



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:24 AM UTC

PDB ID : 3E3B / pdb_00003e3b
Title : Crystal structure of catalytic subunit of human protein kinase CK2alpha prime with a potent indazole-derivative inhibitor
Authors : Kinoshita, T.; Nakaniwa, T.; Tada, T.
Deposited on : 2008-08-07
Resolution : 3.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

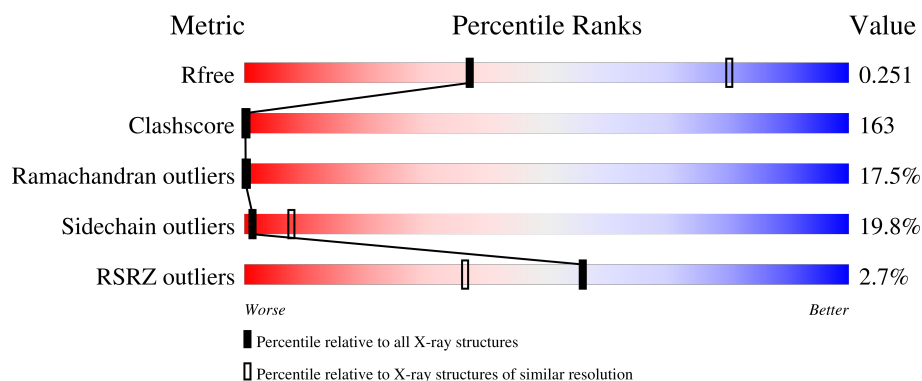
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	X	339	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2938 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.

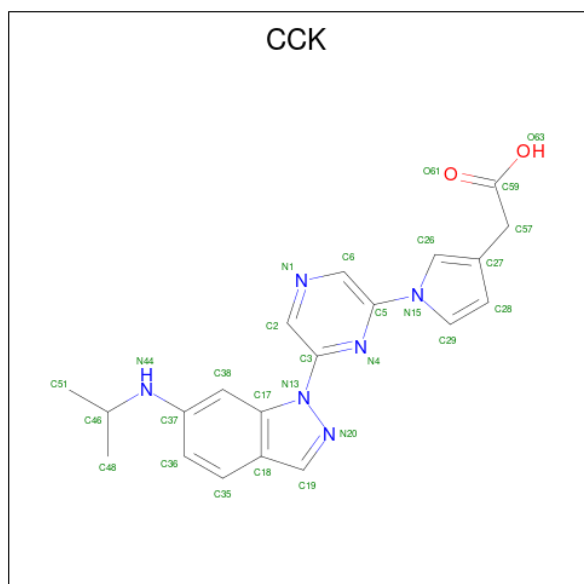
- Molecule 1 is a protein called Casein kinase II subunit alpha'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	334	Total	C	N	O	S	0	0	0
			2804	1803	490	500	11			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	-4	GLY	-	expression tag	UNP P19784
X	-3	PRO	-	expression tag	UNP P19784
X	-2	LEU	-	expression tag	UNP P19784
X	-1	GLY	-	expression tag	UNP P19784
X	0	SER	-	expression tag	UNP P19784

- Molecule 2 is [1-(6-{6-[(1-methylethyl)amino]-1H-indazol-1-yl}pyrazin-2-yl)-1H-pyrrol-3-yl] acetic acid (CCD ID: CCK) (formula: C₂₀H₂₀N₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	X	1	Total	C	N	O	0	0
			28	20	6	2		

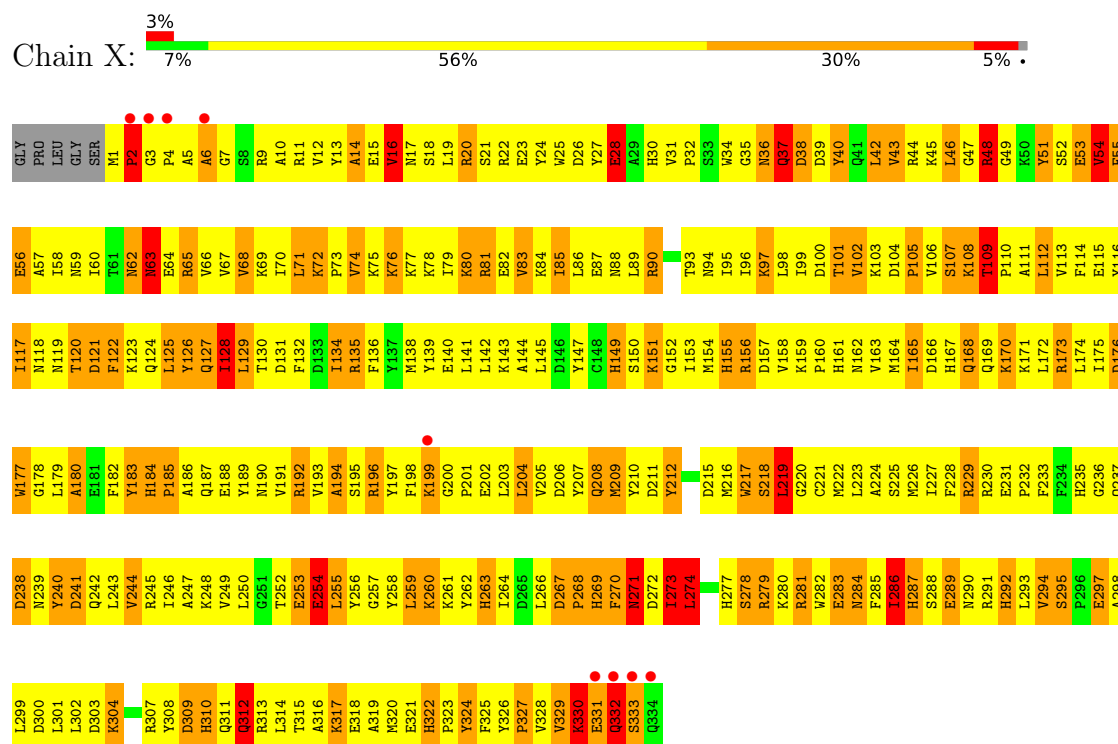
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	106	Total	O	0	0
			106	106		

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: Casein kinase II subunit alpha'



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	69.81Å 102.13Å 46.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.64 – 3.20 57.63 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (57.64-3.20) 99.9 (57.63-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.20 (at 3.19Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.248 , 0.274 0.236 , 0.251	Depositor DCC
R_{free} test set	273 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 84.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	2938	wwPDB-VP
Average B, all atoms (Å ²)	8.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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: CCK

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	X	0.51	0/2877	1.12	28/3885 (0.7%)

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	X	0	1

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	107	SER	N-CA-C	-9.52	101.79	113.97
1	X	37	GLN	N-CA-C	-9.20	98.99	111.96
1	X	239	ASN	N-CA-C	-9.18	101.85	112.87
1	X	135	ARG	N-CA-C	-9.18	101.28	111.28
1	X	260	LYS	N-CA-C	-8.28	100.12	112.04
1	X	109	THR	CA-C-N	8.07	128.01	119.85
1	X	109	THR	C-N-CA	8.07	128.01	119.85
1	X	87	GLU	N-CA-C	-8.00	102.56	111.28
1	X	28	GLU	N-CA-C	-7.61	103.88	113.01
1	X	283	GLU	N-CA-C	-6.97	104.03	112.54
1	X	217	TRP	N-CA-C	-6.73	103.87	111.07
1	X	208	GLN	N-CA-C	6.62	119.51	111.82
1	X	128	ILE	N-CA-C	-6.43	106.42	113.43
1	X	149	HIS	N-CA-C	-6.25	104.39	111.14
1	X	322	HIS	CA-C-N	6.25	127.65	119.84
1	X	322	HIS	C-N-CA	6.25	127.65	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	54	VAL	N-CA-C	6.23	117.06	107.78
1	X	56	GLU	N-CA-C	-6.03	99.42	109.24
1	X	271	ASN	N-CA-C	-5.99	104.44	110.97
1	X	53	GLU	N-CA-C	-5.91	100.66	110.17
1	X	81	ARG	N-CA-C	5.81	118.11	111.02
1	X	241	ASP	N-CA-C	-5.61	105.26	111.71
1	X	286	ILE	N-CA-C	5.52	115.27	106.88
1	X	184	HIS	CA-C-N	5.49	126.70	119.84
1	X	184	HIS	C-N-CA	5.49	126.70	119.84
1	X	204	LEU	N-CA-C	-5.41	106.74	113.55
1	X	40	TYR	N-CA-C	5.20	117.37	108.90
1	X	16	VAL	N-CA-C	5.18	120.12	109.34

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	183	TYR	Sidechain

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	X	2804	0	2780	915	0
2	X	28	0	19	6	0
3	X	106	0	0	42	0
All	All	2938	0	2799	917	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 163.

All (917) 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:X:223:LEU:HD12	1:X:302:LEU:HD13	1.17	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:294:VAL:HG13	1:X:299:LEU:HD21	1.24	1.15
1:X:199:LYS:HZ1	1:X:242:GLN:HG3	1.04	1.13
1:X:107:SER:C	1:X:108:LYS:HE2	1.72	1.13
1:X:65:ARG:HB3	1:X:65:ARG:HH21	1.00	1.10
1:X:256:TYR:HA	1:X:259:LEU:HD11	1.28	1.09
1:X:256:TYR:HA	1:X:259:LEU:CD1	1.85	1.07
1:X:288:SER:O	1:X:291:ARG:HG2	1.54	1.07
1:X:46:LEU:HD21	1:X:56:GLU:HB2	1.35	1.07
1:X:72:LYS:H	1:X:72:LYS:HD2	1.13	1.07
1:X:75:LYS:HE3	1:X:77:LYS:HE2	1.30	1.07
1:X:13:TYR:HB2	1:X:212:TYR:HE2	1.18	1.06
1:X:48:ARG:HB2	1:X:53:GLU:HA	1.13	1.06
1:X:107:SER:HB2	1:X:109:THR:OG1	1.56	1.06
1:X:309:ASP:HB3	1:X:312:GLN:HG2	1.34	1.05
1:X:48:ARG:CB	1:X:53:GLU:HA	1.86	1.05
1:X:65:ARG:HB3	1:X:65:ARG:NH2	1.69	1.05
1:X:294:VAL:HG12	1:X:295:SER:H	0.90	1.05
1:X:72:LYS:HD2	1:X:72:LYS:N	1.71	1.04
1:X:249:VAL:HG12	1:X:250:LEU:HD23	1.38	1.04
1:X:307:ARG:NH2	1:X:312:GLN:HE22	1.57	1.03
1:X:121:ASP:OD2	1:X:123:LYS:HB2	1.58	1.02
1:X:286:ILE:HD11	1:X:291:ARG:HA	1.38	1.02
1:X:309:ASP:HB3	1:X:312:GLN:CG	1.89	1.02
1:X:37:GLN:HE21	1:X:38:ASP:HA	1.25	1.01
1:X:35:GLY:H	1:X:102:VAL:HA	1.24	1.00
1:X:307:ARG:HH21	1:X:312:GLN:NE2	1.57	1.00
1:X:294:VAL:CG1	1:X:295:SER:H	1.73	1.00
1:X:294:VAL:HG12	1:X:295:SER:N	1.70	0.99
1:X:48:ARG:HG2	1:X:52:SER:O	1.63	0.98
1:X:13:TYR:HB2	1:X:212:TYR:CE2	1.99	0.98
1:X:119:ASN:HD22	1:X:120:THR:N	1.62	0.97
1:X:279:ARG:HD3	1:X:279:ARG:C	1.87	0.97
1:X:273:ILE:HD12	1:X:273:ILE:H	1.29	0.97
1:X:105:PRO:O	1:X:108:LYS:HD3	1.64	0.97
1:X:294:VAL:CG1	1:X:299:LEU:HD21	1.95	0.97
1:X:115:GLU:CD	1:X:173:ARG:HH22	1.73	0.96
1:X:204:LEU:HD12	1:X:243:LEU:HD13	1.46	0.96
1:X:131:ASP:O	1:X:135:ARG:HG3	1.65	0.96
1:X:76:LYS:O	1:X:80:LYS:HG2	1.65	0.96
1:X:199:LYS:NZ	1:X:242:GLN:HG3	1.82	0.95
1:X:315:THR:CG2	1:X:318:GLU:H	1.80	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:329:VAL:C	1:X:330:LYS:HD2	1.92	0.94
1:X:72:LYS:H	1:X:72:LYS:CD	1.80	0.94
1:X:304:LYS:HE2	1:X:314:LEU:HD21	1.45	0.94
1:X:205:VAL:HG11	1:X:264:ILE:HG21	1.46	0.94
1:X:119:ASN:HB2	1:X:164:MET:SD	2.07	0.94
1:X:199:LYS:HD3	1:X:204:LEU:CD2	1.99	0.93
1:X:128:ILE:HD13	1:X:129:LEU:N	1.84	0.93
1:X:42:LEU:HD11	1:X:68:VAL:CG1	1.99	0.93
1:X:269:HIS:C	1:X:273:ILE:HD13	1.93	0.92
1:X:10:ALA:HB2	1:X:183:TYR:CE2	2.05	0.92
1:X:37:GLN:HE21	1:X:38:ASP:CA	1.81	0.92
1:X:297:GLU:CB	1:X:324:TYR:HD1	1.82	0.92
1:X:138:MET:SD	1:X:226:MET:HE1	2.10	0.92
1:X:189:TYR:N	1:X:208:GLN:HB3	1.84	0.91
1:X:199:LYS:HZ1	1:X:242:GLN:CG	1.82	0.91
1:X:62:ASN:HD22	1:X:64:GLU:HG3	1.36	0.91
1:X:315:THR:HG22	1:X:318:GLU:HB2	1.51	0.91
1:X:199:LYS:HD3	1:X:204:LEU:HD21	1.53	0.91
1:X:286:ILE:CD1	1:X:291:ARG:HA	2.01	0.91
1:X:304:LYS:HA	1:X:307:ARG:HE	1.36	0.91
1:X:269:HIS:ND1	1:X:273:ILE:HD11	1.87	0.90
1:X:74:VAL:HG13	1:X:75:LYS:N	1.87	0.90
1:X:295:SER:O	1:X:299:LEU:HD23	1.70	0.90
1:X:104:ASP:C	1:X:106:VAL:H	1.80	0.90
1:X:125:LEU:C	1:X:125:LEU:HD13	1.97	0.90
1:X:134:ILE:CG2	1:X:135:ARG:N	2.35	0.90
1:X:205:VAL:HG11	1:X:264:ILE:CG2	2.01	0.90
1:X:273:ILE:HD12	1:X:273:ILE:N	1.87	0.90
1:X:119:ASN:HD22	1:X:120:THR:H	1.11	0.89
1:X:199:LYS:HZ2	1:X:204:LEU:HD11	1.37	0.89
1:X:125:LEU:O	1:X:128:ILE:HD12	1.72	0.89
1:X:20:ARG:HH12	1:X:151:LYS:HZ1	1.17	0.88
1:X:297:GLU:HB3	1:X:324:TYR:HD1	1.35	0.88
1:X:48:ARG:HB2	1:X:53:GLU:CA	2.00	0.88
1:X:223:LEU:CD1	1:X:302:LEU:HD13	2.01	0.88
1:X:315:THR:HG22	1:X:318:GLU:CB	2.02	0.88
1:X:125:LEU:CD1	1:X:126:TYR:HD1	1.87	0.88
1:X:31:VAL:O	1:X:31:VAL:HG13	1.74	0.88
1:X:190:ASN:HD21	1:X:192:ARG:HB2	1.39	0.87
1:X:244:VAL:HG11	1:X:273:ILE:HG22	1.57	0.87
1:X:107:SER:O	1:X:108:LYS:HB2	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:252:THR:CG2	1:X:277:HIS:H	1.87	0.87
1:X:51:TYR:H	1:X:51:TYR:HD2	1.20	0.86
1:X:37:GLN:HB2	1:X:104:ASP:CG	1.99	0.86
1:X:278:SER:O	1:X:280:LYS:HD2	1.76	0.86
1:X:65:ARG:HH21	1:X:65:ARG:CB	1.86	0.85
1:X:12:VAL:HG23	1:X:13:TYR:N	1.91	0.85
1:X:189:TYR:H	1:X:208:GLN:HB3	1.38	0.85
1:X:191:VAL:HG13	1:X:203:LEU:CD2	2.07	0.84
1:X:261:LYS:C	1:X:262:TYR:HD2	1.84	0.84
1:X:119:ASN:ND2	1:X:120:THR:N	2.24	0.84
1:X:248:LYS:HG2	1:X:277:HIS:ND1	1.92	0.84
1:X:271:ASN:H	1:X:271:ASN:ND2	1.72	0.84
1:X:294:VAL:HG13	1:X:299:LEU:CD2	2.04	0.84
1:X:125:LEU:HD12	1:X:126:TYR:CD1	2.13	0.84
1:X:309:ASP:CB	1:X:312:GLN:HG2	2.07	0.84
1:X:204:LEU:HD12	1:X:243:LEU:CD1	2.08	0.83
1:X:217:TRP:HB2	1:X:313:ARG:NH2	1.92	0.83
1:X:191:VAL:HA	1:X:203:LEU:HD22	1.58	0.83
1:X:16:VAL:HG12	1:X:17:ASN:N	1.93	0.83
1:X:227:ILE:HD11	1:X:293:LEU:O	1.79	0.83
1:X:271:ASN:ND2	1:X:271:ASN:N	2.23	0.83
1:X:134:ILE:HG22	1:X:135:ARG:H	1.42	0.83
1:X:71:LEU:HD22	1:X:72:LYS:N	1.94	0.82
1:X:14:ALA:O	1:X:185:PRO:HG3	1.77	0.82
1:X:126:TYR:C	1:X:127:GLN:HG3	2.05	0.82
1:X:273:ILE:H	1:X:273:ILE:CD1	1.91	0.82
1:X:10:ALA:O	1:X:14:ALA:HB2	1.79	0.82
1:X:322:HIS:CE1	1:X:324:TYR:H	1.98	0.82
1:X:74:VAL:HG13	1:X:75:LYS:H	1.41	0.82
1:X:104:ASP:CB	1:X:106:VAL:HG22	2.10	0.81
1:X:315:THR:HG23	1:X:318:GLU:H	1.43	0.81
1:X:292:HIS:CD2	1:X:292:HIS:H	1.98	0.81
1:X:42:LEU:HD11	1:X:68:VAL:HG12	1.62	0.81
1:X:117:ILE:HD13	1:X:117:ILE:C	2.05	0.81
1:X:71:LEU:HD13	1:X:71:LEU:O	1.79	0.81
1:X:106:VAL:HG23	1:X:107:SER:H	1.46	0.81
1:X:293:LEU:HG	3:X:375:HOH:O	1.79	0.81
1:X:12:VAL:HG23	1:X:13:TYR:H	1.47	0.80
1:X:71:LEU:HD22	1:X:71:LEU:C	2.06	0.80
1:X:51:TYR:O	1:X:71:LEU:HD23	1.81	0.80
1:X:164:MET:O	1:X:165:ILE:HG13	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:294:VAL:O	1:X:295:SER:HB3	1.80	0.80
1:X:328:VAL:O	1:X:330:LYS:HE3	1.82	0.80
1:X:51:TYR:N	1:X:51:TYR:CD2	2.49	0.80
1:X:193:VAL:HA	3:X:363:HOH:O	1.80	0.80
1:X:122:PHE:HE1	1:X:161:HIS:CD2	1.99	0.80
1:X:271:ASN:N	1:X:271:ASN:HD22	1.77	0.80
1:X:79:ILE:O	1:X:83:VAL:HG23	1.81	0.80
1:X:5:ALA:HB1	3:X:390:HOH:O	1.82	0.79
1:X:156:ARG:NH2	1:X:156:ARG:HG3	1.97	0.79
1:X:37:GLN:O	1:X:39:ASP:N	2.15	0.79
1:X:156:ARG:HG3	1:X:156:ARG:HH21	1.47	0.79
1:X:199:LYS:CD	1:X:204:LEU:HD21	2.12	0.79
1:X:199:LYS:HD2	1:X:199:LYS:O	1.81	0.79
1:X:104:ASP:O	1:X:106:VAL:HG22	1.82	0.79
1:X:269:HIS:O	1:X:271:ASN:N	2.16	0.79
1:X:20:ARG:HH22	1:X:151:LYS:HZ3	1.31	0.79
1:X:67:VAL:CG1	1:X:114:PHE:HB2	2.13	0.79
1:X:199:LYS:CE	1:X:204:LEU:HD21	2.13	0.78
1:X:297:GLU:HB3	1:X:324:TYR:CD1	2.18	0.78
1:X:34:TRP:HB2	3:X:381:HOH:O	1.84	0.78
1:X:172:LEU:O	1:X:173:ARG:HD3	1.83	0.78
1:X:204:LEU:CD1	1:X:243:LEU:HD13	2.13	0.78
1:X:105:PRO:O	1:X:108:LYS:CD	2.30	0.78
1:X:42:LEU:HD11	1:X:68:VAL:HG11	1.66	0.78
1:X:158:VAL:HB	1:X:218:SER:HB3	1.66	0.77
1:X:34:TRP:CZ3	1:X:110:PRO:HB2	2.20	0.77
1:X:74:VAL:CG1	1:X:75:LYS:H	1.97	0.77
1:X:20:ARG:HH22	1:X:151:LYS:NZ	1.82	0.77
1:X:75:LYS:HG3	1:X:78:LYS:HB3	1.65	0.77
1:X:298:ALA:O	1:X:302:LEU:HB2	1.85	0.77
1:X:256:TYR:O	1:X:259:LEU:HD12	1.85	0.77
1:X:20:ARG:NH1	1:X:151:LYS:HZ1	1.82	0.77
1:X:70:ILE:HD11	3:X:382:HOH:O	1.84	0.77
1:X:125:LEU:HD13	1:X:126:TYR:N	1.99	0.77
1:X:37:GLN:NE2	1:X:38:ASP:N	2.33	0.76
1:X:222:MET:HB3	1:X:226:MET:HE2	1.66	0.76
1:X:34:TRP:CZ3	1:X:101:THR:HG23	2.19	0.76
1:X:199:LYS:NZ	1:X:242:GLN:CG	2.46	0.76
1:X:328:VAL:C	1:X:330:LYS:H	1.93	0.76
1:X:315:THR:HG22	1:X:318:GLU:CG	2.14	0.76
1:X:258:TYR:CE1	1:X:309:ASP:HA	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:104:ASP:C	1:X:106:VAL:N	2.41	0.76
1:X:34:TRP:CZ3	1:X:110:PRO:CB	2.69	0.76
1:X:22:ARG:HG3	1:X:25:TRP:CZ2	2.21	0.76
1:X:37:GLN:NE2	1:X:38:ASP:CG	2.44	0.76
1:X:81:ARG:HG3	1:X:82:GLU:N	2.01	0.76
1:X:198:PHE:O	1:X:199:LYS:C	2.29	0.76
1:X:156:ARG:HH21	1:X:156:ARG:CG	1.98	0.76
1:X:104:ASP:O	1:X:106:VAL:N	2.18	0.75
1:X:58:ILE:HD11	1:X:63:ASN:C	2.11	0.75
1:X:106:VAL:HG23	1:X:107:SER:N	2.01	0.75
1:X:37:GLN:O	1:X:40:TYR:N	2.17	0.75
1:X:330:LYS:HB2	3:X:415:HOH:O	1.85	0.75
1:X:154:MET:HE1	1:X:211:ASP:C	2.12	0.75
1:X:6:ALA:HB2	3:X:442:HOH:O	1.87	0.75
1:X:37:GLN:NE2	1:X:38:ASP:CA	2.49	0.75
1:X:107:SER:O	1:X:108:LYS:HE2	1.84	0.75
1:X:252:THR:HG21	1:X:277:HIS:H	1.50	0.75
1:X:75:LYS:CE	1:X:77:LYS:HE2	2.15	0.75
1:X:199:LYS:NZ	1:X:204:LEU:HD11	2.01	0.75
1:X:104:ASP:HB3	1:X:106:VAL:HG22	1.68	0.75
1:X:279:ARG:C	1:X:279:ARG:CD	2.61	0.74
1:X:122:PHE:HE2	1:X:231:GLU:OE2	1.70	0.74
1:X:75:LYS:O	1:X:77:LYS:N	2.20	0.74
1:X:155:HIS:O	1:X:156:ARG:HB2	1.87	0.74
1:X:46:LEU:CD2	1:X:56:GLU:HB2	2.15	0.74
1:X:156:ARG:NE	1:X:210:TYR:OH	2.20	0.74
1:X:219:LEU:HD13	1:X:219:LEU:O	1.87	0.74
1:X:112:LEU:HB2	1:X:114:PHE:CZ	2.23	0.74
1:X:187:GLN:O	1:X:189:TYR:CD2	2.40	0.74
1:X:270:PHE:HB3	1:X:274:LEU:HD22	1.69	0.74
1:X:244:VAL:HG11	1:X:273:ILE:CG2	2.16	0.74
1:X:103:LYS:HD3	1:X:108:LYS:O	1.88	0.73
1:X:45:LYS:HA	1:X:55:PHE:HA	1.70	0.73
1:X:154:MET:HE1	1:X:211:ASP:O	1.88	0.73
1:X:48:ARG:CG	1:X:53:GLU:HA	2.18	0.73
1:X:75:LYS:HB2	1:X:77:LYS:NZ	2.02	0.73
1:X:82:GLU:HG3	1:X:178:GLY:HA2	1.71	0.73
1:X:67:VAL:HG11	2:X:351:CCK:H29	1.70	0.73
1:X:168:GLN:HA	1:X:168:GLN:NE2	2.03	0.73
1:X:196:ARG:O	1:X:197:TYR:CD1	2.41	0.73
1:X:36:ASN:HB2	3:X:383:HOH:O	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:154:MET:CE	1:X:211:ASP:C	2.62	0.72
1:X:309:ASP:HB3	1:X:312:GLN:HG3	1.71	0.72
1:X:191:VAL:CA	1:X:203:LEU:HD22	2.19	0.72
1:X:122:PHE:CE2	1:X:231:GLU:OE2	2.42	0.72
1:X:20:ARG:HG3	3:X:407:HOH:O	1.88	0.72
1:X:207:TYR:CD1	1:X:264:ILE:HD11	2.25	0.72
1:X:1:MET:O	1:X:2:PRO:C	2.33	0.71
1:X:157:ASP:OD2	1:X:159:LYS:HE2	1.90	0.71
1:X:74:VAL:CG1	1:X:75:LYS:N	2.52	0.71
1:X:119:ASN:CB	1:X:164:MET:SD	2.79	0.71
1:X:202:GLU:OE1	1:X:310:HIS:HB2	1.90	0.71
1:X:176:ASP:OD1	1:X:177:TRP:N	2.23	0.71
1:X:97:LYS:CB	1:X:115:GLU:OE2	2.39	0.71
1:X:191:VAL:HG13	1:X:203:LEU:HD22	1.73	0.71
1:X:199:LYS:HD2	1:X:199:LYS:C	2.15	0.71
1:X:292:HIS:H	1:X:292:HIS:HD2	1.38	0.71
1:X:122:PHE:HD1	1:X:122:PHE:H	1.37	0.71
1:X:135:ARG:HH11	1:X:324:TYR:HA	1.55	0.71
1:X:269:HIS:O	1:X:273:ILE:HD13	1.89	0.71
1:X:37:GLN:NE2	1:X:38:ASP:H	1.90	0.70
1:X:125:LEU:HD22	1:X:128:ILE:CD1	2.21	0.70
1:X:134:ILE:HG23	1:X:135:ARG:N	2.05	0.70
1:X:122:PHE:CE1	1:X:161:HIS:CD2	2.80	0.70
1:X:228:PHE:O	1:X:229:ARG:CG	2.39	0.70
1:X:216:MET:CE	1:X:316:ALA:HA	2.21	0.70
1:X:267:ASP:CG	1:X:268:PRO:HD2	2.16	0.70
1:X:326:TYR:O	1:X:328:VAL:N	2.24	0.70
1:X:328:VAL:O	1:X:330:LYS:CE	2.39	0.70
1:X:125:LEU:CD1	1:X:126:TYR:CD1	2.70	0.70
1:X:10:ALA:HB3	1:X:14:ALA:HA	1.72	0.70
1:X:97:LYS:HB3	1:X:115:GLU:OE2	1.91	0.70
1:X:71:LEU:HD22	1:X:72:LYS:HD2	1.74	0.69
1:X:86:LEU:HD21	1:X:177:TRP:CD1	2.27	0.69
1:X:37:GLN:CB	1:X:104:ASP:CG	2.65	0.69
1:X:103:LYS:HG3	1:X:109:THR:C	2.17	0.69
1:X:122:PHE:CG	1:X:160:PRO:HB3	2.26	0.69
1:X:58:ILE:HD11	1:X:63:ASN:CA	2.22	0.69
1:X:189:TYR:O	1:X:208:GLN:HG2	1.91	0.69
1:X:217:TRP:HB2	1:X:313:ARG:HH22	1.56	0.69
1:X:11:ARG:NH1	1:X:318:GLU:OE1	2.26	0.69
1:X:18:SER:O	1:X:20:ARG:N	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:79:ILE:O	1:X:80:LYS:C	2.35	0.69
1:X:125:LEU:HD22	1:X:128:ILE:HD11	1.73	0.69
1:X:192:ARG:NH1	1:X:206:ASP:OD2	2.26	0.68
1:X:75:LYS:C	3:X:450:HOH:O	2.36	0.68
1:X:37:GLN:HE22	1:X:38:ASP:CG	2.02	0.68
1:X:42:LEU:HD12	1:X:55:PHE:HB2	1.76	0.68
1:X:55:PHE:CD1	1:X:55:PHE:N	2.62	0.68
1:X:227:ILE:HD11	1:X:293:LEU:C	2.19	0.68
1:X:326:TYR:C	1:X:328:VAL:H	2.00	0.68
1:X:329:VAL:HG22	1:X:329:VAL:O	1.93	0.68
1:X:4:PRO:O	1:X:263:HIS:CG	2.47	0.68
1:X:230:ARG:HE	1:X:233:PHE:HD2	1.40	0.68
1:X:279:ARG:HD3	1:X:279:ARG:O	1.93	0.68
1:X:190:ASN:HD21	1:X:192:ARG:CB	2.06	0.68
1:X:75:LYS:C	1:X:77:LYS:N	2.50	0.68
1:X:117:ILE:HD13	1:X:118:ASN:N	2.09	0.68
1:X:270:PHE:HB3	1:X:274:LEU:CD2	2.24	0.68
1:X:138:MET:SD	1:X:226:MET:CE	2.81	0.68
1:X:191:VAL:HG13	1:X:203:LEU:HA	1.76	0.68
1:X:193:VAL:O	1:X:194:ALA:HB3	1.92	0.68
1:X:310:HIS:C	1:X:310:HIS:CD2	2.72	0.68
1:X:288:SER:HA	1:X:291:ARG:HD2	1.76	0.67
1:X:155:HIS:O	1:X:180:ALA:HA	1.94	0.67
1:X:328:VAL:O	1:X:330:LYS:NZ	2.27	0.67
1:X:158:VAL:HB	1:X:218:SER:CB	2.25	0.67
1:X:248:LYS:O	1:X:280:LYS:HD3	1.95	0.67
1:X:141:LEU:HD23	1:X:219:LEU:CD2	2.23	0.67
1:X:138:MET:HE1	1:X:219:LEU:HD13	1.76	0.67
1:X:20:ARG:NH2	1:X:151:LYS:NZ	2.42	0.67
1:X:168:GLN:O	1:X:169:GLN:C	2.34	0.67
1:X:27:TYR:CD1	1:X:27:TYR:C	2.72	0.67
1:X:12:VAL:HG11	1:X:315:THR:OG1	1.95	0.66
1:X:30:HIS:HD2	3:X:425:HOH:O	1.79	0.66
1:X:34:TRP:CE3	1:X:101:THR:HG23	2.30	0.66
1:X:48:ARG:HD3	1:X:49:GLY:O	1.95	0.66
1:X:121:ASP:OD1	1:X:123:LYS:HG2	1.95	0.66
1:X:196:ARG:HD2	1:X:237:GLN:O	1.96	0.66
1:X:228:PHE:O	1:X:229:ARG:HG2	1.95	0.66
1:X:138:MET:HE2	1:X:223:LEU:HB2	1.75	0.66
1:X:203:LEU:HD21	1:X:210:TYR:CE2	2.30	0.66
1:X:248:LYS:HG2	1:X:277:HIS:CE1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:228:PHE:O	1:X:229:ARG:CB	2.43	0.66
1:X:258:TYR:HE1	1:X:309:ASP:HA	1.60	0.66
1:X:20:ARG:NH2	1:X:151:LYS:HZ3	1.94	0.66
1:X:37:GLN:CG	1:X:38:ASP:N	2.58	0.66
1:X:191:VAL:HA	1:X:203:LEU:CD2	2.24	0.66
1:X:75:LYS:HB2	1:X:77:LYS:CE	2.25	0.66
1:X:287:HIS:CD2	1:X:290:ASN:HD21	2.13	0.66
1:X:67:VAL:HG12	1:X:114:PHE:O	1.95	0.66
1:X:164:MET:HE3	1:X:175:ILE:HD13	1.77	0.66
1:X:45:LYS:HE2	1:X:55:PHE:CZ	2.31	0.66
1:X:156:ARG:HD2	1:X:193:VAL:HG21	1.77	0.66
1:X:9:ARG:NH2	1:X:185:PRO:HB3	2.11	0.65
1:X:253:GLU:O	1:X:255:LEU:N	2.29	0.65
1:X:105:PRO:C	1:X:108:LYS:HD3	2.20	0.65
1:X:71:LEU:CD2	1:X:72:LYS:CD	2.75	0.65
1:X:135:ARG:NE	1:X:324:TYR:O	2.29	0.65
1:X:189:TYR:O	1:X:190:ASN:C	2.40	0.65
1:X:315:THR:HG23	1:X:318:GLU:N	2.12	0.65
1:X:209:MET:HA	3:X:361:HOH:O	1.97	0.65
1:X:297:GLU:HB2	1:X:324:TYR:HD1	1.59	0.65
1:X:119:ASN:ND2	1:X:120:THR:H	1.87	0.65
1:X:67:VAL:HG13	1:X:114:PHE:HB2	1.76	0.65
1:X:164:MET:O	1:X:165:ILE:CG1	2.45	0.64
1:X:298:ALA:HB2	1:X:324:TYR:CE1	2.32	0.64
1:X:256:TYR:CA	1:X:259:LEU:CD1	2.71	0.64
1:X:149:HIS:HD2	1:X:316:ALA:HB2	1.62	0.64
1:X:13:TYR:CZ	1:X:150:SER:HA	2.32	0.64
1:X:104:ASP:HB3	1:X:106:VAL:CG2	2.27	0.64
1:X:238:ASP:C	1:X:240:TYR:N	2.52	0.64
1:X:315:THR:HA	3:X:400:HOH:O	1.96	0.64
1:X:37:GLN:NE2	1:X:38:ASP:HA	2.06	0.64
1:X:75:LYS:HB2	1:X:77:LYS:HE2	1.79	0.64
1:X:163:VAL:HG12	1:X:163:VAL:O	1.96	0.64
1:X:307:ARG:NH2	1:X:312:GLN:NE2	2.30	0.64
1:X:176:ASP:O	1:X:177:TRP:CD1	2.51	0.64
1:X:187:GLN:N	1:X:209:MET:HE2	2.12	0.64
1:X:96:ILE:HG22	1:X:177:TRP:HE1	1.63	0.64
1:X:169:GLN:O	1:X:170:LYS:CG	2.46	0.64
1:X:149:HIS:HE1	1:X:215:ASP:OD2	1.81	0.63
1:X:44:ARG:HG2	1:X:56:GLU:OE2	1.98	0.63
1:X:216:MET:HE2	1:X:315:THR:C	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:128:ILE:HD13	1:X:128:ILE:C	2.24	0.63
1:X:169:GLN:O	1:X:170:LYS:CB	2.46	0.63
1:X:200:GLY:HA2	1:X:217:TRP:CD1	2.34	0.63
1:X:322:HIS:ND1	1:X:323:PRO:N	2.45	0.63
1:X:93:THR:O	1:X:95:ILE:HG12	1.98	0.63
1:X:59:ASN:OD1	1:X:59:ASN:C	2.41	0.63
1:X:115:GLU:CD	1:X:173:ARG:NH2	2.53	0.63
1:X:12:VAL:CG2	1:X:13:TYR:N	2.62	0.63
1:X:34:TRP:HA	1:X:101:THR:O	1.99	0.63
1:X:164:MET:HG2	1:X:175:ILE:CG2	2.29	0.63
1:X:244:VAL:CG2	1:X:245:ARG:N	2.61	0.63
1:X:293:LEU:N	1:X:293:LEU:HD22	2.13	0.62
1:X:294:VAL:O	1:X:295:SER:CB	2.47	0.62
1:X:34:TRP:CE3	1:X:101:THR:CG2	2.81	0.62
1:X:71:LEU:CD2	1:X:72:LYS:HD2	2.29	0.62
1:X:218:SER:O	1:X:221:CYS:N	2.32	0.62
1:X:16:VAL:CG1	1:X:17:ASN:N	2.63	0.62
1:X:125:LEU:O	1:X:128:ILE:CD1	2.45	0.62
1:X:47:GLY:O	1:X:54:VAL:N	2.27	0.62
1:X:75:LYS:C	1:X:77:LYS:H	2.06	0.62
1:X:103:LYS:HA	1:X:110:PRO:HA	1.81	0.62
1:X:252:THR:HG23	1:X:277:HIS:H	1.63	0.62
1:X:240:TYR:CE1	1:X:269:HIS:CD2	2.87	0.62
1:X:256:TYR:CD1	1:X:259:LEU:HD11	2.34	0.62
1:X:322:HIS:CG	1:X:323:PRO:HD2	2.34	0.62
1:X:154:MET:CE	1:X:211:ASP:O	2.47	0.62
1:X:58:ILE:HG13	1:X:64:GLU:C	2.24	0.62
1:X:75:LYS:CG	1:X:78:LYS:HB3	2.28	0.62
1:X:78:LYS:HA	1:X:81:ARG:NH2	2.13	0.62
1:X:94:ASN:HB3	1:X:172:LEU:HD23	1.81	0.62
1:X:106:VAL:O	1:X:108:LYS:NZ	2.31	0.62
1:X:97:LYS:NZ	1:X:97:LYS:HB2	2.14	0.62
1:X:37:GLN:HE21	1:X:38:ASP:N	1.95	0.62
1:X:42:LEU:HA	1:X:57:ALA:HB2	1.81	0.62
1:X:125:LEU:C	1:X:125:LEU:CD1	2.73	0.62
1:X:37:GLN:HB2	1:X:104:ASP:OD2	1.99	0.61
1:X:304:LYS:HA	1:X:307:ARG:NE	2.10	0.61
1:X:12:VAL:CG2	1:X:13:TYR:H	2.13	0.61
1:X:10:ALA:CB	1:X:183:TYR:CE2	2.81	0.61
1:X:76:LYS:O	1:X:80:LYS:CG	2.44	0.61
1:X:281:ARG:N	1:X:284:ASN:ND2	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:283:GLU:C	1:X:285:PHE:H	2.06	0.61
1:X:66:VAL:HG11	1:X:113:VAL:HG12	1.83	0.61
1:X:75:LYS:HE3	1:X:77:LYS:CE	2.20	0.61
1:X:171:LYS:HB2	3:X:402:HOH:O	2.00	0.61
1:X:176:ASP:OD1	1:X:176:ASP:C	2.43	0.61
1:X:176:ASP:O	1:X:177:TRP:CG	2.53	0.61
1:X:330:LYS:HD2	1:X:330:LYS:N	2.14	0.61
1:X:147:TYR:O	1:X:150:SER:OG	2.17	0.61
1:X:149:HIS:CE1	1:X:215:ASP:OD2	2.53	0.61
1:X:287:HIS:CD2	1:X:287:HIS:H	2.19	0.61
1:X:256:TYR:CA	1:X:259:LEU:HD11	2.17	0.61
1:X:270:PHE:HA	1:X:273:ILE:HB	1.83	0.61
1:X:188:GLU:HB3	1:X:208:GLN:CD	2.26	0.61
1:X:237:GLN:O	1:X:238:ASP:C	2.44	0.61
1:X:278:SER:O	1:X:280:LYS:CD	2.48	0.61
1:X:319:ALA:O	1:X:322:HIS:HB3	2.01	0.61
1:X:191:VAL:HG13	1:X:203:LEU:HD23	1.83	0.61
1:X:240:TYR:N	1:X:240:TYR:HD2	1.99	0.61
1:X:116:TYR:HD1	3:X:374:HOH:O	1.83	0.61
1:X:269:HIS:C	1:X:271:ASN:H	2.08	0.61
1:X:37:GLN:CD	1:X:38:ASP:H	2.09	0.60
1:X:107:SER:HB2	1:X:109:THR:HG1	1.61	0.60
1:X:254:GLU:HA	3:X:379:HOH:O	2.01	0.60
1:X:4:PRO:O	1:X:263:HIS:CD2	2.55	0.60
1:X:85:ILE:HG22	1:X:86:LEU:N	2.16	0.60
1:X:122:PHE:CD1	1:X:122:PHE:N	2.67	0.60
1:X:134:ILE:HD11	1:X:226:MET:HB3	1.82	0.60
1:X:238:ASP:C	1:X:240:TYR:H	2.07	0.60
1:X:298:ALA:O	1:X:302:LEU:CB	2.49	0.60
1:X:104:ASP:HB3	1:X:106:VAL:HG13	1.82	0.60
1:X:196:ARG:O	1:X:197:TYR:HD1	1.83	0.60
1:X:48:ARG:HG3	1:X:53:GLU:OE1	2.01	0.60
1:X:135:ARG:HG2	1:X:324:TYR:CE2	2.35	0.60
1:X:152:GLY:HA2	1:X:212:TYR:OH	2.02	0.60
1:X:261:LYS:C	1:X:262:TYR:CD2	2.75	0.60
1:X:106:VAL:CG2	1:X:107:SER:H	2.15	0.59
1:X:282:TRP:HB2	1:X:299:LEU:HD12	1.84	0.59
1:X:205:VAL:HG12	1:X:205:VAL:O	2.02	0.59
1:X:307:ARG:HH21	1:X:312:GLN:HE22	0.76	0.59
1:X:267:ASP:O	1:X:268:PRO:O	2.19	0.59
1:X:119:ASN:ND2	1:X:121:ASP:H	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:126:TYR:C	1:X:127:GLN:CG	2.75	0.59
1:X:48:ARG:CG	1:X:52:SER:O	2.43	0.59
1:X:62:ASN:O	1:X:64:GLU:HG3	2.02	0.59
1:X:232:PRO:HG2	1:X:235:HIS:HA	1.83	0.59
1:X:51:TYR:HB2	1:X:71:LEU:HG	1.85	0.59
1:X:64:GLU:O	1:X:66:VAL:HG23	2.01	0.59
1:X:126:TYR:O	1:X:127:GLN:CG	2.50	0.59
1:X:287:HIS:CD2	1:X:290:ASN:ND2	2.71	0.59
1:X:191:VAL:HG13	1:X:203:LEU:CA	2.32	0.58
1:X:44:ARG:CG	1:X:56:GLU:OE2	2.51	0.58
1:X:288:SER:HA	3:X:369:HOH:O	2.03	0.58
1:X:74:VAL:HG13	1:X:75:LYS:HG2	1.85	0.58
1:X:80:LYS:O	1:X:83:VAL:HG23	2.04	0.58
1:X:149:HIS:CD2	1:X:316:ALA:HB2	2.38	0.58
1:X:172:LEU:HD23	1:X:172:LEU:C	2.27	0.58
1:X:130:THR:O	1:X:131:ASP:C	2.46	0.58
1:X:216:MET:HE1	1:X:316:ALA:HA	1.85	0.58
1:X:71:LEU:HD22	1:X:72:LYS:CD	2.33	0.58
1:X:75:LYS:HG3	1:X:75:LYS:O	2.04	0.58
1:X:187:GLN:NE2	3:X:403:HOH:O	2.36	0.58
1:X:268:PRO:O	1:X:269:HIS:CB	2.49	0.58
1:X:315:THR:CG2	1:X:318:GLU:N	2.59	0.58
1:X:330:LYS:O	1:X:331:GLU:C	2.45	0.58
1:X:169:GLN:O	1:X:170:LYS:HG2	2.04	0.58
1:X:22:ARG:HG3	1:X:25:TRP:CH2	2.38	0.58
1:X:59:ASN:OD1	1:X:59:ASN:O	2.22	0.58
1:X:69:LYS:HE3	1:X:114:PHE:HZ	1.68	0.58
1:X:75:LYS:HG3	1:X:78:LYS:H	1.69	0.58
1:X:35:GLY:H	1:X:102:VAL:CA	2.09	0.58
1:X:48:ARG:HA	1:X:54:VAL:HG23	1.85	0.58
1:X:69:LYS:HE2	2:X:351:CCK:O61	2.04	0.58
1:X:103:LYS:O	1:X:105:PRO:HD3	2.03	0.58
1:X:37:GLN:CB	1:X:104:ASP:OD2	2.52	0.57
1:X:182:PHE:HB2	3:X:380:HOH:O	2.03	0.57
1:X:218:SER:O	1:X:220:GLY:N	2.36	0.57
1:X:122:PHE:CD2	1:X:160:PRO:HB3	2.39	0.57
1:X:176:ASP:N	2:X:351:CCK:O63	2.36	0.57
1:X:287:HIS:H	1:X:287:HIS:HD2	1.51	0.57
1:X:9:ARG:HH22	1:X:185:PRO:HB3	1.69	0.57
1:X:269:HIS:C	1:X:271:ASN:N	2.60	0.57
1:X:322:HIS:ND1	1:X:323:PRO:HD2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:37:GLN:HG2	1:X:38:ASP:N	2.17	0.57
1:X:166:ASP:O	1:X:170:LYS:CA	2.52	0.57
1:X:287:HIS:CE1	1:X:289:GLU:HG3	2.39	0.57
1:X:62:ASN:O	1:X:64:GLU:N	2.38	0.57
1:X:131:ASP:O	1:X:135:ARG:CG	2.48	0.57
1:X:218:SER:O	1:X:219:LEU:C	2.47	0.57
1:X:270:PHE:N	1:X:273:ILE:HD13	2.19	0.57
1:X:30:HIS:CG	1:X:84:LYS:HD3	2.40	0.56
1:X:269:HIS:O	1:X:273:ILE:CD1	2.53	0.56
1:X:104:ASP:HB2	1:X:106:VAL:HG22	1.87	0.56
1:X:253:GLU:C	1:X:255:LEU:N	2.62	0.56
1:X:304:LYS:HG2	1:X:307:ARG:HH11	1.70	0.56
1:X:37:GLN:NE2	1:X:38:ASP:OD1	2.36	0.56
1:X:66:VAL:CG1	1:X:99:ILE:HD12	2.36	0.56
1:X:164:MET:C	1:X:165:ILE:HG13	2.30	0.56
1:X:138:MET:HE1	1:X:219:LEU:CD1	2.35	0.56
1:X:166:ASP:O	1:X:170:LYS:N	2.38	0.56
1:X:44:ARG:O	1:X:56:GLU:N	2.38	0.56
1:X:164:MET:HG2	1:X:175:ILE:HG21	1.88	0.56
1:X:253:GLU:O	1:X:254:GLU:C	2.49	0.56
1:X:155:HIS:O	1:X:180:ALA:CA	2.54	0.56
1:X:208:GLN:N	3:X:452:HOH:O	2.39	0.56
1:X:18:SER:C	1:X:20:ARG:H	2.11	0.56
1:X:244:VAL:O	1:X:245:ARG:C	2.48	0.56
1:X:244:VAL:CG1	1:X:273:ILE:HG22	2.32	0.56
1:X:317:LYS:O	1:X:318:GLU:C	2.48	0.56
1:X:304:LYS:CE	1:X:314:LEU:HD21	2.29	0.56
1:X:22:ARG:O	1:X:23:GLU:C	2.49	0.55
1:X:255:LEU:O	1:X:258:TYR:HB3	2.07	0.55
1:X:42:LEU:CD1	1:X:55:PHE:HB2	2.37	0.55
1:X:105:PRO:O	1:X:108:LYS:NZ	2.37	0.55
1:X:332:GLN:O	1:X:333:SER:C	2.49	0.55
1:X:96:ILE:HB	1:X:175:ILE:HA	1.88	0.55
1:X:109:THR:HG22	1:X:110:PRO:HD2	1.88	0.55
1:X:168:GLN:HA	1:X:168:GLN:HE21	1.72	0.55
1:X:240:TYR:N	1:X:240:TYR:CD2	2.71	0.55
1:X:246:ILE:O	1:X:249:VAL:N	2.27	0.55
1:X:75:LYS:HG3	1:X:78:LYS:CB	2.37	0.55
1:X:94:ASN:HB3	1:X:172:LEU:CD2	2.37	0.55
1:X:282:TRP:NE1	1:X:303:ASP:OD1	2.38	0.55
1:X:30:HIS:CD2	3:X:425:HOH:O	2.57	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:317:LYS:HG3	1:X:318:GLU:H	1.71	0.55
1:X:36:ASN:HA	1:X:105:PRO:HD3	1.87	0.55
1:X:75:LYS:HD3	1:X:78:LYS:HB2	1.88	0.55
1:X:104:ASP:HB3	1:X:106:VAL:CG1	2.37	0.55
1:X:166:ASP:O	1:X:170:LYS:HA	2.06	0.55
1:X:287:HIS:O	1:X:288:SER:C	2.50	0.55
1:X:35:GLY:N	1:X:102:VAL:HA	2.08	0.55
1:X:121:ASP:OD2	1:X:123:LYS:CB	2.42	0.55
1:X:207:TYR:CE2	1:X:310:HIS:HE1	2.25	0.55
1:X:58:ILE:HD11	1:X:63:ASN:HA	1.88	0.54
1:X:228:PHE:O	1:X:229:ARG:HB2	2.08	0.54
1:X:117:ILE:HD13	1:X:118:ASN:C	2.32	0.54
1:X:326:TYR:HE1	3:X:395:HOH:O	1.89	0.54
1:X:329:VAL:HG13	3:X:438:HOH:O	2.06	0.54
1:X:42:LEU:CD1	1:X:68:VAL:HG12	2.37	0.54
1:X:250:LEU:O	1:X:254:GLU:HG3	2.07	0.54
1:X:315:THR:CG2	1:X:318:GLU:HG3	2.37	0.54
1:X:205:VAL:CG1	1:X:264:ILE:CG2	2.80	0.54
1:X:269:HIS:C	1:X:273:ILE:CD1	2.75	0.54
1:X:326:TYR:C	1:X:328:VAL:N	2.59	0.54
1:X:117:ILE:HD12	1:X:164:MET:HB3	1.87	0.54
1:X:250:LEU:HB2	1:X:308:TYR:CE2	2.43	0.54
1:X:169:GLN:O	1:X:170:LYS:HB2	2.08	0.54
1:X:185:PRO:O	1:X:186:ALA:HB3	2.07	0.54
1:X:196:ARG:HH21	1:X:196:ARG:HG2	1.72	0.54
1:X:71:LEU:HD23	1:X:72:LYS:CD	2.37	0.54
1:X:75:LYS:O	1:X:76:LYS:C	2.49	0.54
1:X:224:ALA:HA	1:X:227:ILE:HG22	1.90	0.54
1:X:37:GLN:CD	1:X:38:ASP:N	2.65	0.54
1:X:191:VAL:CG1	1:X:203:LEU:HD22	2.36	0.54
1:X:17:ASN:N	3:X:398:HOH:O	2.42	0.53
1:X:18:SER:C	1:X:20:ARG:N	2.67	0.53
1:X:188:GLU:OE1	1:X:209:MET:HE3	2.08	0.53
1:X:269:HIS:ND1	1:X:273:ILE:CD1	2.68	0.53
1:X:69:LYS:HE3	1:X:114:PHE:CZ	2.42	0.53
1:X:173:ARG:NH2	1:X:173:ARG:HG3	2.22	0.53
1:X:292:HIS:CD2	1:X:292:HIS:N	2.71	0.53
1:X:326:TYR:N	1:X:327:PRO:CD	2.70	0.53
1:X:81:ARG:O	1:X:82:GLU:C	2.52	0.53
1:X:199:LYS:NZ	1:X:204:LEU:HD21	2.23	0.53
1:X:286:ILE:O	1:X:286:ILE:HG13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:104:ASP:CB	1:X:106:VAL:CG2	2.83	0.53
1:X:198:PHE:O	1:X:217:TRP:CD1	2.61	0.53
1:X:230:ARG:NH1	1:X:233:PHE:CE2	2.75	0.53
1:X:218:SER:C	1:X:220:GLY:N	2.66	0.53
1:X:34:TRP:CZ3	1:X:110:PRO:HB3	2.41	0.53
1:X:34:TRP:CH2	1:X:110:PRO:HB2	2.43	0.53
1:X:126:TYR:O	1:X:127:GLN:HG3	2.07	0.53
1:X:267:ASP:C	1:X:268:PRO:O	2.52	0.53
1:X:280:LYS:HD2	1:X:280:LYS:N	2.24	0.53
1:X:167:HIS:HD2	1:X:170:LYS:HD3	1.74	0.53
1:X:283:GLU:HA	1:X:286:ILE:HG22	1.91	0.53
1:X:73:PRO:O	1:X:74:VAL:C	2.52	0.53
1:X:155:HIS:HB2	1:X:177:TRP:CZ3	2.44	0.52
1:X:205:VAL:CG1	1:X:264:ILE:HG23	2.39	0.52
1:X:322:HIS:ND1	1:X:323:PRO:CD	2.72	0.52
1:X:141:LEU:CD2	1:X:219:LEU:CD2	2.87	0.52
1:X:193:VAL:O	1:X:194:ALA:CB	2.56	0.52
1:X:317:LYS:HG3	1:X:318:GLU:N	2.24	0.52
1:X:70:ILE:HG22	1:X:111:ALA:HB2	1.90	0.52
1:X:85:ILE:O	1:X:88:ASN:HB2	2.10	0.52
1:X:89:LEU:O	1:X:90:ARG:C	2.52	0.52
1:X:105:PRO:HA	1:X:108:LYS:HA	1.91	0.52
1:X:132:PHE:O	1:X:134:ILE:N	2.42	0.52
1:X:156:ARG:CD	1:X:193:VAL:HG21	2.39	0.52
1:X:125:LEU:O	1:X:127:GLN:N	2.39	0.52
1:X:258:TYR:CD1	1:X:309:ASP:HA	2.43	0.52
1:X:89:LEU:HB3	1:X:95:ILE:HG21	1.92	0.52
1:X:122:PHE:CZ	1:X:160:PRO:HB2	2.45	0.52
1:X:159:LYS:HE2	1:X:162:ASN:ND2	2.25	0.52
1:X:297:GLU:CB	1:X:324:TYR:CD1	2.74	0.52
1:X:36:ASN:OD1	1:X:36:ASN:N	2.41	0.52
1:X:115:GLU:OE1	1:X:173:ARG:NH1	2.42	0.52
1:X:121:ASP:OD1	1:X:123:LYS:CG	2.57	0.52
1:X:196:ARG:O	1:X:196:ARG:CG	2.57	0.52
1:X:329:VAL:O	1:X:330:LYS:C	2.52	0.52
1:X:34:TRP:CH2	1:X:110:PRO:CB	2.93	0.52
1:X:199:LYS:HD3	1:X:204:LEU:CG	2.39	0.52
1:X:316:ALA:HB3	3:X:354:HOH:O	2.09	0.52
1:X:279:ARG:HD3	1:X:280:LYS:N	2.24	0.52
1:X:330:LYS:N	1:X:330:LYS:CD	2.73	0.52
1:X:10:ALA:HB3	1:X:14:ALA:CA	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:154:MET:O	1:X:155:HIS:C	2.53	0.52
1:X:227:ILE:HD12	1:X:293:LEU:HB3	1.91	0.52
1:X:99:ILE:HB	1:X:113:VAL:O	2.10	0.51
1:X:167:HIS:CD2	1:X:170:LYS:HZ3	2.27	0.51
1:X:196:ARG:O	1:X:196:ARG:HG2	2.10	0.51
1:X:281:ARG:O	1:X:284:ASN:ND2	2.43	0.51
1:X:315:THR:HG21	1:X:317:LYS:HG3	1.92	0.51
1:X:322:HIS:ND1	1:X:324:TYR:N	2.58	0.51
1:X:141:LEU:O	1:X:144:ALA:HB3	2.09	0.51
1:X:166:ASP:HB3	1:X:171:LYS:HG2	1.91	0.51
1:X:309:ASP:C	1:X:311:GLN:H	2.17	0.51
1:X:176:ASP:CG	1:X:177:TRP:N	2.68	0.51
1:X:202:GLU:OE1	1:X:310:HIS:CB	2.58	0.51
1:X:227:ILE:CD1	1:X:293:LEU:O	2.56	0.51
1:X:172:LEU:O	1:X:172:LEU:HD23	2.09	0.51
1:X:207:TYR:HD1	1:X:264:ILE:HD11	1.74	0.51
1:X:244:VAL:HG12	1:X:274:LEU:HD12	1.91	0.51
1:X:35:GLY:O	1:X:103:LYS:N	2.43	0.51
1:X:112:LEU:N	1:X:112:LEU:HD22	2.25	0.51
1:X:315:THR:CG2	1:X:318:GLU:CG	2.88	0.51
1:X:66:VAL:HG11	1:X:99:ILE:HD12	1.93	0.51
1:X:67:VAL:HG11	2:X:351:CCK:C29	2.38	0.51
1:X:130:THR:C	1:X:132:PHE:N	2.66	0.51
1:X:149:HIS:HE1	1:X:215:ASP:CG	2.19	0.51
1:X:217:TRP:O	1:X:220:GLY:N	2.44	0.51
1:X:232:PRO:HG2	1:X:235:HIS:CA	2.40	0.51
1:X:328:VAL:HG12	1:X:330:LYS:H	1.76	0.51
1:X:49:GLY:N	1:X:52:SER:O	2.37	0.51
1:X:191:VAL:HG12	1:X:191:VAL:O	2.09	0.51
1:X:244:VAL:C	1:X:246:ILE:N	2.67	0.51
1:X:125:LEU:CD1	1:X:126:TYR:N	2.71	0.51
1:X:130:THR:O	1:X:132:PHE:N	2.44	0.51
1:X:191:VAL:HG21	1:X:206:ASP:HA	1.93	0.51
1:X:288:SER:HA	1:X:291:ARG:CD	2.40	0.51
1:X:112:LEU:CB	1:X:114:PHE:CE1	2.94	0.51
1:X:256:TYR:O	1:X:257:GLY:C	2.53	0.51
1:X:219:LEU:HD13	1:X:219:LEU:C	2.36	0.51
1:X:236:GLY:HA3	1:X:242:GLN:OE1	2.10	0.51
1:X:38:ASP:O	1:X:60:ILE:HD12	2.11	0.50
1:X:75:LYS:N	3:X:450:HOH:O	2.42	0.50
1:X:135:ARG:HH11	1:X:324:TYR:CA	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:187:GLN:O	1:X:189:TYR:HD2	1.93	0.50
1:X:188:GLU:HB3	1:X:208:GLN:NE2	2.26	0.50
1:X:244:VAL:HG23	1:X:245:ARG:N	2.25	0.50
1:X:66:VAL:HG12	1:X:67:VAL:N	2.27	0.50
1:X:122:PHE:CD2	1:X:160:PRO:CB	2.95	0.50
1:X:308:TYR:O	1:X:310:HIS:N	2.45	0.50
1:X:262:TYR:CD2	1:X:262:TYR:N	2.78	0.50
1:X:297:GLU:O	1:X:300:ASP:N	2.44	0.50
1:X:51:TYR:O	1:X:71:LEU:HB2	2.12	0.50
1:X:108:LYS:HB2	3:X:371:HOH:O	2.12	0.50
1:X:201:PRO:HD3	1:X:217:TRP:CE2	2.46	0.50
1:X:217:TRP:O	1:X:218:SER:C	2.55	0.50
1:X:37:GLN:C	3:X:383:HOH:O	2.54	0.50
1:X:278:SER:O	1:X:279:ARG:C	2.55	0.50
1:X:55:PHE:N	1:X:55:PHE:HD1	2.07	0.50
1:X:52:SER:HB2	1:X:69:LYS:HG3	1.93	0.49
1:X:141:LEU:HD23	1:X:219:LEU:HD21	1.94	0.49
1:X:216:MET:HE2	1:X:316:ALA:HA	1.92	0.49
1:X:241:ASP:O	1:X:244:VAL:HG22	2.11	0.49
1:X:261:LYS:HG2	1:X:262:TYR:CE2	2.48	0.49
1:X:267:ASP:OD1	1:X:268:PRO:CD	2.60	0.49
1:X:262:TYR:HD2	1:X:262:TYR:N	2.11	0.49
1:X:294:VAL:CG1	1:X:299:LEU:CD2	2.76	0.49
1:X:20:ARG:NH1	1:X:151:LYS:NZ	2.57	0.49
1:X:66:VAL:CG1	1:X:99:ILE:CD1	2.91	0.49
1:X:145:LEU:HD12	1:X:215:ASP:HB3	1.94	0.49
1:X:222:MET:O	1:X:225:SER:OG	2.26	0.49
1:X:71:LEU:HD23	1:X:72:LYS:HD3	1.95	0.49
1:X:187:GLN:H	1:X:209:MET:HE2	1.77	0.49
1:X:224:ALA:O	1:X:227:ILE:HG22	2.13	0.49
1:X:266:LEU:O	1:X:267:ASP:C	2.54	0.49
1:X:281:ARG:N	1:X:284:ASN:HD22	2.09	0.49
1:X:225:SER:HB2	1:X:230:ARG:O	2.13	0.49
1:X:304:LYS:CG	1:X:307:ARG:HH11	2.26	0.49
1:X:140:GLU:O	1:X:141:LEU:C	2.56	0.48
1:X:159:LYS:HE2	1:X:162:ASN:HD21	1.78	0.48
1:X:131:ASP:O	1:X:134:ILE:HG22	2.12	0.48
1:X:317:LYS:CG	1:X:318:GLU:N	2.75	0.48
1:X:168:GLN:HE21	1:X:168:GLN:CA	2.27	0.48
1:X:279:ARG:HH21	1:X:279:ARG:HG3	1.77	0.48
1:X:71:LEU:HD22	1:X:72:LYS:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:164:MET:HG2	1:X:175:ILE:HG23	1.95	0.48
1:X:240:TYR:HE1	1:X:269:HIS:CD2	2.30	0.48
1:X:281:ARG:NH2	1:X:283:GLU:OE1	2.46	0.48
1:X:124:GLN:O	1:X:127:GLN:OE1	2.32	0.48
1:X:128:ILE:HD13	1:X:129:LEU:H	1.73	0.48
1:X:307:ARG:HD3	1:X:312:GLN:OE1	2.13	0.48
1:X:173:ARG:HG3	1:X:173:ARG:HH21	1.78	0.48
1:X:262:TYR:HE1	1:X:310:HIS:CE1	2.32	0.48
1:X:297:GLU:HB2	1:X:324:TYR:CD1	2.44	0.48
1:X:322:HIS:CG	1:X:323:PRO:CD	2.97	0.48
1:X:103:LYS:HB3	3:X:381:HOH:O	2.13	0.48
1:X:135:ARG:HA	1:X:325:PHE:HE1	1.78	0.48
1:X:39:ASP:HB2	3:X:429:HOH:O	2.13	0.47
1:X:125:LEU:HD22	1:X:128:ILE:HD12	1.94	0.47
1:X:31:VAL:O	1:X:31:VAL:CG1	2.47	0.47
1:X:223:LEU:HD12	1:X:302:LEU:CD1	2.12	0.47
1:X:164:MET:CG	1:X:175:ILE:HG21	2.43	0.47
1:X:201:PRO:HD3	1:X:217:TRP:CD2	2.49	0.47
1:X:46:LEU:N	1:X:54:VAL:O	2.48	0.47
1:X:62:ASN:O	1:X:64:GLU:CG	2.62	0.47
1:X:69:LYS:O	1:X:111:ALA:HB1	2.14	0.47
1:X:112:LEU:HB3	1:X:114:PHE:CE1	2.49	0.47
1:X:173:ARG:HH21	1:X:173:ARG:CG	2.27	0.47
1:X:237:GLN:H	1:X:241:ASP:HB3	1.80	0.47
1:X:30:HIS:O	1:X:32:PRO:HD3	2.15	0.47
1:X:154:MET:O	1:X:156:ARG:HG2	2.15	0.47
1:X:156:ARG:NE	1:X:193:VAL:HG21	2.30	0.47
1:X:211:ASP:O	1:X:212:TYR:C	2.57	0.47
1:X:10:ALA:HB2	1:X:183:TYR:CZ	2.48	0.47
1:X:37:GLN:OE1	1:X:106:VAL:HG13	2.15	0.47
1:X:48:ARG:HG3	1:X:53:GLU:HA	1.95	0.47
1:X:66:VAL:HG12	1:X:67:VAL:H	1.80	0.47
1:X:122:PHE:O	1:X:126:TYR:N	2.42	0.47
1:X:287:HIS:CD2	1:X:287:HIS:N	2.83	0.47
1:X:293:LEU:HD22	1:X:293:LEU:H	1.78	0.47
1:X:317:LYS:HD3	1:X:317:LYS:C	2.40	0.47
2:X:351:CCK:N4	2:X:351:CCK:H38	2.30	0.47
1:X:48:ARG:HG3	1:X:53:GLU:CD	2.40	0.47
1:X:191:VAL:CG1	1:X:203:LEU:HA	2.45	0.47
1:X:191:VAL:HG21	1:X:206:ASP:C	2.40	0.47
1:X:187:GLN:HB3	1:X:189:TYR:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:261:LYS:O	1:X:262:TYR:HD2	1.97	0.47
1:X:330:LYS:O	1:X:330:LYS:HG2	2.15	0.47
1:X:237:GLN:O	1:X:238:ASP:O	2.33	0.47
1:X:322:HIS:ND1	1:X:322:HIS:C	2.73	0.47
1:X:13:TYR:CE2	1:X:150:SER:HA	2.49	0.46
1:X:66:VAL:HG13	1:X:99:ILE:CD1	2.45	0.46
1:X:288:SER:CA	3:X:369:HOH:O	2.62	0.46
1:X:48:ARG:HG2	1:X:49:GLY:N	2.30	0.46
1:X:204:LEU:HD13	1:X:243:LEU:HB2	1.97	0.46
1:X:228:PHE:C	1:X:229:ARG:HG2	2.40	0.46
1:X:279:ARG:C	1:X:280:LYS:HD2	2.40	0.46
1:X:282:TRP:HB2	1:X:299:LEU:CD1	2.46	0.46
1:X:43:VAL:N	1:X:56:GLU:O	2.48	0.46
1:X:46:LEU:HD21	1:X:56:GLU:CB	2.24	0.46
1:X:71:LEU:HD13	1:X:71:LEU:C	2.41	0.46
1:X:156:ARG:NH2	1:X:179:LEU:O	2.48	0.46
1:X:207:TYR:HE2	1:X:310:HIS:HE1	1.63	0.46
1:X:283:GLU:HA	1:X:286:ILE:CG2	2.45	0.46
1:X:37:GLN:HG3	3:X:360:HOH:O	2.13	0.46
1:X:112:LEU:CB	1:X:114:PHE:CZ	2.96	0.46
1:X:138:MET:CE	1:X:219:LEU:HD11	2.46	0.46
1:X:228:PHE:O	1:X:290:ASN:ND2	2.49	0.46
1:X:299:LEU:CD2	1:X:299:LEU:N	2.78	0.46
1:X:309:ASP:C	1:X:311:GLN:N	2.73	0.46
1:X:321:GLU:HB2	3:X:405:HOH:O	2.15	0.46
1:X:11:ARG:NH1	1:X:318:GLU:CD	2.74	0.46
1:X:23:GLU:O	1:X:84:LYS:NZ	2.49	0.46
1:X:122:PHE:CE2	1:X:160:PRO:HB2	2.50	0.46
1:X:138:MET:HE3	1:X:219:LEU:HD11	1.97	0.46
1:X:70:ILE:HG22	1:X:111:ALA:CB	2.44	0.46
1:X:310:HIS:HA	1:X:313:ARG:NE	2.31	0.46
1:X:97:LYS:HB2	1:X:97:LYS:HZ2	1.80	0.46
1:X:236:GLY:HA2	1:X:245:ARG:HG3	1.98	0.46
1:X:262:TYR:O	1:X:263:HIS:C	2.58	0.46
1:X:216:MET:O	1:X:220:GLY:N	2.48	0.46
1:X:256:TYR:HA	1:X:259:LEU:HD12	1.89	0.46
1:X:268:PRO:O	1:X:269:HIS:HB3	2.16	0.45
1:X:310:HIS:C	1:X:310:HIS:HD2	2.20	0.45
1:X:317:LYS:O	1:X:320:MET:N	2.49	0.45
1:X:250:LEU:HD23	1:X:250:LEU:N	2.31	0.45
1:X:21:SER:HB3	1:X:23:GLU:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:48:ARG:CA	1:X:54:VAL:HG23	2.46	0.45
1:X:288:SER:OG	1:X:289:GLU:N	2.48	0.45
1:X:52:SER:CB	1:X:69:LYS:HD2	2.46	0.45
1:X:81:ARG:CG	1:X:82:GLU:N	2.76	0.45
1:X:97:LYS:HB3	1:X:115:GLU:CD	2.40	0.45
1:X:97:LYS:N	1:X:115:GLU:OE2	2.46	0.45
1:X:304:LYS:CD	1:X:307:ARG:NH1	2.78	0.45
1:X:85:ILE:HG12	1:X:153:ILE:HD13	1.97	0.45
1:X:138:MET:CE	1:X:223:LEU:HB2	2.44	0.45
1:X:205:VAL:HG11	1:X:264:ILE:HD13	1.98	0.45
1:X:227:ILE:HG23	1:X:228:PHE:N	2.30	0.45
1:X:244:VAL:CG1	1:X:273:ILE:CG2	2.92	0.45
1:X:62:ASN:O	1:X:63:ASN:C	2.60	0.45
1:X:99:ILE:HD11	1:X:115:GLU:HA	1.99	0.45
1:X:107:SER:CA	1:X:108:LYS:HE2	2.44	0.45
1:X:205:VAL:HG11	1:X:264:ILE:HG23	1.87	0.45
1:X:51:TYR:CD1	1:X:78:LYS:HE2	2.52	0.45
1:X:140:GLU:OE1	1:X:140:GLU:HA	2.16	0.45
1:X:195:SER:C	1:X:197:TYR:H	2.25	0.45
1:X:138:MET:CE	1:X:219:LEU:CD1	2.95	0.45
1:X:156:ARG:HH21	1:X:156:ARG:CB	2.29	0.45
1:X:261:LYS:HG2	1:X:262:TYR:HE2	1.81	0.45
1:X:288:SER:O	1:X:290:ASN:N	2.50	0.45
1:X:298:ALA:N	1:X:324:TYR:CD1	2.85	0.45
1:X:240:TYR:CD1	1:X:269:HIS:CD2	3.05	0.45
1:X:252:THR:HG21	1:X:277:HIS:N	2.26	0.45
1:X:277:HIS:N	1:X:277:HIS:CD2	2.84	0.45
1:X:283:GLU:C	1:X:285:PHE:N	2.71	0.45
1:X:27:TYR:CD1	1:X:28:GLU:N	2.85	0.44
1:X:141:LEU:HD23	1:X:219:LEU:HD22	1.97	0.44
1:X:231:GLU:HA	1:X:232:PRO:HA	1.80	0.44
1:X:168:GLN:O	1:X:169:GLN:O	2.35	0.44
1:X:58:ILE:HD11	1:X:63:ASN:O	2.18	0.44
1:X:216:MET:HE2	1:X:316:ALA:N	2.32	0.44
1:X:15:GLU:O	1:X:15:GLU:HG2	2.17	0.44
1:X:75:LYS:CB	1:X:77:LYS:NZ	2.79	0.44
1:X:191:VAL:HG13	1:X:203:LEU:CB	2.47	0.44
1:X:3:GLY:H	1:X:4:PRO:CD	2.31	0.44
1:X:75:LYS:HB2	1:X:77:LYS:HZ3	1.77	0.44
1:X:83:VAL:O	1:X:84:LYS:C	2.59	0.44
1:X:13:TYR:CE1	1:X:150:SER:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:35:GLY:C	1:X:102:VAL:HB	2.43	0.44
1:X:166:ASP:CB	1:X:171:LYS:HG2	2.47	0.44
1:X:154:MET:HA	1:X:215:ASP:OD2	2.17	0.44
1:X:173:ARG:HD3	3:X:402:HOH:O	2.18	0.44
1:X:44:ARG:HG3	1:X:56:GLU:HB3	1.99	0.44
1:X:68:VAL:HG22	1:X:112:LEU:O	2.17	0.44
1:X:149:HIS:CE1	1:X:215:ASP:CB	3.01	0.44
1:X:209:MET:HG3	3:X:433:HOH:O	2.17	0.44
1:X:225:SER:CB	1:X:230:ARG:O	2.65	0.44
1:X:270:PHE:O	1:X:274:LEU:HB2	2.18	0.44
1:X:315:THR:CG2	1:X:317:LYS:HG3	2.48	0.44
1:X:71:LEU:O	1:X:72:LYS:C	2.61	0.43
1:X:93:THR:HA	3:X:420:HOH:O	2.17	0.43
1:X:99:ILE:HA	3:X:443:HOH:O	2.18	0.43
1:X:262:TYR:O	1:X:263:HIS:O	2.37	0.43
1:X:77:LYS:O	1:X:78:LYS:C	2.59	0.43
1:X:156:ARG:HB2	1:X:180:ALA:HA	2.00	0.43
1:X:202:GLU:H	1:X:202:GLU:HG2	1.66	0.43
1:X:34:TRP:CH2	1:X:110:PRO:HB3	2.53	0.43
1:X:149:HIS:CE1	1:X:215:ASP:HB2	2.54	0.43
1:X:328:VAL:HG12	1:X:330:LYS:N	2.33	0.43
2:X:351:CCK:N4	2:X:351:CCK:C38	2.80	0.43
1:X:54:VAL:HG13	1:X:69:LYS:HB2	1.99	0.43
1:X:157:ASP:OD2	1:X:162:ASN:ND2	2.52	0.43
1:X:190:ASN:ND2	1:X:192:ARG:H	2.17	0.43
1:X:20:ARG:CZ	1:X:151:LYS:HZ1	2.30	0.43
1:X:117:ILE:C	1:X:117:ILE:CD1	2.76	0.43
1:X:216:MET:HE2	1:X:316:ALA:CA	2.49	0.43
1:X:244:VAL:O	1:X:246:ILE:N	2.52	0.43
1:X:256:TYR:O	1:X:260:LYS:HG3	2.18	0.43
1:X:172:LEU:O	1:X:173:ARG:CD	2.61	0.43
1:X:323:PRO:O	1:X:325:PHE:N	2.52	0.43
1:X:62:ASN:HD22	1:X:64:GLU:CG	2.17	0.43
1:X:136:PHE:CD2	1:X:136:PHE:C	2.95	0.43
1:X:190:ASN:ND2	1:X:192:ARG:N	2.66	0.43
1:X:191:VAL:CG1	1:X:203:LEU:CA	2.96	0.43
1:X:308:TYR:O	1:X:309:ASP:C	2.62	0.43
1:X:5:ALA:O	1:X:6:ALA:C	2.62	0.43
1:X:102:VAL:O	1:X:111:ALA:N	2.46	0.43
1:X:134:ILE:HG22	1:X:135:ARG:HG3	2.00	0.43
1:X:139:TYR:CE1	1:X:320:MET:HE3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:245:ARG:HE	1:X:245:ARG:HA	1.84	0.43
1:X:45:LYS:CE	1:X:55:PHE:CE2	3.02	0.43
1:X:103:LYS:O	1:X:105:PRO:CD	2.67	0.43
1:X:104:ASP:C	1:X:106:VAL:HG22	2.43	0.43
1:X:182:PHE:HB3	1:X:184:HIS:CE1	2.53	0.43
1:X:237:GLN:C	1:X:238:ASP:O	2.60	0.43
1:X:269:HIS:O	1:X:272:ASP:N	2.52	0.43
1:X:330:LYS:O	1:X:332:GLN:N	2.51	0.43
1:X:5:ALA:HA	1:X:263:HIS:HB2	2.00	0.43
1:X:179:LEU:HD23	1:X:179:LEU:HA	1.81	0.43
1:X:256:TYR:HD1	1:X:259:LEU:HD11	1.84	0.43
1:X:44:ARG:HG3	1:X:56:GLU:OE2	2.19	0.42
1:X:119:ASN:ND2	3:X:373:HOH:O	2.51	0.42
1:X:143:LYS:HB2	1:X:143:LYS:HE3	1.71	0.42
1:X:323:PRO:O	1:X:324:TYR:C	2.62	0.42
1:X:89:LEU:HD23	1:X:89:LEU:HA	1.79	0.42
1:X:125:LEU:CD2	1:X:128:ILE:HD11	2.45	0.42
1:X:139:TYR:HE1	1:X:320:MET:HB3	1.84	0.42
1:X:47:GLY:C	1:X:54:VAL:HG23	2.44	0.42
1:X:11:ARG:HH12	1:X:318:GLU:CD	2.27	0.42
1:X:119:ASN:ND2	1:X:119:ASN:C	2.68	0.42
1:X:164:MET:CG	1:X:175:ILE:CG2	2.97	0.42
1:X:198:PHE:O	1:X:217:TRP:HD1	2.03	0.42
1:X:250:LEU:CB	1:X:308:TYR:CE2	3.02	0.42
1:X:299:LEU:N	1:X:299:LEU:HD22	2.34	0.42
1:X:20:ARG:CZ	1:X:151:LYS:NZ	2.82	0.42
1:X:22:ARG:HG2	1:X:26:ASP:HB2	2.02	0.42
1:X:283:GLU:O	1:X:285:PHE:N	2.53	0.42
1:X:52:SER:HB2	1:X:69:LYS:CG	2.49	0.42
1:X:222:MET:O	1:X:223:LEU:C	2.62	0.42
1:X:267:ASP:C	1:X:267:ASP:OD1	2.62	0.42
1:X:287:HIS:CE1	1:X:289:GLU:HB2	2.54	0.42
1:X:187:GLN:N	1:X:209:MET:CE	2.80	0.42
1:X:37:GLN:O	1:X:38:ASP:C	2.62	0.42
1:X:176:ASP:C	1:X:177:TRP:CD1	2.98	0.42
1:X:217:TRP:CZ2	1:X:246:ILE:HD13	2.55	0.42
1:X:10:ALA:N	1:X:183:TYR:OH	2.46	0.42
1:X:12:VAL:HG23	1:X:13:TYR:CD2	2.55	0.42
1:X:120:THR:O	1:X:121:ASP:O	2.38	0.42
1:X:122:PHE:CE2	1:X:160:PRO:CB	3.03	0.42
1:X:307:ARG:HD2	1:X:312:GLN:CD	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:34:TRP:CZ3	1:X:101:THR:CG2	2.97	0.41
1:X:58:ILE:CD1	1:X:63:ASN:HA	2.50	0.41
1:X:96:ILE:HG23	1:X:96:ILE:O	2.18	0.41
1:X:287:HIS:NE2	1:X:290:ASN:ND2	2.68	0.41
1:X:119:ASN:HD21	1:X:121:ASP:H	1.66	0.41
1:X:219:LEU:C	1:X:219:LEU:CD1	2.93	0.41
1:X:316:ALA:N	3:X:400:HOH:O	2.52	0.41
1:X:98:LEU:HD11	1:X:112:LEU:HD12	2.02	0.41
1:X:105:PRO:O	1:X:108:LYS:CE	2.68	0.41
1:X:134:ILE:O	1:X:135:ARG:C	2.64	0.41
1:X:242:GLN:O	1:X:246:ILE:HG13	2.20	0.41
1:X:267:ASP:OD1	1:X:268:PRO:N	2.53	0.41
1:X:317:LYS:HD3	1:X:318:GLU:N	2.35	0.41
1:X:67:VAL:HG11	1:X:114:PHE:HB2	1.96	0.41
1:X:129:LEU:O	1:X:130:THR:HG23	2.19	0.41
1:X:139:TYR:O	1:X:142:LEU:HB2	2.20	0.41
1:X:280:LYS:CD	1:X:280:LYS:N	2.83	0.41
1:X:286:ILE:HB	1:X:294:VAL:HG21	2.01	0.41
1:X:329:VAL:O	1:X:330:LYS:HD2	2.19	0.41
1:X:10:ALA:CB	1:X:183:TYR:HE2	2.32	0.41
1:X:37:GLN:C	1:X:39:ASP:N	2.74	0.41
1:X:42:LEU:HD12	1:X:55:PHE:CG	2.55	0.41
1:X:104:ASP:O	1:X:105:PRO:C	2.64	0.41
1:X:62:ASN:ND2	1:X:64:GLU:HG3	2.17	0.41
1:X:155:HIS:C	1:X:155:HIS:CD2	2.99	0.41
1:X:232:PRO:HD2	1:X:235:HIS:CG	2.56	0.41
1:X:27:TYR:CD1	1:X:81:ARG:HB3	2.56	0.41
1:X:106:VAL:CG2	1:X:107:SER:N	2.70	0.41
1:X:155:HIS:ND1	1:X:174:LEU:HD21	2.35	0.41
1:X:37:GLN:OE1	1:X:106:VAL:CG1	2.69	0.41
1:X:119:ASN:CG	1:X:164:MET:SD	3.04	0.41
1:X:196:ARG:HG2	1:X:196:ARG:NH2	2.36	0.41
1:X:253:GLU:O	1:X:256:TYR:N	2.54	0.41
1:X:300:ASP:O	1:X:301:LEU:C	2.64	0.41
1:X:7:GLY:HA2	3:X:433:HOH:O	2.21	0.41
1:X:154:MET:O	1:X:156:ARG:N	2.54	0.41
1:X:154:MET:CB	1:X:215:ASP:OD2	2.68	0.41
1:X:159:LYS:HG2	1:X:162:ASN:HD22	1.86	0.41
1:X:173:ARG:O	1:X:175:ILE:N	2.54	0.41
1:X:253:GLU:C	1:X:255:LEU:H	2.29	0.41
1:X:3:GLY:N	1:X:4:PRO:CD	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:135:ARG:NH1	1:X:324:TYR:CD1	2.89	0.40
1:X:255:LEU:HG	1:X:308:TYR:CZ	2.56	0.40
1:X:278:SER:O	1:X:280:LYS:CE	2.69	0.40
1:X:71:LEU:HD13	1:X:72:LYS:O	2.21	0.40
1:X:204:LEU:C	1:X:206:ASP:H	2.27	0.40
1:X:304:LYS:HD2	1:X:307:ARG:NH1	2.35	0.40
1:X:207:TYR:HE1	3:X:390:HOH:O	2.04	0.40
1:X:263:HIS:O	1:X:264:ILE:HG13	2.22	0.40
1:X:190:ASN:HD21	1:X:192:ARG:CA	2.34	0.40
1:X:226:MET:O	3:X:375:HOH:O	2.22	0.40
1:X:270:PHE:CA	1:X:273:ILE:HD13	2.51	0.40
1:X:75:LYS:CG	1:X:78:LYS:CB	2.99	0.40
1:X:142:LEU:C	1:X:144:ALA:N	2.79	0.40
1:X:281:ARG:H	1:X:284:ASN:ND2	2.18	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	X	332/339 (98%)	201 (60%)	73 (22%)	58 (18%)	0 0

All (58) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	6	ALA
1	X	38	ASP
1	X	63	ASN
1	X	121	ASP
1	X	126	TYR
1	X	134	ILE
1	X	170	LYS

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Mol	Chain	Res	Type
1	X	229	ARG
1	X	270	PHE
1	X	274	LEU
1	X	294	VAL
1	X	295	SER
1	X	332	GLN
1	X	14	ALA
1	X	19	LEU
1	X	76	LYS
1	X	90	ARG
1	X	129	LEU
1	X	185	PRO
1	X	194	ALA
1	X	254	GLU
1	X	263	HIS
1	X	268	PRO
1	X	289	GLU
1	X	330	LYS
1	X	331	GLU
1	X	333	SER
1	X	48	ARG
1	X	105	PRO
1	X	127	GLN
1	X	155	HIS
1	X	168	GLN
1	X	176	ASP
1	X	180	ALA
1	X	196	ARG
1	X	219	LEU
1	X	238	ASP
1	X	269	HIS
1	X	284	ASN
1	X	297	GLU
1	X	309	ASP
1	X	324	TYR
1	X	327	PRO
1	X	329	VAL
1	X	2	PRO
1	X	108	LYS
1	X	177	TRP
1	X	212	TYR
1	X	218	SER

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Mol	Chain	Res	Type
1	X	273	ILE
1	X	312	GLN
1	X	74	VAL
1	X	80	LYS
1	X	247	ALA
1	X	24	TYR
1	X	165	ILE
1	X	43	VAL
1	X	16	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	X	303/306 (99%)	243 (80%)	60 (20%)	1 8

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	2	PRO
1	X	16	VAL
1	X	20	ARG
1	X	28	GLU
1	X	36	ASN
1	X	37	GLN
1	X	42	LEU
1	X	46	LEU
1	X	48	ARG
1	X	51	TYR
1	X	54	VAL
1	X	55	PHE
1	X	62	ASN
1	X	63	ASN
1	X	65	ARG
1	X	68	VAL
1	X	71	LEU

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Mol	Chain	Res	Type
1	X	72	LYS
1	X	83	VAL
1	X	85	ILE
1	X	97	LYS
1	X	100	ASP
1	X	101	THR
1	X	102	VAL
1	X	109	THR
1	X	112	LEU
1	X	117	ILE
1	X	120	THR
1	X	122	PHE
1	X	125	LEU
1	X	128	ILE
1	X	151	LYS
1	X	156	ARG
1	X	173	ARG
1	X	192	ARG
1	X	199	LYS
1	X	209	MET
1	X	219	LEU
1	X	240	TYR
1	X	244	VAL
1	X	253	GLU
1	X	254	GLU
1	X	255	LEU
1	X	259	LEU
1	X	267	ASP
1	X	271	ASN
1	X	273	ILE
1	X	274	LEU
1	X	278	SER
1	X	279	ARG
1	X	281	ARG
1	X	286	ILE
1	X	287	HIS
1	X	292	HIS
1	X	304	LYS
1	X	310	HIS
1	X	312	GLN
1	X	317	LYS
1	X	330	LYS

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Mol	Chain	Res	Type
1	X	332	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	30	HIS
1	X	37	GLN
1	X	41	GLN
1	X	62	ASN
1	X	88	ASN
1	X	119	ASN
1	X	124	GLN
1	X	149	HIS
1	X	161	HIS
1	X	162	ASN
1	X	168	GLN
1	X	169	GLN
1	X	184	HIS
1	X	187	GLN
1	X	190	ASN
1	X	208	GLN
1	X	271	ASN
1	X	276	GLN
1	X	277	HIS
1	X	284	ASN
1	X	287	HIS
1	X	292	HIS
1	X	311	GLN
1	X	312	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	CCK	X	351	-	31,31,31	3.19	9 (29%)	39,44,44	3.80	20 (51%)

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	CCK	X	351	-	-	4/16/16/16	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	351	CCK	N13-N20	-12.15	1.25	1.38
2	X	351	CCK	C5-N15	-8.79	1.28	1.43
2	X	351	CCK	C3-N13	-4.54	1.34	1.42
2	X	351	CCK	C19-N20	4.09	1.36	1.32
2	X	351	CCK	C29-N15	3.62	1.45	1.38
2	X	351	CCK	C26-N15	3.52	1.43	1.38
2	X	351	CCK	C36-C37	2.47	1.43	1.39
2	X	351	CCK	C36-C35	2.09	1.42	1.38
2	X	351	CCK	O63-C59	-2.00	1.24	1.30

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	351	CCK	C29-N15-C26	-10.72	99.13	108.58
2	X	351	CCK	C27-C26-N15	9.41	113.72	108.39
2	X	351	CCK	C28-C29-N15	9.13	114.35	108.56
2	X	351	CCK	C17-N13-C3	-6.62	124.53	130.21
2	X	351	CCK	C17-C18-C19	-5.83	101.16	104.48
2	X	351	CCK	C35-C18-C17	5.15	124.54	119.31
2	X	351	CCK	C36-C35-C18	-5.15	114.79	121.74
2	X	351	CCK	C19-N20-N13	4.64	109.09	106.14
2	X	351	CCK	N4-C3-N13	3.80	117.89	115.31
2	X	351	CCK	C51-C46-C48	-3.70	102.27	111.55
2	X	351	CCK	C6-N1-C2	3.57	122.36	117.51
2	X	351	CCK	C18-C19-N20	-3.51	109.40	112.05
2	X	351	CCK	C5-C6-N1	-3.49	117.49	121.21
2	X	351	CCK	C38-C17-C18	-3.34	119.53	122.29
2	X	351	CCK	C3-C2-N1	-2.37	118.68	121.21
2	X	351	CCK	N4-C5-N15	2.30	116.83	113.95
2	X	351	CCK	C5-N15-C26	2.22	130.25	126.93
2	X	351	CCK	O63-C59-C57	2.20	121.33	114.51
2	X	351	CCK	O61-C59-C57	-2.12	116.09	122.11
2	X	351	CCK	C5-N15-C29	2.06	130.02	126.93

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	X	351	CCK	C28-C27-C57-C59
2	X	351	CCK	C51-C46-N44-C37
2	X	351	CCK	C36-C37-N44-C46
2	X	351	CCK	C38-C37-N44-C46

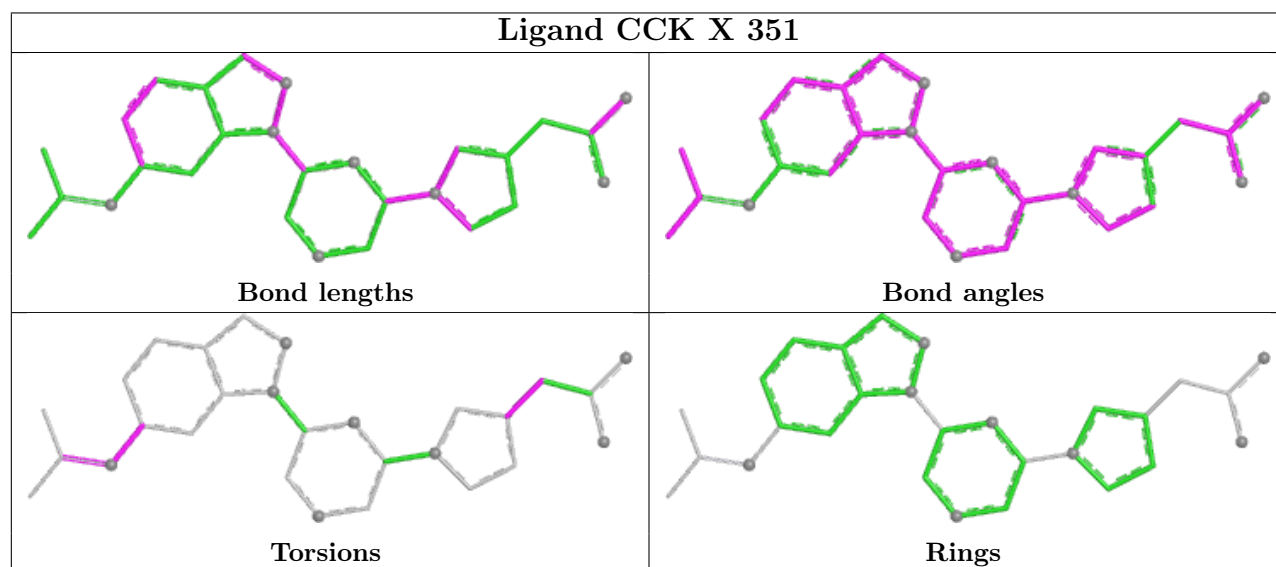
There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	X	351	CCK	6	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 [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	X	334/339 (98%)	0.07	9 (2%) 56 36	0, 6, 26, 74	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	333	SER	3.6
1	X	332	GLN	3.4
1	X	6	ALA	3.0
1	X	2	PRO	2.6
1	X	331	GLU	2.6
1	X	4	PRO	2.5
1	X	3	GLY	2.3
1	X	199	LYS	2.2
1	X	334	GLN	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](#)

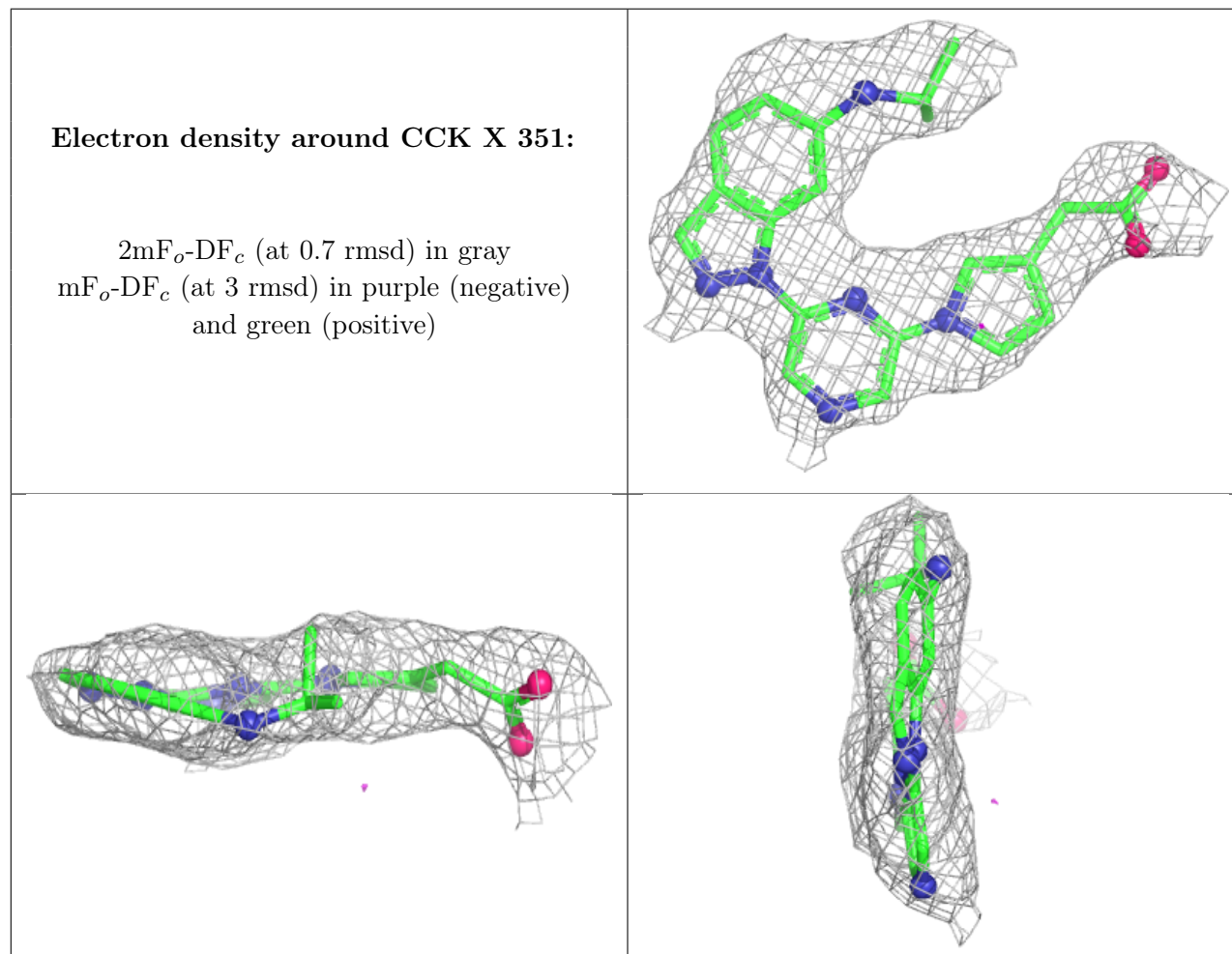
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	CCK	X	351	28/28	0.90	0.12	11,25,29,29	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.