



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2021 – 01:15 PM EDT

PDB ID : 1S1V
Title : Crystal structure of L100I mutant HIV-1 reverse transcriptase in complex with TNK-651
Authors : Ren, J.; Nichols, C.E.; Chamberlain, P.P.; Stammers, D.K.
Deposited on : 2004-01-07
Resolution : 2.60 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)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

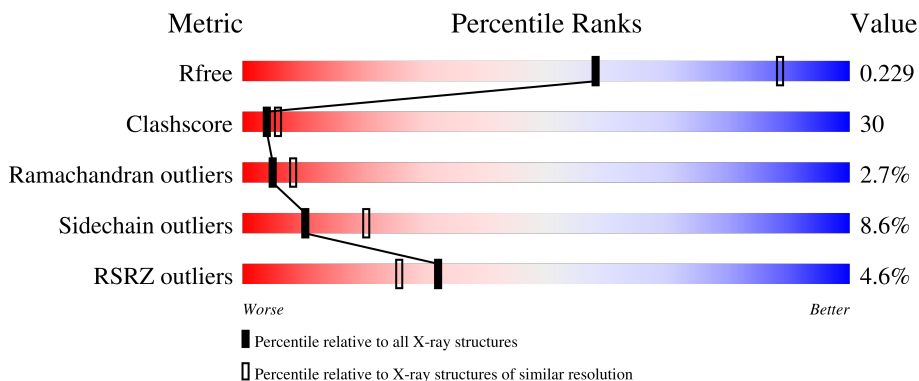
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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

Mol	Chain	Length	Quality of chain
1	A	560	
2	B	440	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7803 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 Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	534	4370	2830	727	805	8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ILE	LEU	engineered mutation	UNP P04585
A	280	CSD	CYS	modified residue	UNP P04585

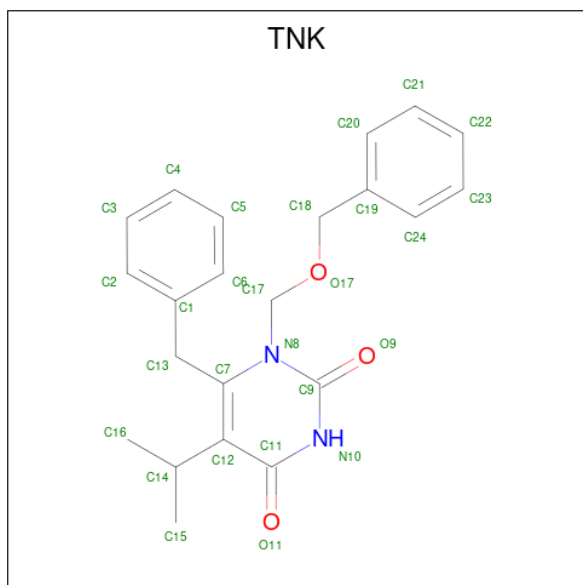
- Molecule 2 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	404	3339	2172	555	605	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	100	ILE	LEU	engineered mutation	UNP P04585

- Molecule 3 is 6-BENZYL-1-BENZYLOXYMETHYL-5-ISOPROPYL URACIL (three-letter code: TNK) (formula: C₂₂H₂₄N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	27	22	2	3	0	0

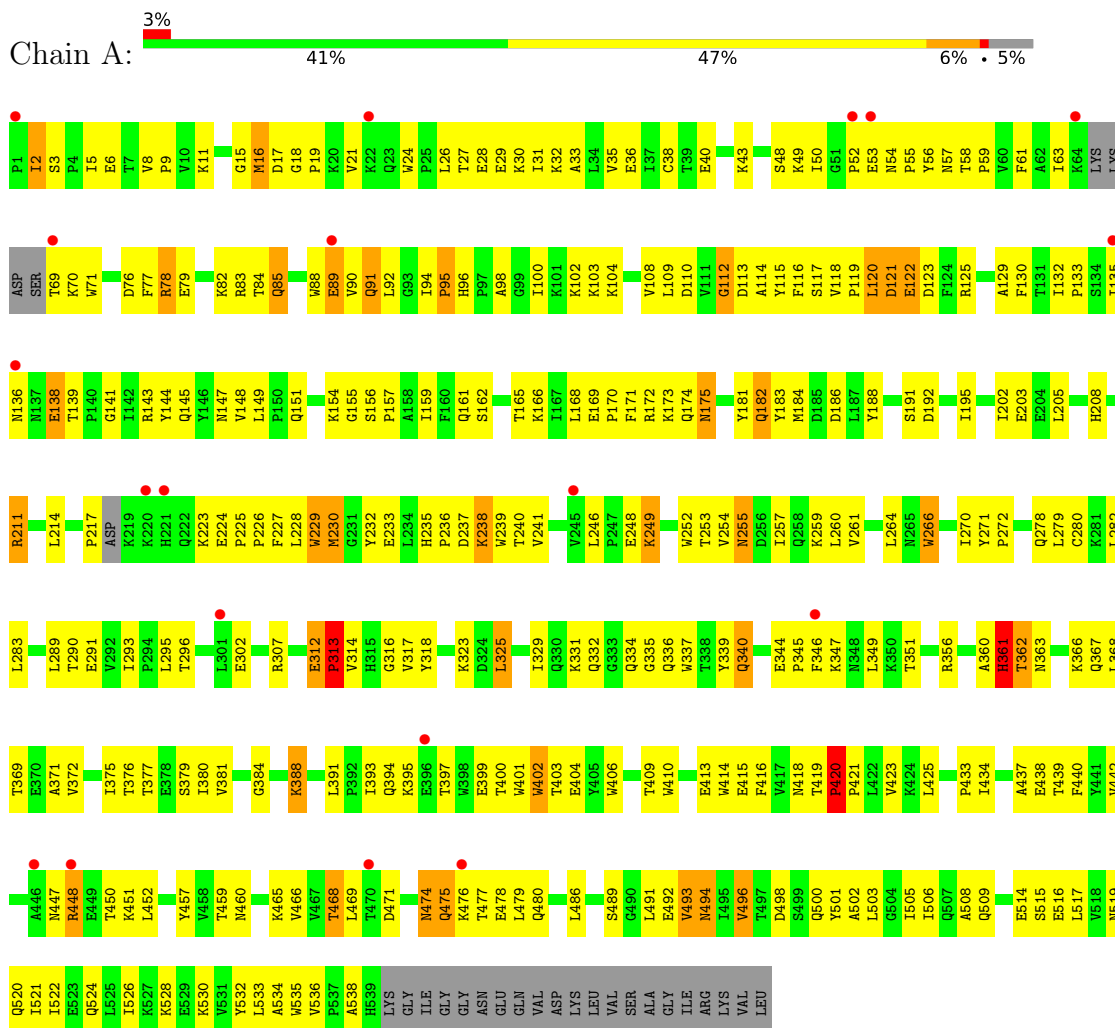
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	28	Total	O	0	0
			28	28		

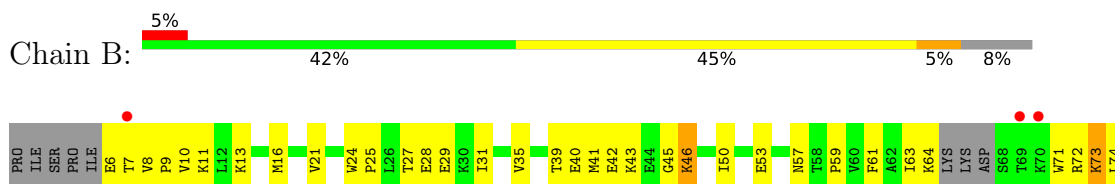
3 Residue-property plots

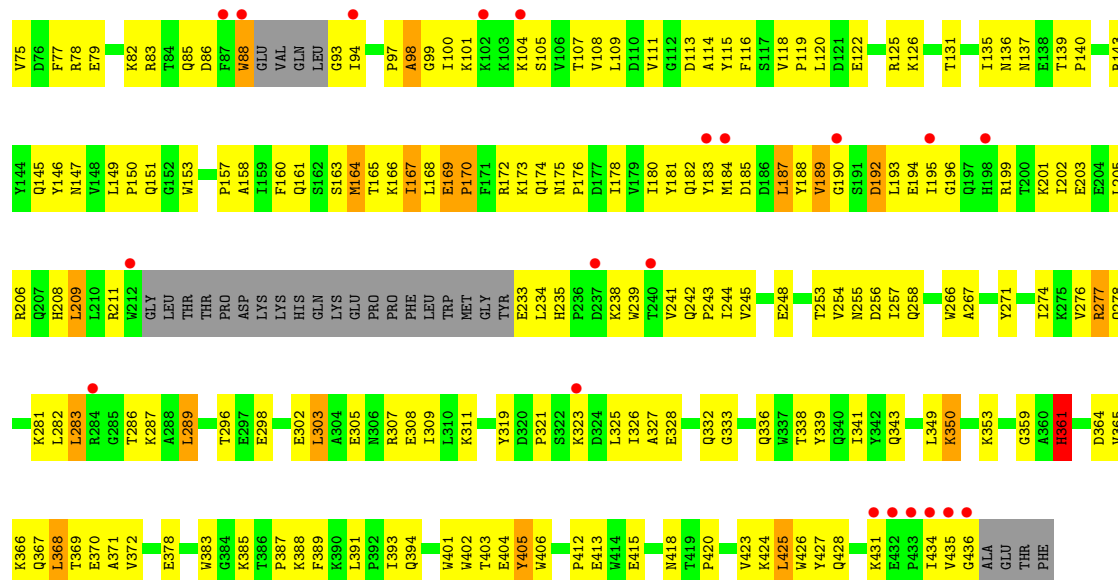
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Reverse transcriptase



- Molecule 2: Reverse transcriptase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	138.10Å 110.30Å 72.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.51 – 2.60 29.51 – 2.59	Depositor EDS
% Data completeness (in resolution range)	94.1 (29.51-2.60) 93.4 (29.51-2.59)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.57Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.233 , 0.313 0.217 , 0.229	Depositor DCC
R_{free} test set	1632 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	69.1	Xtrriage
Anisotropy	0.320	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 69.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7803	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: CSD, TNK

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	0.44	0/4477	0.69	2/6085 (0.0%)
2	B	0.46	0/3432	0.69	0/4661
All	All	0.45	0/7909	0.69	2/10746 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	494	ASN	N-CA-C	-5.32	96.64	111.00
1	A	388	LYS	N-CA-C	-5.07	97.32	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4370	0	4413	272	1
2	B	3339	0	3367	209	0
3	A	27	0	24	5	0
4	A	39	0	0	3	1
4	B	28	0	0	0	0
All	All	7803	0	7804	470	1

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 30.

All (470) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:57:ASN:HD22	2:B:143:ARG:NH1	1.59	1.01
2:B:111:VAL:HG11	2:B:187:LEU:HD22	1.44	0.98
1:A:182:GLN:HE21	1:A:182:GLN:C	1.68	0.97
2:B:169:GLU:HB2	2:B:170:PRO:HD3	1.44	0.96
1:A:270:ILE:HG22	1:A:314:VAL:HG21	1.48	0.96
1:A:241:VAL:HG21	1:A:270:ILE:HG21	1.54	0.90
1:A:469:LEU:HD12	1:A:477:THR:HG22	1.53	0.90
1:A:502:ALA:HA	1:A:505:ILE:HD12	1.55	0.88
2:B:235:HIS:O	2:B:238:LYS:HG2	1.73	0.88
1:A:38:CYS:SG	1:A:132:ILE:HD11	2.13	0.87
1:A:3:SER:HB3	1:A:5:ILE:HG13	1.53	0.87
2:B:420:PRO:HB2	2:B:423:VAL:HG23	1.57	0.86
2:B:332:GLN:NE2	2:B:424:LYS:HE2	1.89	0.86
2:B:241:VAL:HG22	2:B:350:LYS:HA	1.57	0.85
1:A:108:VAL:HG11	1:A:223:LYS:HD2	1.59	0.83
1:A:356:ARG:HG3	1:A:356:ARG:HH11	1.44	0.83
2:B:366:LYS:O	2:B:370:GLU:HG3	1.79	0.83
1:A:17:ASP:O	1:A:83:ARG:HD3	1.79	0.82
1:A:317:VAL:HG21	1:A:347:LYS:HB3	1.61	0.82
2:B:115:TYR:HB3	2:B:149:LEU:HB2	1.63	0.81
2:B:31:ILE:O	2:B:35:VAL:HG23	1.81	0.81
1:A:388:LYS:HD2	1:A:413:GLU:OE2	1.81	0.81
1:A:16:MET:CE	1:A:83:ARG:HG2	2.14	0.78
1:A:16:MET:HE3	4:A:1004:HOH:O	1.82	0.78
2:B:266:TRP:CH2	2:B:423:VAL:HG22	2.18	0.78
2:B:350:LYS:HE2	2:B:378:GLU:OE1	1.82	0.78
1:A:228:LEU:HD12	1:A:228:LEU:N	1.98	0.78
2:B:57:ASN:HD22	2:B:143:ARG:HH12	1.30	0.78
2:B:332:GLN:HE22	2:B:424:LYS:HE2	1.46	0.78
2:B:195:ILE:HG13	2:B:199:ARG:HE	1.50	0.77
1:A:278:GLN:O	1:A:282:LEU:HD13	1.85	0.77
2:B:195:ILE:HG23	2:B:196:GLY:H	1.49	0.76
1:A:98:ALA:HB2	1:A:349:LEU:O	1.87	0.74
2:B:163:SER:O	2:B:167:ILE:HG23	1.86	0.74
2:B:169:GLU:HB2	2:B:170:PRO:CD	2.17	0.74
1:A:344:GLU:OE1	1:A:347:LYS:HD2	1.86	0.74
1:A:30:LYS:HE2	1:A:71:TRP:CH2	2.23	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:THR:O	1:A:380:ILE:HG12	1.88	0.73
1:A:94:ILE:HG21	1:A:230:MET:CE	2.19	0.73
1:A:120:LEU:HD13	1:A:125:ARG:HG2	1.71	0.73
1:A:270:ILE:CG2	1:A:314:VAL:HG21	2.18	0.72
1:A:16:MET:HE2	1:A:83:ARG:HG2	1.69	0.72
1:A:116:PHE:CE2	1:A:151:GLN:HG2	2.25	0.72
1:A:393:ILE:HB	1:A:423:VAL:CG2	2.20	0.71
1:A:225:PRO:HG3	1:A:227:PHE:CZ	2.26	0.71
1:A:136:ASN:C	1:A:138:GLU:H	1.91	0.70
1:A:129:ALA:HB1	1:A:143:ARG:HH12	1.55	0.70
1:A:19:PRO:O	1:A:56:TYR:HA	1.90	0.70
2:B:139:THR:HG22	2:B:140:PRO:O	1.90	0.70
1:A:516:GLU:O	1:A:520:GLN:HG3	1.92	0.69
2:B:195:ILE:HG23	2:B:196:GLY:N	2.07	0.69
1:A:503:LEU:HA	1:A:506:ILE:HD12	1.75	0.69
1:A:406:TRP:CH2	2:B:418:ASN:HA	2.28	0.69
2:B:61:PHE:CE1	2:B:74:LEU:HD23	2.28	0.69
1:A:362:THR:HG22	1:A:363:ASN:H	1.58	0.68
1:A:225:PRO:HA	1:A:226:PRO:C	2.12	0.68
1:A:58:THR:HG23	1:A:59:PRO:HD2	1.76	0.68
2:B:248:GLU:HG2	2:B:307:ARG:NH2	2.07	0.68
2:B:161:GLN:HA	2:B:161:GLN:NE2	2.06	0.68
2:B:325:LEU:HD21	2:B:383:TRP:CE3	2.29	0.67
1:A:94:ILE:HG21	1:A:230:MET:HE2	1.75	0.67
1:A:439:THR:HG21	2:B:289:LEU:HD13	1.77	0.67
1:A:317:VAL:HG12	1:A:318:TYR:N	2.11	0.66
2:B:323:LYS:HB2	2:B:323:LYS:NZ	2.10	0.66
2:B:180:ILE:HG12	2:B:189:VAL:HG13	1.76	0.66
1:A:420:PRO:HA	1:A:421:PRO:C	2.14	0.66
1:A:136:ASN:HB2	1:A:138:GLU:HG3	1.77	0.66
2:B:35:VAL:O	2:B:39:THR:HG23	1.96	0.66
2:B:208:HIS:O	2:B:211:ARG:HG2	1.95	0.66
1:A:88:TRP:HA	1:A:88:TRP:CE3	2.31	0.65
1:A:96:HIS:HD2	1:A:98:ALA:HB3	1.60	0.65
2:B:195:ILE:HD11	2:B:199:ARG:NE	2.11	0.65
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.77	0.65
1:A:40:GLU:HA	1:A:43:LYS:HE2	1.79	0.65
1:A:312:GLU:N	1:A:313:PRO:HD3	2.12	0.65
1:A:63:ILE:HA	1:A:71:TRP:HZ3	1.62	0.65
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.32	0.64
2:B:78:ARG:O	2:B:82:LYS:HG3	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:LYS:O	1:A:85:GLN:HB3	1.97	0.64
2:B:28:GLU:HG3	2:B:135:ILE:HD11	1.78	0.64
2:B:61:PHE:HE1	2:B:74:LEU:HD23	1.63	0.64
1:A:31:ILE:O	1:A:35:VAL:HG23	1.97	0.64
1:A:271:TYR:OH	1:A:313:PRO:HA	1.98	0.64
1:A:323:LYS:NZ	1:A:344:GLU:HG2	2.13	0.64
2:B:365:VAL:O	2:B:369:THR:HG23	1.98	0.64
1:A:451:LYS:HD3	1:A:471:ASP:OD2	1.98	0.63
2:B:424:LYS:HD3	2:B:424:LYS:C	2.18	0.63
2:B:195:ILE:HG12	2:B:199:ARG:HH21	1.62	0.63
1:A:475:GLN:HG3	1:A:476:LYS:N	2.12	0.63
1:A:433:PRO:HG3	1:A:532:TYR:CE2	2.33	0.63
1:A:255:ASN:O	1:A:259:LYS:HG2	1.99	0.62
2:B:57:ASN:HD22	2:B:143:ARG:HH11	1.46	0.62
2:B:332:GLN:HG3	2:B:338:THR:HG23	1.80	0.62
1:A:79:GLU:HB3	1:A:83:ARG:NH1	2.14	0.62
1:A:257:ILE:O	1:A:261:VAL:HG23	2.00	0.62
1:A:2:ILE:HG22	1:A:3:SER:N	2.14	0.62
1:A:260:LEU:HG	1:A:264:LEU:HD23	1.81	0.62
2:B:73:LYS:NZ	2:B:73:LYS:HB3	2.14	0.61
2:B:175:ASN:ND2	2:B:201:LYS:HD2	2.14	0.61
1:A:503:LEU:HD13	1:A:535:TRP:CG	2.36	0.61
1:A:28:GLU:O	1:A:32:LYS:HG3	2.01	0.60
2:B:278:GLN:NE2	2:B:281:LYS:HD2	2.15	0.60
2:B:319:TYR:HE1	2:B:321:PRO:HG3	1.66	0.60
1:A:368:LEU:O	1:A:372:VAL:HG23	2.01	0.60
2:B:368:LEU:O	2:B:372:VAL:HG23	2.01	0.60
2:B:308:GLU:O	2:B:311:LYS:HB2	2.01	0.60
2:B:434:ILE:HG22	2:B:435:VAL:HG13	1.82	0.60
1:A:536:VAL:HG12	2:B:258:GLN:HB3	1.83	0.60
2:B:79:GLU:O	2:B:83:ARG:HG3	2.01	0.60
2:B:254:VAL:O	2:B:258:GLN:HG3	2.00	0.60
1:A:356:ARG:HG3	1:A:356:ARG:NH1	2.12	0.60
1:A:40:GLU:HA	1:A:43:LYS:CE	2.32	0.60
1:A:228:LEU:N	1:A:228:LEU:CD1	2.64	0.59
2:B:424:LYS:HZ3	2:B:425:LEU:HD12	1.66	0.59
1:A:312:GLU:N	1:A:313:PRO:CD	2.64	0.59
2:B:195:ILE:CG1	2:B:199:ARG:HE	2.14	0.59
1:A:260:LEU:HG	1:A:264:LEU:CD2	2.33	0.59
1:A:419:THR:HG22	1:A:419:THR:O	2.02	0.59
2:B:97:PRO:O	2:B:99:GLY:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:423:VAL:O	2:B:427:TYR:HD2	1.83	0.59
1:A:371:ALA:O	1:A:375:ILE:HG13	2.03	0.59
2:B:94:ILE:HD11	2:B:182:GLN:H	1.68	0.59
2:B:203:GLU:HA	2:B:206:ARG:HB2	1.85	0.59
1:A:246:LEU:O	1:A:307:ARG:NH1	2.32	0.59
2:B:115:TYR:HB3	2:B:149:LEU:CB	2.32	0.58
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.83	0.58
1:A:439:THR:CG2	2:B:289:LEU:HD13	2.34	0.58
1:A:122:GLU:N	1:A:122:GLU:OE1	2.36	0.58
1:A:2:ILE:HG22	1:A:3:SER:H	1.69	0.58
1:A:116:PHE:HE2	1:A:151:GLN:HG2	1.67	0.58
2:B:88:TRP:CZ3	2:B:93:GLY:N	2.71	0.58
1:A:48:SER:O	1:A:144:TYR:HA	2.03	0.58
2:B:27:THR:O	2:B:31:ILE:HG13	2.03	0.58
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.04	0.58
1:A:33:ALA:O	1:A:36:GLU:HB3	2.04	0.57
2:B:98:ALA:HA	2:B:101:LYS:NZ	2.19	0.57
1:A:522:ILE:O	1:A:526:ILE:HG13	2.04	0.57
2:B:57:ASN:ND2	2:B:131:THR:OG1	2.38	0.57
2:B:108:VAL:HG22	2:B:188:TYR:CD2	2.40	0.57
1:A:323:LYS:HZ3	1:A:344:GLU:HG2	1.69	0.57
2:B:169:GLU:HG2	2:B:173:LYS:HZ3	1.70	0.57
2:B:97:PRO:C	2:B:99:GLY:H	2.07	0.57
1:A:380:ILE:O	1:A:384:GLY:HA2	2.05	0.57
2:B:332:GLN:NE2	2:B:428:GLN:HB2	2.19	0.56
1:A:16:MET:HE1	1:A:83:ARG:HG2	1.84	0.56
2:B:160:PHE:O	2:B:160:PHE:CD1	2.57	0.56
1:A:162:SER:O	1:A:165:THR:HB	2.06	0.56
1:A:114:ALA:O	1:A:117:SER:HB2	2.05	0.56
1:A:239:TRP:CE2	1:A:316:GLY:HA3	2.40	0.56
2:B:164:MET:O	2:B:168:LEU:HG	2.05	0.56
2:B:387:PRO:HG2	2:B:389:PHE:CE1	2.40	0.56
2:B:241:VAL:CG2	2:B:350:LYS:HA	2.33	0.56
2:B:173:LYS:O	2:B:176:PRO:HD3	2.06	0.56
1:A:188:TYR:CD2	3:A:999:TNK:H2	2.41	0.56
1:A:90:VAL:O	1:A:91:GLN:C	2.44	0.55
1:A:492:GLU:HA	1:A:530:LYS:O	2.06	0.55
1:A:254:VAL:HB	1:A:289:LEU:HA	1.87	0.55
2:B:202:ILE:O	2:B:205:LEU:N	2.38	0.55
1:A:202:ILE:HG22	1:A:203:GLU:N	2.22	0.55
1:A:110:ASP:O	1:A:217:PRO:HD2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:LEU:H	1:A:289:LEU:HD22	1.70	0.55
2:B:50:ILE:CG1	2:B:143:ARG:HB3	2.37	0.55
2:B:205:LEU:HD13	2:B:209:LEU:HD22	1.88	0.55
1:A:233:GLU:HB2	1:A:240:THR:OG1	2.06	0.55
2:B:28:GLU:HG3	2:B:135:ILE:CD1	2.37	0.55
2:B:107:THR:O	2:B:189:VAL:HG23	2.06	0.55
1:A:11:LYS:NZ	4:A:1003:HOH:O	2.39	0.55
2:B:7:THR:HG22	2:B:119:PRO:HG2	1.88	0.55
2:B:13:LYS:HE2	2:B:86:ASP:OD2	2.07	0.55
2:B:239:TRP:CZ2	2:B:378:GLU:HG2	2.42	0.55
2:B:120:LEU:HD23	2:B:125:ARG:HG2	1.87	0.55
2:B:183:TYR:CE1	2:B:184:MET:HG2	2.42	0.54
2:B:278:GLN:HE21	2:B:278:GLN:HA	1.70	0.54
1:A:136:ASN:C	1:A:138:GLU:N	2.61	0.54
2:B:178:ILE:HG23	2:B:190:GLY:O	2.07	0.54
2:B:257:ILE:HB	2:B:283:LEU:HD11	1.89	0.54
2:B:98:ALA:HA	2:B:101:LYS:HZ1	1.73	0.54
1:A:58:THR:CG2	1:A:59:PRO:HD2	2.36	0.54
1:A:235:HIS:HB3	1:A:236:PRO:HD2	1.90	0.54
2:B:423:VAL:O	2:B:427:TYR:CD2	2.61	0.54
1:A:108:VAL:CG1	1:A:223:LYS:HD2	2.33	0.53
2:B:323:LYS:HB2	2:B:323:LYS:HZ2	1.72	0.53
1:A:182:GLN:C	1:A:182:GLN:NE2	2.51	0.53
2:B:97:PRO:O	2:B:100:ILE:HG22	2.09	0.53
1:A:293:ILE:N	1:A:293:ILE:HD12	2.22	0.53
1:A:94:ILE:HG21	1:A:230:MET:HE1	1.88	0.53
1:A:418:ASN:C	1:A:420:PRO:HD3	2.29	0.53
2:B:328:GLU:O	2:B:339:TYR:HA	2.08	0.53
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.89	0.53
1:A:248:GLU:O	1:A:249:LYS:HG3	2.08	0.53
1:A:486:LEU:O	1:A:528:LYS:NZ	2.42	0.53
2:B:57:ASN:HD21	2:B:131:THR:CB	2.22	0.53
2:B:111:VAL:HG22	2:B:185:ASP:O	2.08	0.53
1:A:112:GLY:O	1:A:114:ALA:N	2.38	0.53
2:B:94:ILE:HD11	2:B:181:TYR:HD2	1.74	0.53
1:A:169:GLU:O	1:A:173:LYS:HG3	2.09	0.53
1:A:225:PRO:HG3	1:A:227:PHE:CE2	2.43	0.53
1:A:27:THR:O	1:A:31:ILE:HG13	2.09	0.53
1:A:114:ALA:HB1	1:A:214:LEU:HD22	1.90	0.53
2:B:46:LYS:HE2	2:B:116:PHE:HD2	1.74	0.53
2:B:267:ALA:HB2	2:B:426:TRP:CZ3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:LYS:CE	1:A:334:GLN:HA	2.38	0.52
1:A:476:LYS:O	1:A:480:GLN:HB2	2.08	0.52
2:B:88:TRP:CE3	2:B:88:TRP:HA	2.44	0.52
2:B:420:PRO:HB2	2:B:423:VAL:CG2	2.33	0.52
1:A:252:TRP:NE1	1:A:295:LEU:HD11	2.25	0.52
2:B:305:GLU:O	2:B:309:ILE:HG13	2.10	0.52
1:A:171:PHE:O	1:A:175:ASN:ND2	2.43	0.52
1:A:394:GLN:HB2	1:A:397:THR:OG1	2.10	0.52
1:A:502:ALA:HA	1:A:505:ILE:CD1	2.33	0.52
2:B:114:ALA:HB1	2:B:160:PHE:CZ	2.44	0.52
2:B:175:ASN:HD21	2:B:201:LYS:HD2	1.75	0.52
1:A:498:ASP:HB2	1:A:538:ALA:HB2	1.92	0.52
2:B:10:VAL:HG11	2:B:153:TRP:CZ2	2.44	0.52
1:A:289:LEU:HD22	1:A:289:LEU:N	2.25	0.52
1:A:474:ASN:O	1:A:478:GLU:HG3	2.09	0.52
2:B:271:TYR:HB2	2:B:274:ILE:CD1	2.40	0.52
2:B:319:TYR:CE1	2:B:321:PRO:HG3	2.43	0.52
1:A:514:GLU:HG3	1:A:515:SER:N	2.26	0.51
1:A:440:PHE:CZ	1:A:489:SER:HB3	2.45	0.51
1:A:181:TYR:HB3	1:A:188:TYR:HB2	1.91	0.51
2:B:195:ILE:HG12	2:B:199:ARG:NH2	2.24	0.51
2:B:97:PRO:C	2:B:99:GLY:N	2.64	0.51
1:A:182:GLN:HE21	1:A:183:TYR:N	2.08	0.51
1:A:239:TRP:CZ2	1:A:316:GLY:HA3	2.46	0.51
1:A:122:GLU:H	1:A:122:GLU:CD	2.15	0.51
1:A:433:PRO:HA	1:A:532:TYR:CD2	2.45	0.51
2:B:139:THR:HG23	2:B:140:PRO:HD2	1.92	0.51
2:B:401:TRP:O	2:B:404:GLU:N	2.37	0.51
2:B:248:GLU:HG2	2:B:307:ARG:CZ	2.40	0.51
2:B:205:LEU:O	2:B:208:HIS:HB3	2.12	0.50
1:A:317:VAL:CG1	1:A:318:TYR:N	2.75	0.50
2:B:359:GLY:HA2	2:B:361:HIS:CE1	2.46	0.50
1:A:49:LYS:HA	1:A:143:ARG:O	2.11	0.50
1:A:253:THR:HB	1:A:290:THR:O	2.11	0.50
2:B:11:LYS:N	2:B:85:GLN:OE1	2.41	0.50
1:A:363:ASN:O	1:A:366:LYS:HB3	2.10	0.50
1:A:494:ASN:HB3	2:B:289:LEU:HD22	1.92	0.50
2:B:169:GLU:O	2:B:172:ARG:N	2.44	0.50
2:B:205:LEU:CD1	2:B:209:LEU:HD22	2.42	0.50
2:B:413:GLU:HA	2:B:413:GLU:OE2	2.11	0.50
1:A:130:PHE:CZ	1:A:144:TYR:HB2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:TRP:HA	2:B:88:TRP:HE3	1.75	0.50
2:B:125:ARG:NE	2:B:147:ASN:HA	2.27	0.50
2:B:195:ILE:CG2	2:B:196:GLY:H	2.21	0.50
2:B:13:LYS:HB2	2:B:16:MET:HG3	1.94	0.49
1:A:122:GLU:HA	1:A:125:ARG:NE	2.27	0.49
1:A:168:LEU:O	1:A:172:ARG:HG3	2.11	0.49
1:A:76:ASP:OD2	1:A:78:ARG:HG3	2.11	0.49
1:A:89:GLU:HG3	1:A:89:GLU:O	2.12	0.49
2:B:24:TRP:HB2	2:B:25:PRO:HD2	1.93	0.49
2:B:349:LEU:O	2:B:350:LYS:HB2	2.12	0.49
1:A:88:TRP:HA	1:A:88:TRP:HE3	1.75	0.49
1:A:63:ILE:CA	1:A:71:TRP:HZ3	2.24	0.49
2:B:267:ALA:HB2	2:B:426:TRP:CH2	2.47	0.49
1:A:112:GLY:C	1:A:114:ALA:H	2.16	0.49
1:A:155:GLY:O	1:A:159:ILE:HG13	2.13	0.49
1:A:329:ILE:HD12	1:A:391:LEU:CD2	2.42	0.49
2:B:169:GLU:O	2:B:173:LYS:HD3	2.13	0.49
2:B:195:ILE:CD1	2:B:199:ARG:NE	2.75	0.49
1:A:79:GLU:O	1:A:82:LYS:HG2	2.12	0.49
1:A:235:HIS:HB2	1:A:238:LYS:O	2.13	0.49
1:A:95:PRO:HG3	2:B:136:ASN:O	2.13	0.48
2:B:6:GLU:OE1	2:B:6:GLU:HA	2.12	0.48
1:A:448:ARG:NE	1:A:474:ASN:HB2	2.28	0.48
2:B:104:LYS:NZ	2:B:192:ASP:HB3	2.28	0.48
1:A:21:VAL:CG1	1:A:59:PRO:HD3	2.43	0.48
2:B:178:ILE:HD11	2:B:201:LYS:HG2	1.95	0.48
1:A:317:VAL:CG2	1:A:347:LYS:HB3	2.38	0.48
2:B:43:LYS:C	2:B:45:GLY:H	2.17	0.48
2:B:282:LEU:HD21	2:B:296:THR:HG23	1.96	0.48
1:A:283:LEU:N	1:A:283:LEU:HD12	2.28	0.48
2:B:109:LEU:HD11	2:B:205:LEU:HD12	1.95	0.48
2:B:319:TYR:OH	2:B:385:LYS:HD3	2.14	0.48
1:A:340:GLN:CB	1:A:351:THR:HG22	2.44	0.48
2:B:10:VAL:HG11	2:B:153:TRP:HZ2	1.79	0.48
1:A:181:TYR:HB2	3:A:999:TNK:H161	1.96	0.48
1:A:332:GLN:O	1:A:332:GLN:HG2	2.14	0.48
1:A:181:TYR:HH	1:A:183:TYR:HD2	1.60	0.48
2:B:169:GLU:CG	2:B:173:LYS:HZ3	2.27	0.48
1:A:26:LEU:O	1:A:31:ILE:HD11	2.13	0.47
1:A:252:TRP:CD1	1:A:295:LEU:HD11	2.48	0.47
1:A:360:ALA:O	1:A:361:HIS:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:242:GLN:HA	2:B:242:GLN:OE1	2.13	0.47
2:B:325:LEU:HA	2:B:343:GLN:HG2	1.96	0.47
1:A:98:ALA:HB1	1:A:349:LEU:HB3	1.96	0.47
1:A:289:LEU:H	1:A:289:LEU:CD2	2.26	0.47
2:B:333:GLY:O	2:B:336:GLN:HB2	2.14	0.47
2:B:122:GLU:HA	2:B:125:ARG:HD2	1.96	0.47
1:A:211:ARG:HG3	1:A:211:ARG:HH11	1.78	0.47
1:A:340:GLN:HB3	1:A:351:THR:HG22	1.95	0.47
1:A:57:ASN:HA	1:A:129:ALA:O	2.15	0.47
2:B:94:ILE:HD11	2:B:181:TYR:CD2	2.49	0.47
2:B:125:ARG:HG2	2:B:146:TYR:O	2.15	0.47
1:A:460:ASN:HA	2:B:286:THR:O	2.14	0.47
2:B:50:ILE:CG2	2:B:145:GLN:HG2	2.45	0.47
2:B:57:ASN:ND2	2:B:143:ARG:NH1	2.44	0.47
2:B:136:ASN:O	2:B:137:ASN:HB2	2.15	0.47
2:B:239:TRP:CH2	2:B:378:GLU:HG2	2.49	0.47
2:B:368:LEU:O	2:B:371:ALA:HB3	2.14	0.47
1:A:79:GLU:HA	1:A:82:LYS:HG2	1.96	0.47
2:B:241:VAL:HG12	2:B:241:VAL:O	2.15	0.47
2:B:332:GLN:HE22	2:B:428:GLN:HB2	1.79	0.47
2:B:276:VAL:HA	2:B:302:GLU:OE2	2.14	0.46
1:A:50:ILE:HG21	1:A:145:GLN:HG2	1.98	0.46
1:A:58:THR:HG23	1:A:76:ASP:O	2.15	0.46
1:A:186:ASP:CG	1:A:223:LYS:HE3	2.35	0.46
1:A:402:TRP:CD1	1:A:402:TRP:C	2.89	0.46
1:A:447:ASN:O	1:A:451:LYS:N	2.48	0.46
1:A:77:PHE:O	1:A:78:ARG:C	2.54	0.46
1:A:409:THR:O	1:A:410:TRP:HB2	2.14	0.46
2:B:169:GLU:HA	2:B:173:LYS:HZ2	1.79	0.46
1:A:8:VAL:O	1:A:121:ASP:HB2	2.15	0.46
1:A:312:GLU:H	1:A:313:PRO:HD3	1.81	0.46
2:B:173:LYS:HD2	2:B:173:LYS:N	2.30	0.46
2:B:278:GLN:NE2	2:B:278:GLN:HA	2.29	0.46
1:A:3:SER:HB3	1:A:5:ILE:CG1	2.37	0.46
2:B:116:PHE:HE1	2:B:151:GLN:CG	2.28	0.46
1:A:356:ARG:NH1	1:A:356:ARG:CG	2.78	0.46
1:A:169:GLU:HB2	1:A:170:PRO:HD3	1.97	0.46
1:A:118:VAL:O	1:A:148:VAL:HB	2.16	0.46
1:A:21:VAL:HG13	1:A:59:PRO:HD3	1.97	0.46
1:A:362:THR:HG22	1:A:363:ASN:N	2.28	0.46
1:A:415:GLU:HG2	1:A:416:PHE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:HIS:CD2	1:A:98:ALA:HB3	2.46	0.45
1:A:317:VAL:HG12	1:A:318:TYR:O	2.17	0.45
1:A:345:PRO:O	1:A:346:PHE:HB2	2.17	0.45
2:B:131:THR:HG1	2:B:143:ARG:HH11	1.64	0.45
2:B:195:ILE:CG1	2:B:199:ARG:NE	2.78	0.45
2:B:245:VAL:O	2:B:245:VAL:HG23	2.16	0.45
2:B:326:ILE:HG22	2:B:327:ALA:N	2.31	0.45
1:A:257:ILE:HG22	1:A:283:LEU:HD11	1.97	0.45
1:A:468:THR:O	1:A:469:LEU:HD23	2.16	0.45
2:B:115:TYR:OH	2:B:157:PRO:HB3	2.16	0.45
2:B:158:ALA:O	2:B:161:GLN:HB2	2.16	0.45
1:A:122:GLU:HA	1:A:125:ARG:HG3	1.97	0.45
1:A:434:ILE:CG2	1:A:437:ALA:HB2	2.46	0.45
1:A:208:HIS:O	1:A:211:ARG:HB3	2.16	0.45
2:B:39:THR:O	2:B:42:GLU:HB3	2.17	0.45
1:A:58:THR:CG2	1:A:76:ASP:O	2.65	0.45
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.99	0.45
1:A:278:GLN:HB2	1:A:302:GLU:CD	2.37	0.45
1:A:266:TRP:CD1	1:A:266:TRP:C	2.90	0.45
1:A:118:VAL:HB	1:A:149:LEU:HD13	1.99	0.45
2:B:139:THR:HG23	2:B:140:PRO:CD	2.47	0.45
1:A:100:ILE:HD12	2:B:136:ASN:HD21	1.82	0.44
1:A:418:ASN:O	1:A:420:PRO:HD3	2.17	0.44
1:A:516:GLU:O	1:A:519:ASN:HB2	2.18	0.44
2:B:368:LEU:HD23	2:B:368:LEU:HA	1.87	0.44
1:A:120:LEU:O	1:A:122:GLU:N	2.50	0.44
1:A:317:VAL:HG12	1:A:318:TYR:H	1.78	0.44
1:A:498:ASP:HA	1:A:536:VAL:O	2.17	0.44
2:B:118:VAL:HG12	2:B:119:PRO:O	2.18	0.44
1:A:181:TYR:CZ	1:A:183:TYR:HB2	2.52	0.44
1:A:340:GLN:HA	1:A:351:THR:HA	1.99	0.44
2:B:116:PHE:HE1	2:B:151:GLN:CD	2.20	0.44
2:B:239:TRP:CH2	2:B:378:GLU:HA	2.52	0.44
1:A:169:GLU:N	1:A:170:PRO:CD	2.79	0.44
2:B:53:GLU:CD	2:B:53:GLU:H	2.21	0.44
2:B:63:ILE:HG13	2:B:72:ARG:HB3	1.97	0.44
2:B:149:LEU:HA	2:B:150:PRO:HD3	1.86	0.44
2:B:332:GLN:HE22	2:B:424:LYS:CE	2.24	0.44
2:B:105:SER:HA	2:B:234:LEU:O	2.17	0.44
1:A:508:ALA:O	1:A:509:GLN:C	2.56	0.44
2:B:303:LEU:HD13	2:B:307:ARG:NH2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:TYR:CG	1:A:151:GLN:NE2	2.86	0.44
1:A:399:GLU:O	1:A:403:THR:HB	2.17	0.44
2:B:73:LYS:HB3	2:B:73:LYS:HZ2	1.82	0.44
2:B:163:SER:O	2:B:167:ILE:CG2	2.62	0.44
1:A:63:ILE:HD12	1:A:63:ILE:O	2.18	0.44
1:A:457:TYR:CD1	1:A:457:TYR:C	2.91	0.44
2:B:435:VAL:HG23	2:B:436:GLY:N	2.33	0.44
1:A:100:ILE:HG12	3:A:999:TNK:H6	1.99	0.44
1:A:279:LEU:CD2	1:A:302:GLU:OE1	2.66	0.44
2:B:46:LYS:CE	2:B:116:PHE:HD2	2.31	0.43
1:A:161:GLN:HA	1:A:161:GLN:OE1	2.18	0.43
2:B:75:VAL:HG11	2:B:77:PHE:CZ	2.53	0.43
2:B:388:LYS:HE2	2:B:415:GLU:HB3	2.00	0.43
1:A:434:ILE:HB	1:A:437:ALA:HB3	2.01	0.43
2:B:173:LYS:C	2:B:175:ASN:N	2.72	0.43
1:A:228:LEU:HD12	1:A:228:LEU:H	1.81	0.43
1:A:479:LEU:O	1:A:521:ILE:HD11	2.18	0.43
2:B:353:LYS:HE3	2:B:353:LYS:HB2	1.84	0.43
1:A:377:THR:O	1:A:381:VAL:HG23	2.18	0.43
1:A:516:GLU:HA	1:A:519:ASN:HD22	1.84	0.43
2:B:277:ARG:HG2	2:B:278:GLN:H	1.84	0.43
2:B:393:ILE:HG12	2:B:394:GLN:N	2.34	0.43
1:A:132:ILE:HA	1:A:133:PRO:HD3	1.84	0.43
2:B:170:PRO:O	2:B:174:GLN:HG3	2.18	0.43
1:A:325:LEU:HA	1:A:325:LEU:HD23	1.64	0.43
2:B:245:VAL:HG13	2:B:431:LYS:HB2	2.01	0.43
1:A:232:TYR:HA	1:A:240:THR:O	2.19	0.43
2:B:108:VAL:HA	2:B:187:LEU:O	2.18	0.43
2:B:404:GLU:HB2	2:B:405:TYR:CE1	2.54	0.43
1:A:228:LEU:CD1	1:A:228:LEU:H	2.31	0.43
2:B:64:LYS:HE2	2:B:71:TRP:CZ2	2.54	0.43
1:A:229:TRP:O	1:A:232:TYR:HB2	2.18	0.42
1:A:254:VAL:HB	1:A:289:LEU:O	2.18	0.42
1:A:400:THR:O	1:A:403:THR:HG22	2.19	0.42
1:A:439:THR:HA	1:A:494:ASN:HB2	2.01	0.42
1:A:465:LYS:HG2	1:A:466:VAL:N	2.33	0.42
1:A:182:GLN:NE2	1:A:183:TYR:N	2.67	0.42
1:A:317:VAL:CG1	1:A:318:TYR:H	2.33	0.42
2:B:169:GLU:O	2:B:172:ARG:HB2	2.19	0.42
1:A:84:THR:HB	1:A:154:LYS:HD3	2.01	0.42
2:B:8:VAL:HG23	2:B:9:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:406:TRP:CH2	2:B:412:PRO:HD2	2.55	0.42
1:A:18:GLY:HA3	1:A:56:TYR:CD1	2.54	0.42
1:A:118:VAL:HA	1:A:119:PRO:HD3	1.74	0.42
1:A:24:TRP:CB	1:A:61:PHE:HE1	2.32	0.42
1:A:54:ASN:O	1:A:56:TYR:N	2.52	0.42
1:A:170:PRO:O	1:A:174:GLN:HG3	2.20	0.42
1:A:307:ARG:NH1	1:A:307:ARG:HG2	2.35	0.42
1:A:442:VAL:HG22	1:A:496:VAL:O	2.19	0.42
2:B:253:THR:O	2:B:256:ASP:HB2	2.18	0.42
1:A:236:PRO:HB3	3:A:999:TNK:C22	2.50	0.42
2:B:326:ILE:O	2:B:341:ILE:HA	2.20	0.42
1:A:94:ILE:CG2	1:A:230:MET:HE2	2.48	0.42
1:A:307:ARG:HG2	1:A:307:ARG:HH11	1.85	0.42
1:A:438:GLU:OE1	1:A:459:THR:CB	2.68	0.42
1:A:451:LYS:O	1:A:471:ASP:N	2.53	0.42
2:B:254:VAL:O	2:B:255:ASN:C	2.58	0.42
2:B:278:GLN:HG3	2:B:298:GLU:HB3	2.02	0.42
1:A:339:TYR:CD1	1:A:339:TYR:C	2.93	0.42
1:A:379:SER:O	1:A:380:ILE:C	2.57	0.42
1:A:489:SER:HB2	1:A:493:VAL:HG13	2.02	0.42
2:B:139:THR:CG2	2:B:140:PRO:N	2.83	0.42
2:B:401:TRP:O	2:B:402:TRP:C	2.57	0.42
1:A:50:ILE:CG2	1:A:145:GLN:HG2	2.50	0.42
1:A:270:ILE:CG2	1:A:314:VAL:CG2	2.93	0.42
1:A:406:TRP:CZ3	2:B:418:ASN:HA	2.53	0.42
3:A:999:TNK:H131	3:A:999:TNK:H172	1.80	0.42
1:A:9:PRO:HG2	2:B:53:GLU:HG3	2.02	0.41
1:A:28:GLU:HG3	1:A:29:GLU:N	2.35	0.41
1:A:79:GLU:HA	1:A:82:LYS:CD	2.49	0.41
1:A:224:GLU:HA	1:A:225:PRO:HD3	1.83	0.41
2:B:88:TRP:CH2	2:B:93:GLY:N	2.88	0.41
2:B:389:PHE:HB3	2:B:391:LEU:HD21	2.02	0.41
1:A:94:ILE:HG22	1:A:229:TRP:CH2	2.55	0.41
1:A:393:ILE:HB	1:A:423:VAL:HG22	2.00	0.41
1:A:82:LYS:HA	4:A:1007:HOH:O	2.19	0.41
1:A:70:LYS:HB3	1:A:70:LYS:HE2	1.88	0.41
1:A:254:VAL:HG23	1:A:293:ILE:HD11	2.01	0.41
1:A:496:VAL:HA	1:A:534:ALA:O	2.20	0.41
2:B:168:LEU:O	2:B:169:GLU:C	2.58	0.41
2:B:41:MET:HB3	2:B:41:MET:HE2	1.91	0.41
2:B:125:ARG:O	2:B:126:LYS:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:131:THR:OG1	2:B:143:ARG:HD2	2.20	0.41
1:A:95:PRO:HD2	1:A:229:TRP:HH2	1.85	0.41
1:A:279:LEU:HD23	1:A:302:GLU:OE1	2.21	0.41
1:A:440:PHE:CE1	1:A:489:SER:HB3	2.56	0.41
1:A:536:VAL:CG1	2:B:258:GLN:HB3	2.49	0.41
1:A:120:LEU:CD2	1:A:121:ASP:N	2.83	0.41
1:A:138:GLU:HB3	1:A:139:THR:H	1.51	0.41
1:A:335:GLY:HA2	1:A:367:GLN:OE1	2.21	0.41
1:A:337:TRP:CZ3	1:A:368:LEU:HD23	2.55	0.41
1:A:503:LEU:HD13	1:A:535:TRP:CB	2.50	0.41
2:B:364:ASP:O	2:B:367:GLN:N	2.54	0.41
1:A:95:PRO:HB3	2:B:136:ASN:ND2	2.37	0.40
1:A:132:ILE:O	1:A:141:GLY:HA3	2.21	0.40
1:A:253:THR:HA	1:A:291:GLU:O	2.22	0.40
1:A:15:GLY:O	1:A:16:MET:C	2.60	0.40
1:A:114:ALA:HA	1:A:117:SER:HB2	2.02	0.40
1:A:103:LYS:HB3	1:A:191:SER:O	2.21	0.40
1:A:401:TRP:HB2	1:A:425:LEU:HD21	2.03	0.40
2:B:244:ILE:HG13	2:B:426:TRP:CZ2	2.57	0.40
1:A:96:HIS:CD2	1:A:98:ALA:H	2.40	0.40
1:A:486:LEU:HB3	1:A:524:GLN:HB3	2.03	0.40
2:B:46:LYS:HG2	2:B:116:PHE:CD2	2.56	0.40
2:B:151:GLN:H	2:B:151:GLN:HG3	1.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:GLU:OE1	4:A:1057:HOH:O[1_556]	2.15	0.05

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	527/560 (94%)	460 (87%)	49 (9%)	18 (3%)	3	5
2	B	396/440 (90%)	344 (87%)	45 (11%)	7 (2%)	8	16
All	All	923/1000 (92%)	804 (87%)	94 (10%)	25 (3%)	5	8

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	138	GLU
1	A	272	PRO
1	A	16	MET
1	A	85	GLN
1	A	112	GLY
1	A	296	THR
1	A	313	PRO
2	B	98	ALA
2	B	361	HIS
1	A	95	PRO
1	A	113	ASP
1	A	361	HIS
1	A	420	PRO
2	B	193	LEU
1	A	78	ARG
1	A	121	ASP
2	B	40	GLU
2	B	166	LYS
2	B	350	LYS
1	A	91	GLN
1	A	52	PRO
1	A	312	GLU
2	B	169	GLU
1	A	55	PRO

5.3.2 Protein sidechains [i](#)

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	478/499 (96%)	431 (90%)	47 (10%)	8	15
2	B	367/400 (92%)	341 (93%)	26 (7%)	14	29
All	All	845/899 (94%)	772 (91%)	73 (9%)	10	20

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	53	GLU
1	A	69	THR
1	A	89	GLU
1	A	92	LEU
1	A	102	LYS
1	A	109	LEU
1	A	120	LEU
1	A	122	GLU
1	A	123	ASP
1	A	135	ILE
1	A	166	LYS
1	A	175	ASN
1	A	182	GLN
1	A	184	MET
1	A	195	ILE
1	A	205	LEU
1	A	211	ARG
1	A	229	TRP
1	A	230	MET
1	A	237	ASP
1	A	238	LYS
1	A	249	LYS
1	A	255	ASN
1	A	266	TRP
1	A	313	PRO
1	A	325	LEU
1	A	336	GLN
1	A	340	GLN
1	A	361	HIS
1	A	362	THR
1	A	369	THR
1	A	402	TRP
1	A	404	GLU
1	A	420	PRO

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Mol	Chain	Res	Type
1	A	448	ARG
1	A	452	LEU
1	A	468	THR
1	A	474	ASN
1	A	475	GLN
1	A	491	LEU
1	A	493	VAL
1	A	496	VAL
1	A	500	GLN
1	A	501	TYR
1	A	517	LEU
1	A	533	LEU
2	B	29	GLU
2	B	46	LYS
2	B	73	LYS
2	B	88	TRP
2	B	113	ASP
2	B	164	MET
2	B	165	THR
2	B	167	ILE
2	B	170	PRO
2	B	187	LEU
2	B	189	VAL
2	B	192	ASP
2	B	194	GLU
2	B	209	LEU
2	B	233	GLU
2	B	243	PRO
2	B	277	ARG
2	B	283	LEU
2	B	287	LYS
2	B	289	LEU
2	B	303	LEU
2	B	361	HIS
2	B	368	LEU
2	B	403	THR
2	B	405	TYR
2	B	425	LEU

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

Mol	Chain	Res	Type
1	A	91	GLN
1	A	96	HIS
1	A	136	ASN
1	A	151	GLN
1	A	174	GLN
1	A	175	ASN
1	A	182	GLN
1	A	242	GLN
1	A	255	ASN
1	A	278	GLN
1	A	334	GLN
1	A	336	GLN
1	A	361	HIS
1	A	474	ASN
1	A	475	GLN
1	A	500	GLN
1	A	507	GLN
1	A	512	GLN
2	B	57	ASN
2	B	161	GLN
2	B	175	ASN
2	B	197	GLN
2	B	208	HIS
2	B	235	HIS
2	B	255	ASN
2	B	269	GLN
2	B	278	GLN
2	B	332	GLN
2	B	361	HIS
2	B	394	GLN
2	B	428	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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
1	CSD	A	280	1	3,7,8	0.97	0	1,8,10	4.03	1 (100%)

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
1	CSD	A	280	1	-	2/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280	CSD	OD1-SG-CB	4.03	113.21	105.54

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	280	CSD	N-CA-CB-SG
1	A	280	CSD	CA-CB-SG-OD1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
3	TNK	A	999	-	23,29,29	1.55	4 (17%)	24,39,39	3.28	3 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TNK	A	999	-	-	3/12/14/14	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	999	TNK	C11-N10	3.45	1.39	1.33
3	A	999	TNK	C11-C12	2.50	1.46	1.41
3	A	999	TNK	C7-N8	2.19	1.42	1.36
3	A	999	TNK	C3-C2	2.10	1.43	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	999	TNK	C11-N10-C9	13.86	126.84	115.14
3	A	999	TNK	C12-C11-N10	-6.40	116.31	126.22
3	A	999	TNK	C7-C12-C14	3.36	126.08	121.42

There are no chirality outliers.

All (3) torsion outliers are listed below:

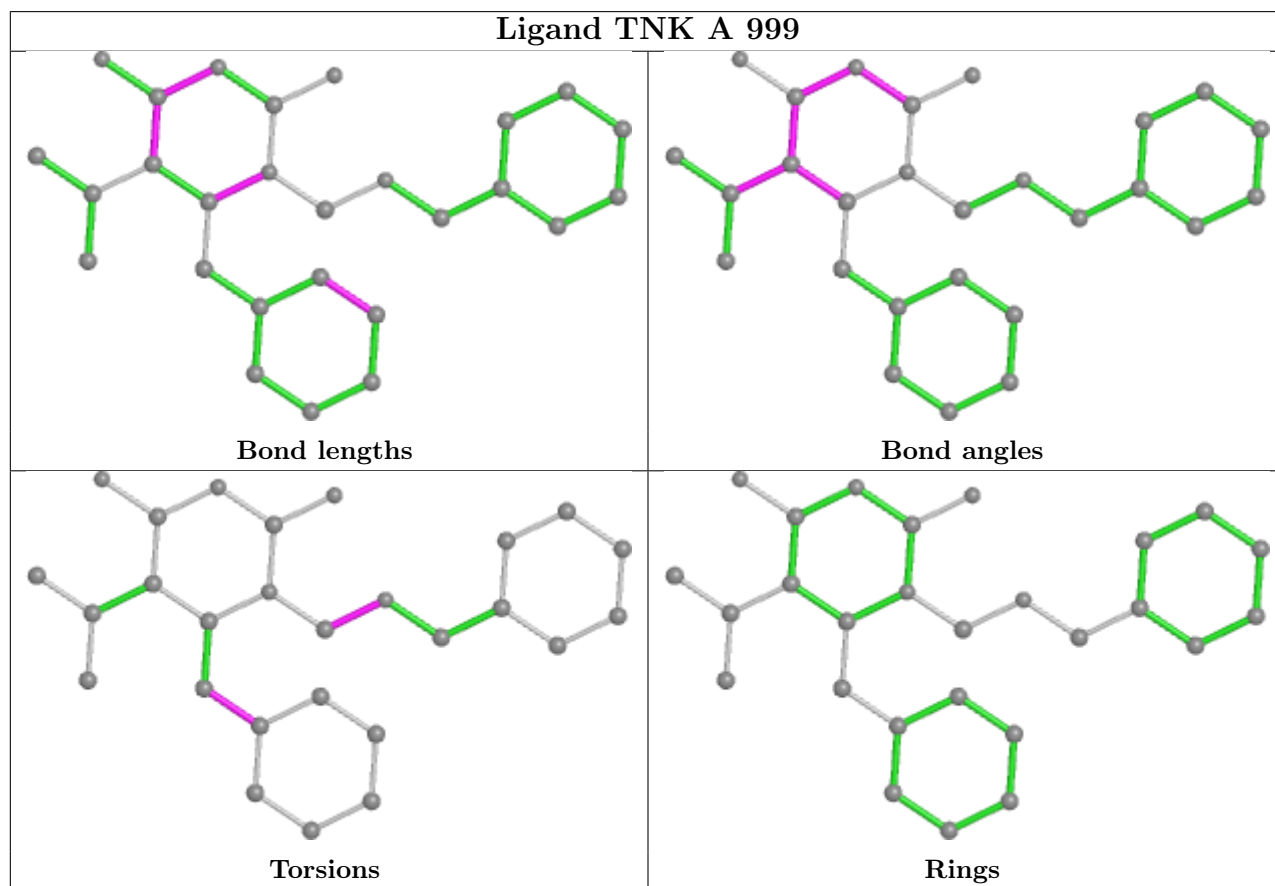
Mol	Chain	Res	Type	Atoms
3	A	999	TNK	N8-C17-O17-C18
3	A	999	TNK	C6-C1-C13-C7
3	A	999	TNK	C2-C1-C13-C7

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	999	TNK	5	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

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	533/560 (95%)	-0.15	19 (3%) 42 35	39, 75, 120, 150	0
2	B	404/440 (91%)	-0.04	24 (5%) 22 17	38, 74, 125, 150	0
All	All	937/1000 (93%)	-0.11	43 (4%) 32 26	38, 74, 122, 150	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	435	VAL	4.8
2	B	434	ILE	4.5
2	B	436	GLY	4.5
2	B	69	THR	4.2
2	B	88	TRP	4.2
2	B	104	LYS	4.0
2	B	432	GLU	4.0
2	B	431	LYS	3.9
1	A	53	GLU	3.8
2	B	70	LYS	3.7
1	A	136	ASN	3.7
1	A	220	LYS	3.6
1	A	89	GLU	3.6
2	B	212	TRP	3.5
1	A	446	ALA	3.5
2	B	433	PRO	3.3
2	B	94	ILE	3.3
1	A	245	VAL	3.3
1	A	470	THR	3.0
2	B	183	TYR	2.9
2	B	195	ILE	2.9
1	A	1	PRO	2.9
1	A	69	THR	2.6
2	B	184	MET	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	240	THR	2.6
1	A	22	LYS	2.5
2	B	87	PHE	2.5
2	B	198	HIS	2.4
1	A	301	LEU	2.4
2	B	284	ARG	2.4
1	A	52	PRO	2.4
1	A	64	LYS	2.3
2	B	237	ASP	2.3
2	B	7	THR	2.2
1	A	221	HIS	2.2
1	A	476	LYS	2.2
2	B	190	GLY	2.1
1	A	396	GLU	2.1
1	A	135	ILE	2.0
1	A	448	ARG	2.0
1	A	346	PHE	2.0
2	B	323	LYS	2.0
2	B	102	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CSD	A	280	8/9	0.95	0.14	74,75,88,95	0

6.3 Carbohydrates [i](#)

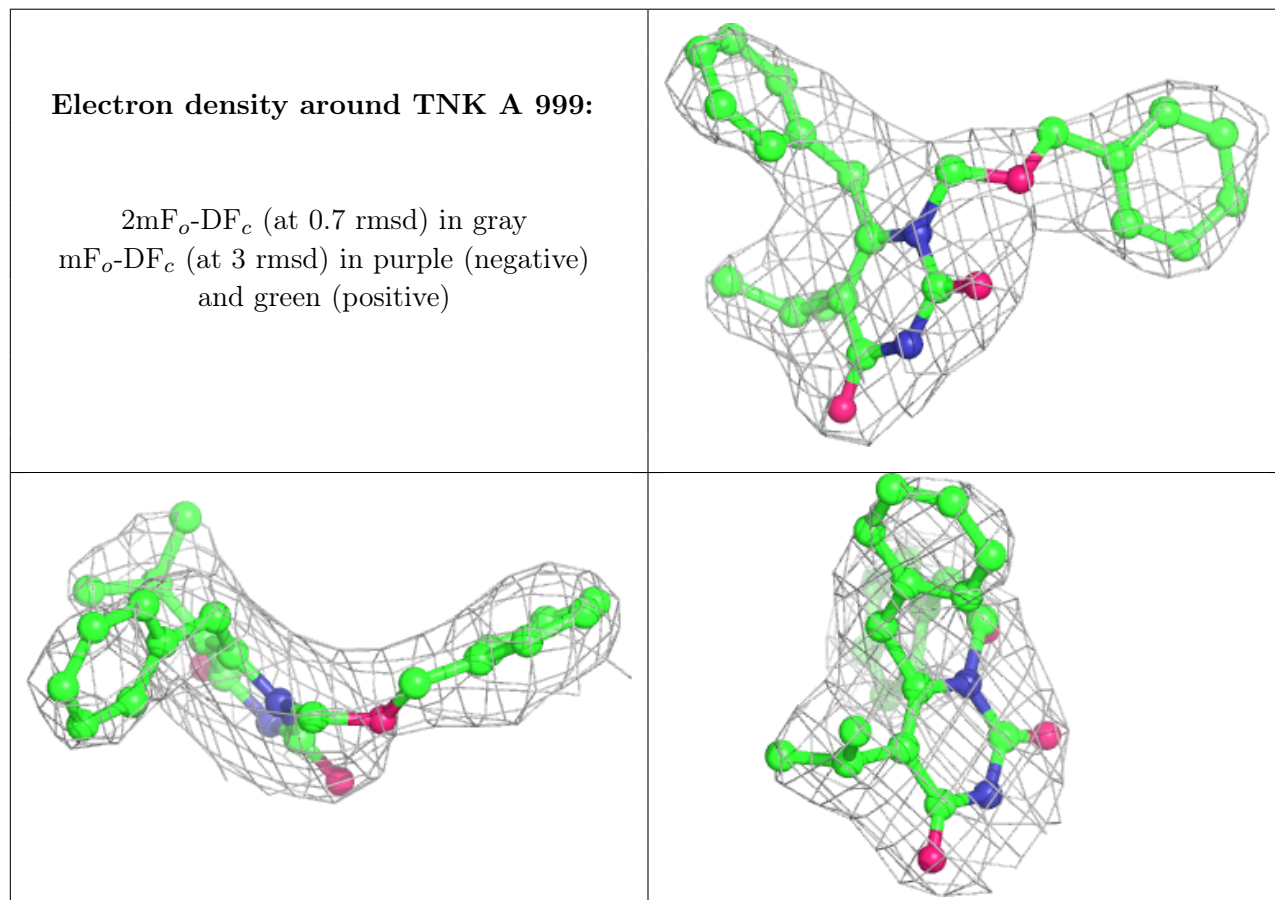
There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	TNK	A	999	27/27	0.95	0.17	42,61,82,86	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.