D:120:PHE:HZ	1.82	0.44
1:A:88:GLY:O	2:A:1:07R:H7	2.17	0.44
1:B:293:HIS:HA	1:B:296:SER:OG	2.17	0.44
1:B:392:LEU:N	1:B:393:PRO:HD3	2.31	0.44
1:A:9:THR:HG22	1:A:12:GLU:OE2	2.18	0.44
1:C:318:THR:O	1:C:323:ARG:HD3	2.18	0.44
1:C:41:LEU:CD2	1:C:387:PHE:CD2	3.00	0.44
1:D:12:GLU:HG3	1:D:16:ASN:OD1	2.18	0.44
1:A:112:MET:O	1:A:115:ARG:N	2.51	0.43
1:A:43:PHE:CD1	1:A:383:ILE:HG23	2.53	0.43
1:A:61:ASP:OD2	1:A:62:THR:N	2.50	0.43
1:B:240:TYR:OH	1:B:270:GLU:OE1	2.32	0.43
1:B:280:ALA:HB2	1:B:289:LYS:HD2	2.00	0.43
1:B:167:ASN:ND2	4:B:423:HOH:O	2.45	0.43
1:B:225:LYS:C	1:B:228:MET:SD	2.96	0.43
1:B:41:LEU:HD13	1:B:52:ILE:HG23	2.00	0.43
1:A:203:ASN:ND2	1:A:216:ASP:HB3	2.33	0.43
1:A:69:LEU:HD23	1:B:13:LYS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:VAL:HG13	1:C:91:GLN:HB3	2.01	0.43
1:D:56:LEU:O	1:D:60:LYS:HB2	2.18	0.43
1:A:159:GLY:HA2	1:A:368:PHE:CE1	2.53	0.43
1:A:195:ILE:HG22	1:A:257:ARG:HB3	2.00	0.43
1:C:139:LEU:HD13	1:C:151:MET:HE3	2.00	0.43
1:C:216:ASP:HB2	2:C:2:07R:S23	2.58	0.43
1:C:9:THR:HG22	1:C:11:PHE:N	2.20	0.43
1:D:189:ILE:O	1:D:192:MET:HG3	2.19	0.43
1:D:244:GLU:HB2	1:D:320:ARG:HH21	1.83	0.43
1:C:206:LEU:HA	1:C:211:HIS:O	2.18	0.43
1:C:197:ARG:CD	1:C:255:TYR:OH	2.61	0.43
1:A:140:PHE:O	1:A:401:SER:HB2	2.18	0.43
1:A:388:VAL:HG23	1:A:389:GLY:N	2.32	0.43
1:A:55:PHE:CE1	1:A:59:TYR:CD1	3.06	0.43
1:B:174:TRP:CD1	1:B:354:PRO:HB3	2.53	0.43
1:B:156:MET:CE	1:B:213:LYS:HB2	2.49	0.43
1:C:216:ASP:OD1	2:C:2:07R:S23	2.76	0.43
1:C:290:ILE:O	1:C:293:HIS:HB3	2.19	0.43
1:D:302:ASP:HB2	1:D:304:ASP:H	1.83	0.43
1:C:336:LEU:H	1:C:336:LEU:HD12	1.84	0.43
1:C:381:PHE:N	1:C:381:PHE:CD2	2.87	0.43
1:C:41:LEU:CD2	1:C:387:PHE:HD2	2.31	0.43
1:B:233:THR:HB	1:B:234:ALA:H	1.64	0.43
1:C:156:MET:HG3	1:C:205:LEU:CB	2.49	0.43
1:C:30:LEU:HA	1:C:30:LEU:HD23	1.80	0.43
1:C:7:PHE:N	4:C:420:HOH:O	2.51	0.43
1:D:112:MET:HG2	1:D:120:PHE:CE2	2.53	0.43
1:A:348:LEU:HD12	1:A:351:THR:HG21	2.01	0.43
1:B:187:ASP:OD2	1:B:329:VAL:HG21	2.19	0.43
1:C:127:ILE:HD11	1:C:194:PHE:CB	2.49	0.43
1:C:348:LEU:HD12	1:C:348:LEU:HA	1.68	0.43
1:D:321:GLU:N	1:D:321:GLU:CD	2.67	0.43
1:D:125:ARG:NH1	1:D:399:TYR:HB2	2.34	0.43
2:A:1:07R:S23	2:A:1:07R:O01	2.77	0.43
1:A:241:ILE:HB	1:A:246:LEU:HD21	2.00	0.43
1:A:361:SER:HB2	1:A:363:ILE:N	2.21	0.43
1:A:28:ASP:OD1	1:A:400:TYR:HE2	2.00	0.43
1:B:317:LEU:HA	1:B:317:LEU:HD12	1.82	0.43
1:D:131:ALA:O	1:D:132:ASN:C	2.56	0.43
1:A:110:PHE:HE1	1:A:380:THR:O	2.02	0.42
1:A:139:LEU:HD22	1:A:141:TYR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ILE:O	1:A:220:CYS:HA	2.19	0.42
1:A:28:ASP:O	1:A:31:LEU:HB2	2.19	0.42
1:A:255:TYR:HA	1:A:320:ARG:NH1	2.33	0.42
1:B:363:ILE:O	1:B:364:ASP:C	2.57	0.42
1:B:56:LEU:HA	1:B:56:LEU:HD23	1.82	0.42
1:C:222:LYS:O	1:C:229:VAL:HG11	2.19	0.42
1:C:30:LEU:HD11	1:D:31:LEU:CD2	2.48	0.42
1:C:187:ASP:HB2	1:C:329:VAL:HG21	2.00	0.42
1:A:329:VAL:O	1:A:332:ILE:HB	2.19	0.42
1:B:104:MET:HE2	1:B:152:VAL:HG22	2.01	0.42
1:C:197:ARG:NE	1:C:219:THR:HG22	2.32	0.42
1:D:87:PHE:CZ	1:D:116:SER:HB3	2.54	0.42
1:B:146:ASP:OD1	1:B:146:ASP:N	2.53	0.42
1:B:170:VAL:HG12	1:B:174:TRP:HB2	2.01	0.42
1:B:312:LEU:HA	1:B:312:LEU:HD23	1.74	0.42
1:D:257:ARG:HH11	1:D:257:ARG:CB	2.32	0.42
1:D:375:LYS:HB3	1:D:376:GLY:H	1.61	0.42
1:B:258:GLU:OE2	1:B:320:ARG:HD2	2.18	0.42
1:C:121:PHE:HE1	1:C:122:TRP:CE2	2.37	0.42
1:C:225:LYS:HG3	1:C:226:GLU:H	1.85	0.42
1:D:244:GLU:CG	1:D:255:TYR:HB2	2.50	0.42
1:D:316:PHE:CZ	1:D:332:ILE:HD13	2.53	0.42
1:D:338:PHE:O	1:D:340:ASN:ND2	2.52	0.42
1:A:49:ASN:HD22	1:A:52:ILE:CD1	2.31	0.42
1:B:15:ASP:HA	1:B:18:LEU:HG	2.02	0.42
1:B:241:ILE:CD1	1:B:246:LEU:HD22	2.49	0.42
1:D:19:ARG:HG3	1:D:21:PRO:HD3	2.00	0.42
1:B:82:ILE:HG13	1:B:82:ILE:O	2.19	0.42
1:C:13:LYS:O	1:C:17:LEU:HD13	2.19	0.42
1:C:49:ASN:HD21	1:D:388:VAL:HA	1.83	0.42
1:C:58:ARG:NH2	1:D:395:VAL:O	2.52	0.42
1:D:37:LEU:O	1:D:41:LEU:HG	2.20	0.42
1:D:60:LYS:O	1:D:63:ILE:HG22	2.19	0.42
1:B:10:ARG:HA	1:B:13:LYS:HB2	2.01	0.42
1:C:74:GLU:N	1:C:74:GLU:OE1	2.51	0.42
1:B:114:LYS:O	1:B:116:SER:N	2.44	0.42
1:B:302:ASP:O	1:B:304:ASP:O	2.37	0.42
1:B:348:LEU:HB3	1:B:349:ARG:H	1.60	0.42
1:B:401:SER:O	1:B:402:ASN:HB2	2.19	0.42
1:C:391:GLN:C	1:C:393:PRO:HD2	2.39	0.42
1:D:219:THR:HB	1:D:237:THR:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:84:ARG:HB2	1:D:84:ARG:HE	1.54	0.42
1:A:84:ARG:HD3	1:A:371:LEU:HD22	2.00	0.42
1:B:186:LEU:HD23	1:B:186:LEU:HA	1.68	0.42
1:B:214:LEU:HD12	1:B:214:LEU:HA	1.92	0.42
1:C:211:HIS:CE1	1:C:353:ALA:HB2	2.55	0.42
1:C:383:ILE:HA	1:C:384:PRO:HD3	1.77	0.42
1:D:283:LEU:HA	1:D:283:LEU:HD23	1.83	0.42
1:A:230:ARG:HG2	1:A:254:TYR:HE2	1.85	0.42
1:A:391:GLN:C	1:A:393:PRO:HD2	2.40	0.42
1:B:258:GLU:H	1:B:258:GLU:HG3	1.43	0.42
1:B:90:VAL:HG23	1:B:218:GLY:H	1.84	0.42
1:A:374:ASP:O	1:A:375:LYS:HB2	2.20	0.41
1:B:113:ILE:HG22	1:B:114:LYS:N	2.35	0.41
1:B:348:LEU:O	1:B:351:THR:N	2.49	0.41
1:C:316:PHE:O	1:C:323:ARG:HD2	2.20	0.41
1:D:375:LYS:HA	1:D:375:LYS:HD2	1.67	0.41
1:A:346:GLU:H	1:A:346:GLU:CD	2.20	0.41
1:B:312:LEU:HD12	1:B:337:PHE:CD1	2.54	0.41
1:D:195:ILE:CG2	1:D:197:ARG:HG3	2.47	0.41
1:D:383:ILE:HA	1:D:384:PRO:HD3	1.65	0.41
1:A:134:PRO:O	1:A:213:LYS:HG2	2.20	0.41
1:B:256:GLY:H	1:B:258:GLU:CD	2.24	0.41
1:B:313:ILE:HG23	1:B:317:LEU:HD22	2.02	0.41
1:C:123:GLU:HB2	1:C:217:PHE:CD2	2.55	0.41
1:C:243:PRO:O	1:C:247:LYS:HB2	2.20	0.41
1:A:320:ARG:HG3	1:A:321:GLU:HG3	2.02	0.41
1:A:49:ASN:HD21	1:A:51:ASN:HB2	1.85	0.41
1:D:100:LYS:HB2	1:D:102:TYR:HE2	1.84	0.41
1:C:30:LEU:HB3	1:D:30:LEU:HB3	2.03	0.41
1:A:311:ASN:OD1	1:A:335:HIS:NE2	2.43	0.41
1:B:73:ALA:HB3	1:B:74:GLU:OE2	2.20	0.41
1:C:105:LYS:N	1:C:153:MET:CE	2.84	0.41
1:D:161:LEU:HD23	1:D:212:LEU:HD12	2.03	0.41
1:B:223:MET:CB	1:B:224:ASN:ND2	2.76	0.41
1:C:135:TRP:HB2	1:C:185:ALA:HA	2.02	0.41
1:C:189:ILE:HG21	1:C:217:PHE:HE1	1.86	0.41
1:C:262:TRP:CZ3	1:C:318:THR:N	2.89	0.41
1:C:41:LEU:HD13	1:C:52:ILE:HG23	2.03	0.41
1:D:12:GLU:HG3	1:D:16:ASN:CG	2.41	0.41
1:D:19:ARG:CG	1:D:21:PRO:HD3	2.50	0.41
1:D:244:GLU:HG2	1:D:245:VAL:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:GLN:HG3	1:A:139:LEU:N	2.35	0.41
1:B:174:TRP:N	1:B:174:TRP:CD1	2.88	0.41
1:C:216:ASP:CG	2:C:2:07R:S23	2.98	0.41
1:A:111:GLU:O	1:A:114:LYS:HB3	2.21	0.41
1:A:124:GLU:HB2	1:A:218:GLY:CA	2.47	0.41
1:B:248:SER:OG	1:B:255:TYR:CD2	2.72	0.41
1:B:46:LEU:HD21	1:B:386:ALA:CA	2.51	0.41
1:C:159:GLY:HA2	1:C:368:PHE:CZ	2.55	0.41
2:C:2:07R:O01	2:C:2:07R:S23	2.78	0.41
1:A:244:GLU:CD	1:A:323:ARG:HH22	2.23	0.41
1:A:343:TRP:C	1:A:343:TRP:CE3	2.93	0.41
1:B:187:ASP:HB2	1:B:329:VAL:HG11	2.03	0.41
1:C:221:MET:CE	1:C:255:TYR:CZ	3.04	0.41
1:D:272:LEU:HB3	1:D:305:ILE:HD13	2.03	0.41
1:D:95:HIS:ND1	1:D:98:THR:HG23	2.36	0.41
1:A:79:VAL:HG11	1:A:92:LEU:HD23	2.03	0.41
1:B:228:MET:HG3	1:B:230:ARG:HD2	2.03	0.41
1:C:29:CYS:O	1:C:32:ASP:HB2	2.21	0.41
1:D:134:PRO:O	1:D:213:LYS:HG2	2.21	0.41
1:D:354:PRO:HA	4:D:425:HOH:O	2.21	0.41
1:A:128:MET:HB3	1:A:139:LEU:HB2	2.02	0.41
1:A:17:LEU:HD12	1:A:17:LEU:HA	1.92	0.41
1:A:197:ARG:HD2	1:A:221:MET:HE1	2.02	0.41
1:A:313:ILE:HG23	1:A:317:LEU:CD2	2.48	0.41
1:B:142:ALA:HA	1:B:150:TYR:O	2.20	0.41
1:B:375:LYS:HG3	1:B:376:GLY:H	1.86	0.41
1:C:59:TYR:O	1:C:62:THR:HB	2.21	0.41
1:D:192:MET:HE2	1:D:192:MET:HB3	1.98	0.41
1:D:279:TYR:C	1:D:279:TYR:CD2	2.93	0.41
1:C:202:ASP:OD1	1:C:202:ASP:N	2.54	0.40
1:D:100:LYS:HD3	1:D:102:TYR:OH	2.20	0.40
1:A:338:PHE:CD1	1:A:345:TRP:HZ2	2.39	0.40
1:A:82:ILE:N	1:A:82:ILE:HD13	2.36	0.40
1:B:94:ARG:NE	1:B:99:ARG:HH21	2.19	0.40
1:C:172:GLU:OE2	1:C:306:SER:CB	2.70	0.40
1:C:299:PHE:HA	1:C:300:PRO:HD3	1.88	0.40
1:C:142:ALA:O	1:C:398:THR:HG23	2.20	0.40
1:C:79:VAL:HG11	1:C:363:ILE:HD11	2.03	0.40
1:C:92:LEU:HA	1:C:92:LEU:HD12	1.85	0.40
1:D:109:LYS:O	1:D:113:ILE:HG12	2.21	0.40
1:A:221:MET:CE	1:A:255:TYR:OH	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:MET:HE3	1:A:227:GLY:CA	2.51	0.40
1:A:50:LYS:HB2	1:A:50:LYS:HE2	1.84	0.40
1:B:223:MET:HB2	1:B:224:ASN:HD21	1.75	0.40
1:D:161:LEU:HA	1:D:161:LEU:HD13	1.89	0.40
1:A:261:TRP:HB3	1:A:316:PHE:CD2	2.56	0.40
1:A:372:GLU:OE2	1:A:375:LYS:HG3	2.21	0.40
1:B:306:SER:O	1:B:307:LYS:C	2.60	0.40
1:C:197:ARG:HB3	1:C:219:THR:CG2	2.52	0.40
1:D:142:ALA:HB3	1:D:399:TYR:HB3	2.03	0.40
1:A:197:ARG:CZ	1:A:221:MET:HE1	2.52	0.40
1:C:127:ILE:CD1	1:C:189:ILE:HG23	2.51	0.40
1:D:19:ARG:HD3	1:D:19:ARG:HA	1.26	0.40
1:D:219:THR:O	1:D:220:CYS:SG	2.80	0.40
1:D:392:LEU:N	1:D:393:PRO:CD	2.85	0.40
1:D:31:LEU:HD22	1:D:66:ILE:HD13	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	394/410 (96%)	364 (92%)	28 (7%)	2 (0%)	29	61
1	B	393/410 (96%)	349 (89%)	39 (10%)	5 (1%)	12	37
1	C	394/410 (96%)	361 (92%)	31 (8%)	2 (0%)	29	61
1	D	393/410 (96%)	347 (88%)	43 (11%)	3 (1%)	19	51
All	All	1574/1640 (96%)	1421 (90%)	141 (9%)	12 (1%)	19	51

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	119	ALA
1	B	305	ILE
1	B	115	ARG
1	C	372	GLU
1	D	115	ARG
1	D	228	MET
1	A	60	LYS
1	A	229	VAL
1	B	359	LEU
1	D	60	LYS
1	B	127	ILE
1	C	127	ILE

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	352/365 (96%)	303 (86%)	49 (14%)	3	10
1	B	351/365 (96%)	291 (83%)	60 (17%)	2	6
1	C	352/365 (96%)	295 (84%)	57 (16%)	2	7
1	D	351/365 (96%)	296 (84%)	55 (16%)	2	8
All	All	1406/1460 (96%)	1185 (84%)	221 (16%)	2	8

All (221) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	68	ASP
1	A	70	ARG
1	A	72	LYS
1	A	75	ASP
1	A	78	VAL
1	A	99	ARG
1	A	107	LEU
1	A	118	SER
1	A	123	GLU

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Mol	Chain	Res	Type
1	A	125	ARG
1	A	132	ASN
1	A	139	LEU
1	A	146	ASP
1	A	199	VAL
1	A	212	LEU
1	A	221	MET
1	A	224	ASN
1	A	229	VAL
1	A	230	ARG
1	A	239	ASP
1	A	241	ILE
1	A	244	GLU
1	A	248	SER
1	A	249	GLN
1	A	257	ARG
1	A	258	GLU
1	A	268	LEU
1	A	270	GLU
1	A	281	ASP
1	A	284	VAL
1	A	288	SER
1	A	294	LYS
1	A	304	ASP
1	A	317	LEU
1	A	318	THR
1	A	321	GLU
1	A	322	VAL
1	A	326	ARG
1	A	334	ARG
1	A	346	GLU
1	A	349	ARG
1	A	359	LEU
1	A	361	SER
1	A	363	ILE
1	A	365	THR
1	A	380	THR
1	A	385	LYS
1	A	401	SER
1	B	9	THR
1	B	11	PHE
1	B	14	MET

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Mol	Chain	Res	Type
1	B	20	ASP
1	B	27	SER
1	B	62	THR
1	B	65	LYS
1	B	72	LYS
1	B	77	GLU
1	B	80	LYS
1	B	84	ARG
1	B	92	LEU
1	B	112	MET
1	B	113	ILE
1	B	114	LYS
1	B	120	PHE
1	B	139	LEU
1	B	154	GLU
1	B	170	VAL
1	B	200	LYS
1	B	209	SER
1	B	213	LYS
1	B	219	THR
1	B	220	CYS
1	B	224	ASN
1	B	225	LYS
1	B	226	GLU
1	B	228	MET
1	B	230	ARG
1	B	233	THR
1	B	235	VAL
1	B	237	THR
1	B	242	SER
1	B	246	LEU
1	B	257	ARG
1	B	258	GLU
1	B	275	ASP
1	B	281	ASP
1	B	312	LEU
1	B	317	LEU
1	B	321	GLU
1	B	322	VAL
1	B	326	ARG
1	B	332	ILE
1	B	333	LYS

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Mol	Chain	Res	Type
1	B	336	LEU
1	B	340	ASN
1	B	341	ASP
1	B	346	GLU
1	B	347	THR
1	B	348	LEU
1	B	349	ARG
1	B	350	ASP
1	B	351	THR
1	B	352	VAL
1	B	355	VAL
1	B	356	VAL
1	B	363	ILE
1	B	373	GLU
1	B	379	GLU
1	C	7	PHE
1	C	8	GLU
1	C	15	ASP
1	C	34	LEU
1	C	46	LEU
1	C	48	LYS
1	C	50	LYS
1	C	53	ASP
1	C	63	ILE
1	C	66	ILE
1	C	67	ARG
1	C	82	ILE
1	C	92	LEU
1	C	96	LYS
1	C	118	SER
1	C	139	LEU
1	C	151	MET
1	C	163	ASN
1	C	172	GLU
1	C	195	ILE
1	C	202	ASP
1	C	212	LEU
1	C	220	CYS
1	C	222	LYS
1	C	225	LYS
1	C	228	MET
1	C	230	ARG

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Mol	Chain	Res	Type
1	C	232	ASP
1	C	233	THR
1	C	248	SER
1	C	252	ASP
1	C	254	TYR
1	C	257	ARG
1	C	258	GLU
1	C	260	ASP
1	C	264	VAL
1	C	268	LEU
1	C	283	LEU
1	C	297	LEU
1	C	306	SER
1	C	316	PHE
1	C	317	LEU
1	C	320	ARG
1	C	329	VAL
1	C	336	LEU
1	C	337	PHE
1	C	339	LYS
1	C	340	ASN
1	C	342	GLN
1	C	348	LEU
1	C	351	THR
1	C	356	VAL
1	C	360	SER
1	C	363	ILE
1	C	364	ASP
1	C	379	GLU
1	C	383	ILE
1	D	9	THR
1	D	19	ARG
1	D	20	ASP
1	D	26	ASN
1	D	27	SER
1	D	39	TYR
1	D	46	LEU
1	D	47	ARG
1	D	62	THR
1	D	65	LYS
1	D	69	LEU
1	D	77	GLU

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Mol	Chain	Res	Type
1	D	80	LYS
1	D	113	ILE
1	D	116	SER
1	D	125	ARG
1	D	139	LEU
1	D	144	GLN
1	D	151	MET
1	D	161	LEU
1	D	162	VAL
1	D	173	LYS
1	D	192	MET
1	D	200	LYS
1	D	202	ASP
1	D	228	MET
1	D	237	THR
1	D	246	LEU
1	D	257	ARG
1	D	268	LEU
1	D	270	GLU
1	D	281	ASP
1	D	284	VAL
1	D	288	SER
1	D	307	LYS
1	D	308	GLU
1	D	312	LEU
1	D	317	LEU
1	D	318	THR
1	D	320	ARG
1	D	321	GLU
1	D	326	ARG
1	D	329	VAL
1	D	330	GLU
1	D	331	GLU
1	D	336	LEU
1	D	341	ASP
1	D	348	LEU
1	D	362	ASP
1	D	364	ASP
1	D	368	PHE
1	D	378	GLU
1	D	385	LYS
1	D	388	VAL

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Mol	Chain	Res	Type
1	D	401	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	51	ASN
1	B	211	HIS
1	B	311	ASN
1	B	390	ASN
1	C	64	ASN
1	C	196	HIS
1	C	211	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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
2	07R	C	2	-	22,25,25	4.12	16 (72%)	26,33,33	1.83	9 (34%)
2	07R	A	1	-	22,25,25	3.57	14 (63%)	26,33,33	1.52	7 (26%)
3	EDO	B	2	-	3,3,3	1.05	0	2,2,2	0.34	0
3	EDO	D	1	-	3,3,3	0.73	0	2,2,2	0.57	0
3	EDO	A	3	-	3,3,3	1.09	0	2,2,2	0.26	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
2	07R	C	2	-	-	2/11/13/13	0/3/3/3
2	07R	A	1	-	-	2/11/13/13	0/3/3/3
3	EDO	B	2	-	-	1/1/1/1	-
3	EDO	D	1	-	-	1/1/1/1	-
3	EDO	A	3	-	-	1/1/1/1	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	07R	C13-N12	8.73	1.51	1.36
2	C	2	07R	C02-N03	8.54	1.53	1.35
2	A	1	07R	C02-N03	7.37	1.50	1.35
2	A	1	07R	C13-N12	6.89	1.48	1.36
2	A	1	07R	C06-C05	5.97	1.49	1.39
2	C	2	07R	C21-C20	5.55	1.49	1.38
2	C	2	07R	C06-C05	5.54	1.48	1.39
2	C	2	07R	C15-N14	5.01	1.53	1.37
2	C	2	07R	C02-N12	4.94	1.47	1.37
2	C	2	07R	C17-C18	4.73	1.48	1.38
2	A	1	07R	C21-C20	4.39	1.47	1.38
2	A	1	07R	C02-N12	4.35	1.46	1.37
2	A	1	07R	C17-C16	4.04	1.47	1.39
2	A	1	07R	C15-N14	4.03	1.50	1.37
2	A	1	07R	C17-C18	3.71	1.46	1.38
2	A	1	07R	C10-C09	3.60	1.46	1.38
2	C	2	07R	C10-C09	3.46	1.46	1.38
2	C	2	07R	C04-N03	3.32	1.52	1.46
2	C	2	07R	O01-C02	3.26	1.30	1.23
2	C	2	07R	C17-C16	3.13	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	07R	O01-C02	3.12	1.29	1.23
2	A	1	07R	C04-N03	2.95	1.51	1.46
2	C	2	07R	C09-C07	2.94	1.44	1.38
2	C	2	07R	C16-C15	2.74	1.53	1.48
2	C	2	07R	O08-C07	2.62	1.43	1.37
2	C	2	07R	C10-C11	2.56	1.44	1.38
2	A	1	07R	C20-N19	2.31	1.40	1.33
2	C	2	07R	C21-C16	2.28	1.44	1.39
2	A	1	07R	O08-C07	2.05	1.41	1.37
2	A	1	07R	C22-S23	-2.01	1.67	1.70

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	07R	C22-C15-C16	-3.75	124.23	129.44
2	C	2	07R	C16-C15-N14	3.40	126.49	120.78
2	C	2	07R	C20-C21-C16	3.13	124.23	119.57
2	C	2	07R	C21-C16-C17	-3.01	111.58	117.59
2	A	1	07R	C21-C16-C15	2.66	125.49	121.28
2	C	2	07R	C07-C06-C05	-2.46	118.53	120.35
2	C	2	07R	C04-N03-C02	-2.33	116.78	121.53
2	C	2	07R	N12-C02-N03	2.33	117.87	113.87
2	A	1	07R	N12-C02-N03	2.32	117.86	113.87
2	A	1	07R	C17-C18-N19	-2.29	119.63	123.62
2	A	1	07R	C11-C05-C06	2.24	121.67	118.54
2	A	1	07R	C18-C17-C16	2.16	122.79	119.57
2	A	1	07R	C17-C16-C15	-2.16	117.88	121.28
2	C	2	07R	O01-C02-N12	-2.12	120.04	123.62
2	C	2	07R	C21-C16-C15	2.11	124.62	121.28
2	A	1	07R	C04-C05-C06	-2.10	116.10	120.64

There are no chirality outliers.

All (7) torsion outliers are listed below:

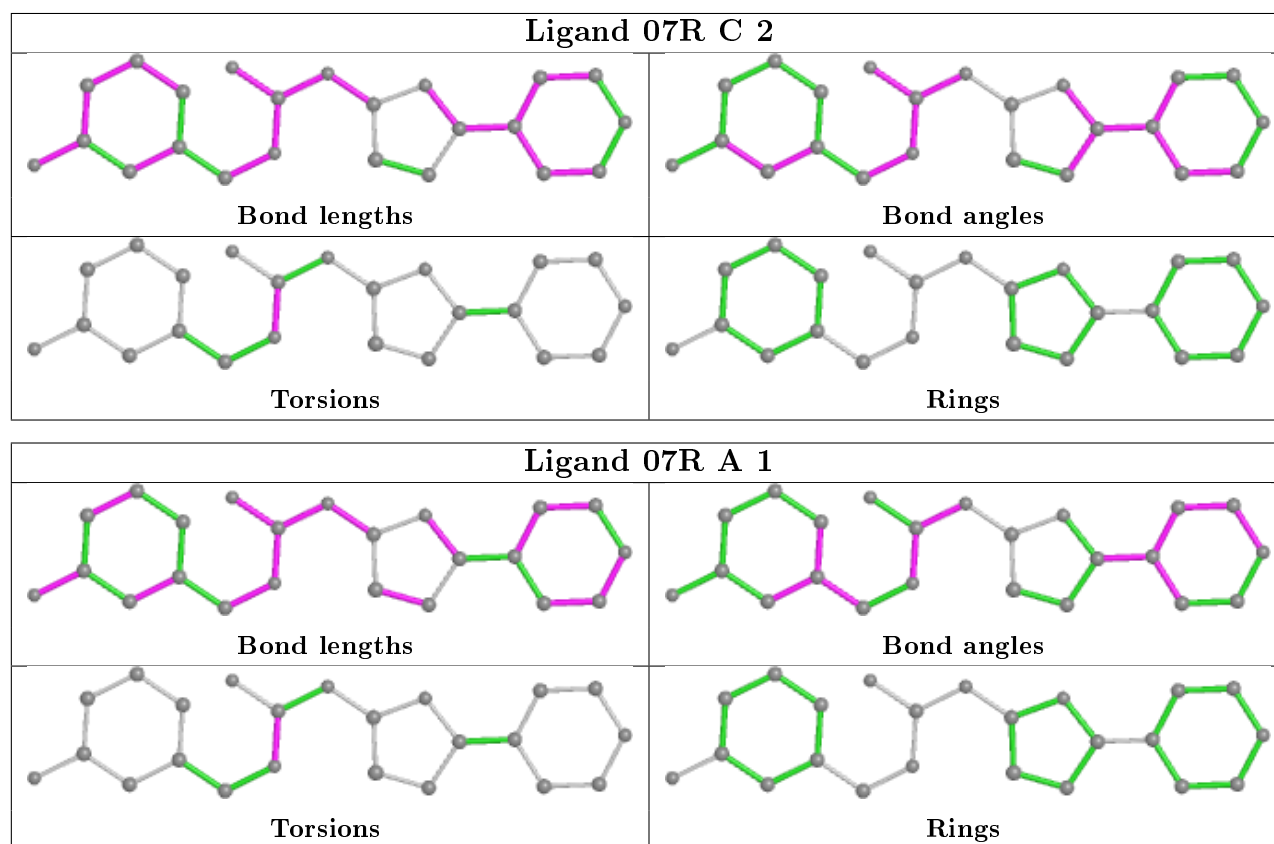
Mol	Chain	Res	Type	Atoms
2	C	2	07R	O01-C02-N03-C04
2	C	2	07R	N12-C02-N03-C04
2	A	1	07R	O01-C02-N03-C04
2	A	1	07R	N12-C02-N03-C04
3	B	2	EDO	O1-C1-C2-O2
3	D	1	EDO	O1-C1-C2-O2
3	A	3	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	07R	14	0
2	A	1	07R	16	0
3	B	2	EDO	2	0
3	D	1	EDO	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	396/410 (96%)	0.07	7 (1%) 68 67	28, 56, 95, 124	0
1	B	395/410 (96%)	0.01	8 (2%) 65 63	26, 47, 86, 117	0
1	C	396/410 (96%)	0.23	20 (5%) 28 24	35, 61, 94, 130	0
1	D	386/410 (94%)	-0.01	6 (1%) 72 71	26, 46, 88, 118	0
All	All	1573/1640 (95%)	0.07	41 (2%) 56 52	26, 53, 90, 130	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	CYS	7.4
1	C	375	LYS	6.5
1	B	223	MET	5.7
1	A	231	CYS	5.5
1	C	234	ALA	5.3
1	A	234	ALA	5.1
1	C	219	THR	4.4
1	C	227	GLY	4.0
1	C	228	MET	4.0
1	C	230	ARG	3.9
1	B	228	MET	3.7
1	C	229	VAL	3.6
1	C	221	MET	3.6
1	B	116	SER	3.6
1	D	235	VAL	3.5
1	C	303	ASN	3.5
1	C	251	GLY	3.3
1	C	374	ASP	3.2
1	B	373	GLU	3.2
1	D	220	CYS	3.0
1	B	366	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	119	ALA	2.9
1	A	375	LYS	2.9
1	A	221	MET	2.6
1	D	115	ARG	2.5
1	C	223	MET	2.5
1	C	302	ASP	2.4
1	C	217	PHE	2.4
1	D	118	SER	2.4
1	D	236	GLY	2.3
1	B	224	ASN	2.3
1	A	229	VAL	2.3
1	C	369	ASP	2.2
1	B	230	ARG	2.2
1	C	231	CYS	2.2
1	C	287	TYR	2.2
1	C	224	ASN	2.1
1	C	226	GLU	2.1
1	A	226	GLU	2.1
1	A	254	TYR	2.1
1	D	380	THR	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 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.

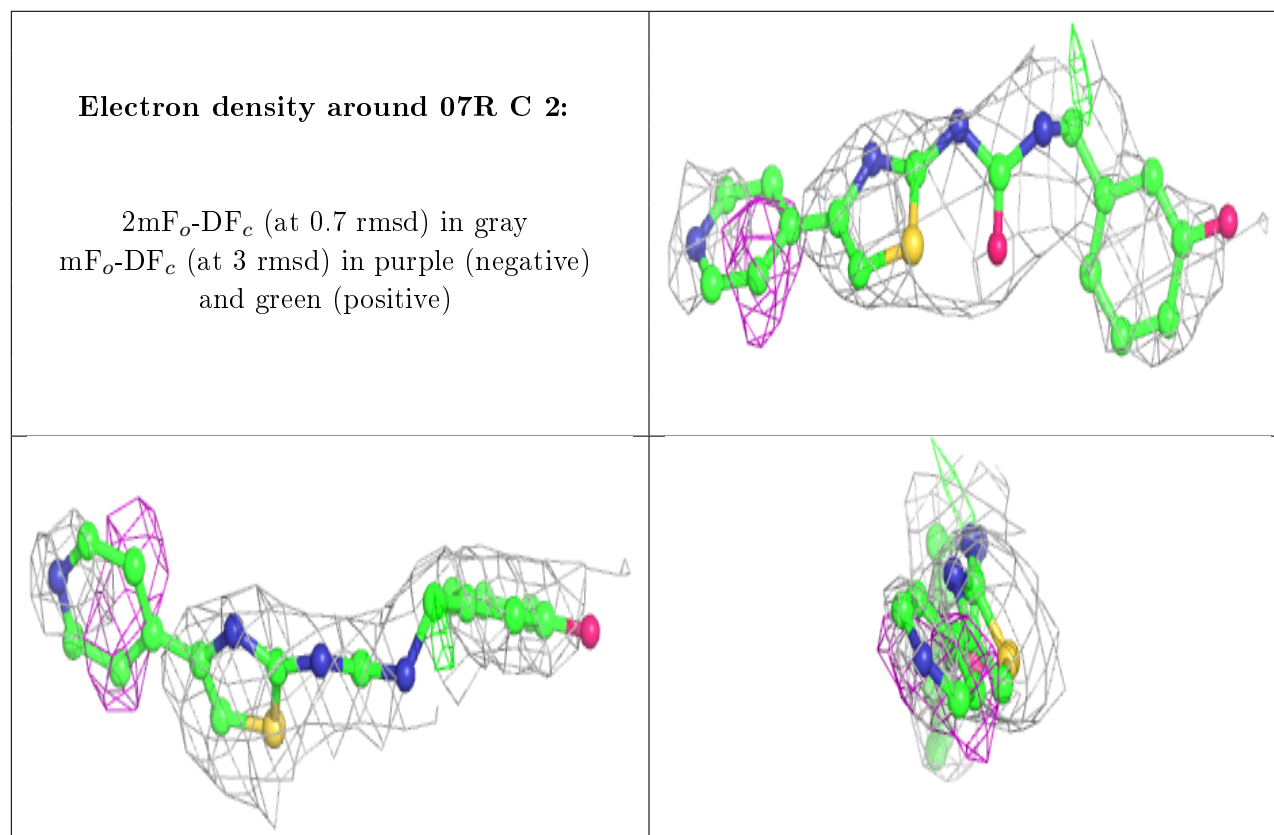
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	07R	C	2	23/23	0.79	0.37	61,72,82,105	0
3	EDO	B	2	4/4	0.93	0.20	40,47,47,48	0
2	07R	A	1	23/23	0.94	0.23	52,68,74,79	0

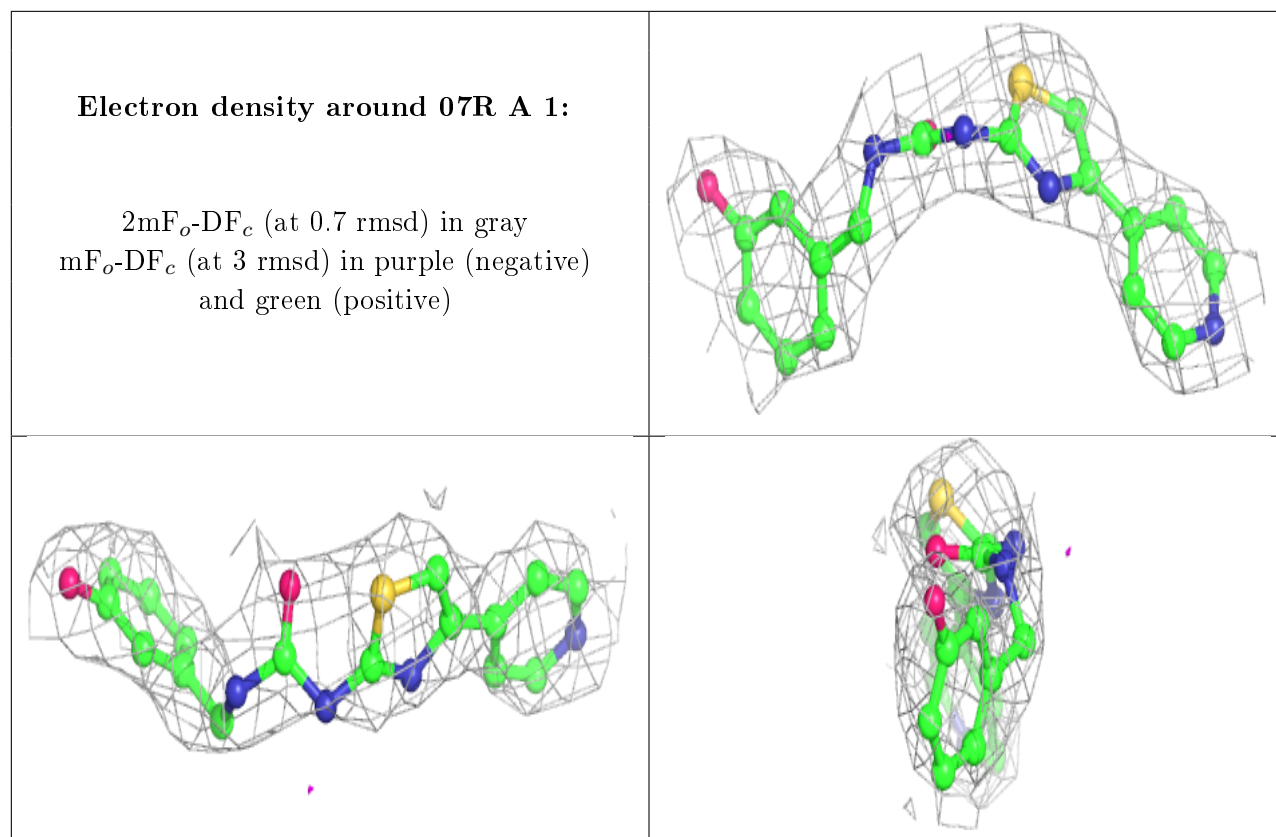
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	A	3	4/4	0.94	0.16	41,45,47,49	0
3	EDO	D	1	4/4	0.95	0.20	42,43,46,46	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.