

Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 09:34 PM EDT

PDB ID	:	2BAN
Title	:	Crystal structure of HIV-1 reverse transcriptase (RT) in complex with
		JANSSEN-R157208
Authors	:	Das, K.; Arnold, E.
Deposited on	:	2005-10-14
Resolution	:	2.95 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
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)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.95 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	3104 (3.00-2.92)
Clashscore	141614	3462(3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 <=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	А	560	34%	52%	11% ••
2	В	430	<mark>6%</mark> 37%	50%	12% •



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2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7922 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 P66 subunit.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	552	Total 4431	C 2864	N 733	0 827	${f S}7$	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	280	SER	CYS	engineered mutation	UNP P03366

• Molecule 2 is a protein called Reverse transcriptase P51 subunit.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	427	Total 3465	C 2256	N 570	O 633	S 6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	280	SER	CYS	engineered mutation	UNP P03366

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Mn 1 1	0	0

• Molecule 4 is 5-ETHYL-3-[(2-METHOXYETHYL)METHYLAMINO]-6-METHYL-4-(3-M ETHYLBENZYL)PYRIDIN-2(1H)-ONE (three-letter code: 357) (formula: C₂₀H₂₈N₂O₂).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	А	1	Total 24	C 20	N 2	O 2	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total O 1 1	0	0



Chain B:

37%

3 Residue-property plots (i)

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 P66 subunit



50%

12%







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	226.24Å 69.43Å 104.45Å	Deperitor
a, b, c, α , β , γ	90.00° 106.49° 90.00°	Depositor
Resolution(A)	19.86 - 2.95	Depositor
Resolution (A)	32.37 - 2.95	EDS
% Data completeness	91.9 (19.86-2.95)	Depositor
(in resolution range)	93.8 (32.37-2.95)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.92 (at 2.95 \text{\AA})$	Xtriage
Refinement program	CNS 1.1	Depositor
D D	0.243 , 0.305	Depositor
n, n_{free}	0.239 , 0.296	DCC
R_{free} test set	1533 reflections (4.94%)	wwPDB-VP
Wilson B-factor $(Å^2)$	80.4	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27, 61.5	EDS
L-test for twinning ²	$ < L >=0.48, < L^2>=0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7922	wwPDB-VP
Average B, all atoms $(Å^2)$	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.76% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: MN, 357

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).

Mal	Chain	Bond lengths		Bond angles	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.45	0/4546	0.78	5/6185~(0.1%)
2	В	0.49	0/3566	0.77	1/4856~(0.0%)
All	All	0.46	0/8112	0.78	6/11041~(0.1%)

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
2	В	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
1	А	55	PRO	N-CA-C	10.91	140.47	112.10
1	А	26	LEU	N-CA-C	7.64	131.63	111.00
1	А	54	ASN	N-CA-C	5.32	125.35	111.00
1	А	55	PRO	CA-C-N	-5.15	105.87	117.20
2	В	89	GLU	N-CA-C	-5.09	97.25	111.00
1	А	151	GLN	N-CA-C	5.07	124.68	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	В	232	TYR	Sidechain



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	А	4431	0	4413	429	0
2	В	3465	0	3456	297	0
3	А	1	0	0	0	0
4	А	24	0	28	6	0
5	А	1	0	0	0	0
All	All	7922	0	7897	711	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 45.

All (711) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:362:THR:HG22	1:A:363:ASN:H	1.08	1.18
1:A:241:VAL:HG11	1:A:266:TRP:HE1	1.06	1.15
1:A:132:ILE:HG13	1:A:142:ILE:HB	1.30	1.13
1:A:27:THR:HG23	1:A:30:LYS:HB2	1.31	1.11
1:A:54:ASN:HB2	1:A:55:PRO:HD3	1.32	1.07
2:B:284:ARG:HH11	2:B:284:ARG:HG3	1.14	1.06
1:A:241:VAL:HG11	1:A:266:TRP:NE1	1.71	1.02
1:A:242:GLN:HB2	1:A:243:PRO:HD3	1.34	1.02
1:A:131:THR:HG23	1:A:143:ARG:HD2	1.39	1.02
1:A:241:VAL:CG1	1:A:266:TRP:HE1	1.78	0.97
1:A:362:THR:HG22	1:A:363:ASN:N	1.79	0.97
1:A:362:THR:CG2	1:A:363:ASN:H	1.80	0.94
2:B:276:VAL:H	2:B:277:ARG:HH11	0.96	0.94
1:A:35:VAL:HG22	1:A:132:ILE:HD12	1.50	0.94
1:A:122:GLU:HA	1:A:125:ARG:HD2	1.47	0.93
1:A:161:GLN:HG2	1:A:182:GLN:HE21	1.31	0.93
1:A:218:ASP:C	1:A:220:LYS:H	1.63	0.92
2:B:11:LYS:HD3	2:B:11:LYS:H	1.35	0.92
2:B:87:PHE:O	2:B:91:GLN:HB2	1.70	0.90
1:A:330:GLN:HE22	1:A:340:GLN:HE22	1.16	0.90
2:B:149:LEU:HD22	2:B:156:SER:HA	1.51	0.89
1:A:494:ASN:HD22	2:B:289:LEU:HD12	1.38	0.89



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:435:VAL:HG22	2:B:290:THR:HG21	1.54	0.88
2:B:85:GLN:HA	2:B:88:TRP:HB2	1.54	0.87
1:A:330:GLN:NE2	1:A:340:GLN:HE22	1.71	0.87
1:A:164:MET:HE3	1:A:187:LEU:HD11	1.57	0.87
1:A:240:THR:HG22	1:A:241:VAL:H	1.38	0.87
2:B:277:ARG:O	2:B:281:LYS:HG3	1.75	0.86
1:A:460:ASN:ND2	1:A:461:LYS:H	1.73	0.86
1:A:108:VAL:HG12	1:A:188:TYR:CD2	2.10	0.86
1:A:270:ILE:O	1:A:272:PRO:HD3	1.76	0.85
1:A:460:ASN:HD22	1:A:461:LYS:H	1.22	0.85
1:A:249:LYS:HG3	1:A:250:ASP:H	1.40	0.85
2:B:276:VAL:N	2:B:277:ARG:HH11	1.74	0.85
1:A:195:ILE:HD12	1:A:195:ILE:H	1.40	0.84
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.59	0.84
2:B:277:ARG:CD	2:B:277:ARG:H	1.90	0.84
1:A:54:ASN:HB2	1:A:55:PRO:CD	2.08	0.84
1:A:90:VAL:HG23	1:A:91:GLN:H	1.44	0.83
1:A:231:GLY:O	1:A:241:VAL:HG13	1.78	0.82
2:B:241:VAL:HG13	2:B:243:PRO:HD3	1.62	0.82
1:A:130:PHE:CE1	1:A:144:TYR:HB2	2.15	0.82
1:A:64:LYS:HE2	1:A:68:SER:HA	1.62	0.82
1:A:450:THR:O	1:A:451:LYS:HG2	1.79	0.82
1:A:233:GLU:CD	1:A:242:GLN:HE21	1.83	0.82
1:A:27:THR:CG2	1:A:30:LYS:HB2	2.09	0.81
2:B:78:ARG:HD3	2:B:412:PRO:O	1.79	0.81
1:A:74:LEU:HD12	1:A:75:VAL:H	1.45	0.81
1:A:132:ILE:CG1	1:A:142:ILE:HB	2.10	0.81
2:B:139:THR:HB	2:B:140:PRO:HD2	1.63	0.80
2:B:276:VAL:H	2:B:277:ARG:NH1	1.78	0.80
2:B:306:ASN:ND2	2:B:309:ILE:HD12	1.97	0.79
1:A:3:SER:HB3	1:A:5:ILE:HG13	1.63	0.79
2:B:350:LYS:HE3	2:B:378:GLU:OE1	1.82	0.79
1:A:131:THR:CG2	1:A:143:ARG:HD2	2.12	0.79
2:B:235:HIS:HB2	2:B:238:LYS:HE3	1.64	0.79
2:B:275:LYS:HA	2:B:277:ARG:NH1	1.98	0.79
2:B:125:ARG:O	2:B:127:TYR:N	2.16	0.79
1:A:354:TYR:HD1	1:A:374:LYS:HD2	1.48	0.78
2:B:241:VAL:HG22	2:B:242:GLN:H	1.48	0.78
2:B:253:THR:HG22	2:B:292:VAL:HG22	1.65	0.78
1:A:74:LEU:HD12	1:A:75:VAL:N	1.98	0.78
2:B:156:SER:N	2:B:157:PRO:HD2	1.99	0.78



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:B:224:GLU:O	2:B:226:PRO:HD3	1.84	0.78
1:A:279:LEU:HD12	1:A:279:LEU:H	1.49	0.78
2:B:31:ILE:O	2:B:35:VAL:HG23	1.83	0.77
2:B:149:LEU:HD21	2:B:159:ILE:HD12	1.66	0.77
2:B:284:ARG:HG3	2:B:284:ARG:NH1	1.90	0.77
2:B:206:ARG:HE	2:B:217:PRO:HB2	1.48	0.77
2:B:296:THR:HG22	2:B:297:GLU:N	2.00	0.77
2:B:11:LYS:HD3	2:B:11:LYS:N	1.97	0.77
2:B:118:VAL:HB	2:B:149:LEU:CD1	2.15	0.76
1:A:218:ASP:C	1:A:220:LYS:N	2.38	0.76
2:B:156:SER:H	2:B:157:PRO:HD2	1.50	0.76
1:A:441:TYR:CE2	1:A:544:GLY:HA3	2.21	0.76
2:B:128:THR:OG1	2:B:146:TYR:HB2	1.86	0.76
1:A:23:GLN:O	1:A:25:PRO:HD3	1.86	0.75
1:A:460:ASN:ND2	1:A:461:LYS:N	2.34	0.75
2:B:296:THR:CG2	2:B:297:GLU:H	1.99	0.75
1:A:66:LYS:C	1:A:68:SER:H	1.89	0.75
2:B:314:VAL:HG12	2:B:315:HIS:H	1.49	0.75
1:A:195:ILE:H	1:A:195:ILE:CD1	2.00	0.74
1:A:183:TYR:CE2	1:A:184:MET:HG3	2.22	0.74
1:A:434:ILE:HG21	1:A:492:GLU:HG2	1.69	0.74
1:A:511:ASP:OD1	1:A:512:LYS:HG2	1.87	0.74
2:B:278:GLN:NE2	2:B:281:LYS:HD2	2.02	0.74
2:B:101:LYS:O	2:B:236:PRO:HB2	1.87	0.74
2:B:66:LYS:C	2:B:68:SER:H	1.90	0.73
2:B:277:ARG:H	2:B:277:ARG:HD3	1.53	0.73
2:B:149:LEU:CD2	2:B:156:SER:HA	2.19	0.72
1:A:92:LEU:HG	1:A:93:GLY:N	2.05	0.72
1:A:278:GLN:HG2	1:A:302:GLU:OE2	1.89	0.72
1:A:317:VAL:HG12	1:A:348:ASN:O	1.90	0.72
1:A:242:GLN:HB2	1:A:243:PRO:CD	2.16	0.71
2:B:28:GLU:HG2	2:B:32:LYS:HE3	1.72	0.71
2:B:174:GLN:O	2:B:176:PRO:HD3	1.89	0.71
2:B:340:GLN:HG2	2:B:426:TRP:CZ2	2.24	0.71
2:B:281:LYS:HA	2:B:284:ARG:NH1	2.06	0.71
2:B:253:THR:O	2:B:257:ILE:HG22	1.90	0.70
2:B:166:LYS:HE2	2:B:212:TRP:HH2	1.57	0.70
1:A:240:THR:HG22	1:A:241:VAL:N	2.07	0.69
2:B:253:THR:H	2:B:256:ASP:HB2	1.57	0.69
2:B:85:GLN:HG3	2:B:154:LYS:HB3	1.74	0.69
1:A:161:GLN:HG2	1:A:182:GLN:NE2	2.05	0.69



	ti a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:163:SER:HA	1:A:166:LYS:HE3	1.74	0.69
1:A:83:ARG:HG3	1:A:83:ARG:HH11	1.58	0.69
2:B:241:VAL:HG22	2:B:242:GLN:N	2.06	0.68
1:A:242:GLN:CB	1:A:243:PRO:HD3	2.19	0.68
2:B:296:THR:CG2	2:B:297:GLU:N	2.55	0.68
1:A:487:GLN:HG3	1:A:524:GLN:HE22	1.58	0.68
2:B:7:THR:O	2:B:9:PRO:HD3	1.94	0.68
1:A:64:LYS:HE2	1:A:68:SER:CA	2.24	0.68
1:A:242:GLN:O	1:A:244:ILE:HG13	1.94	0.68
1:A:195:ILE:HD12	1:A:195:ILE:N	2.08	0.67
2:B:104:LYS:HA	2:B:237:ASP:OD2	1.95	0.67
2:B:306:ASN:HD22	2:B:309:ILE:HD12	1.60	0.67
2:B:279:LEU:HD12	2:B:299:ALA:HB1	1.77	0.67
2:B:314:VAL:HG12	2:B:315:HIS:N	2.09	0.67
2:B:380:ILE:O	2:B:384:GLY:HA2	1.95	0.67
4:A:562:357:H5'1	2:B:138:GLU:HB3	1.77	0.67
2:B:12:LEU:HA	2:B:84:THR:HG22	1.75	0.67
1:A:60:VAL:HG22	1:A:130:PHE:HB2	1.77	0.67
2:B:66:LYS:HZ1	2:B:218:ASP:HB2	1.59	0.66
1:A:210:LEU:HA	1:A:214:LEU:O	1.96	0.66
2:B:118:VAL:HB	2:B:149:LEU:HD12	1.76	0.66
1:A:330:GLN:HE22	1:A:340:GLN:NE2	1.90	0.66
1:A:296:THR:HG22	1:A:297:GLU:N	2.11	0.66
1:A:59:PRO:HB2	1:A:61:PHE:CE1	2.31	0.65
2:B:257:ILE:HG23	2:B:283:LEU:HD21	1.78	0.65
1:A:20:LYS:HG2	1:A:56:TYR:HB3	1.77	0.65
1:A:493:VAL:HG22	1:A:494:ASN:N	2.11	0.65
1:A:65:LYS:HE2	1:A:66:LYS:HA	1.79	0.65
1:A:65:LYS:HE2	1:A:66:LYS:CA	2.26	0.65
1:A:297:GLU:N	1:A:297:GLU:OE1	2.30	0.65
2:B:296:THR:HG22	2:B:297:GLU:H	1.58	0.65
2:B:219:LYS:NZ	2:B:219:LYS:HB3	2.12	0.65
2:B:349:LEU:HD23	2:B:349:LEU:N	2.11	0.65
1:A:60:VAL:C	1:A:61:PHE:HD1	2.00	0.65
1:A:41:MET:HB2	1:A:47:ILE:HD11	1.79	0.64
1:A:298:GLU:H	1:A:298:GLU:CD	2.00	0.64
1:A:138:GLU:O	1:A:138:GLU:HG3	1.98	0.64
1:A:398:TRP:CH2	1:A:411:ILE:HD11	2.32	0.64
1:A:430:GLU:HG3	1:A:434:ILE:HD11	1.80	0.64
1:A:521:ILE:O	1:A:525:LEU:HG	1.97	0.64
1:A:265:ASN:O	1:A:268:SER:N	2.31	0.64



	A i a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:28:GLU:H	1:A:28:GLU:CD	2.02	0.64
1:A:543:GLY:O	2:B:284:ARG:HA	1.97	0.64
2:B:366:LYS:O	2:B:370:GLU:HG3	1.98	0.63
1:A:358:ARG:C	1:A:360:ALA:H	2.02	0.63
1:A:241:VAL:HG11	1:A:266:TRP:CD1	2.32	0.63
2:B:257:ILE:CG2	2:B:283:LEU:HD21	2.29	0.63
2:B:277:ARG:CD	2:B:277:ARG:N	2.58	0.63
1:A:286:THR:HG22	1:A:288:ALA:H	1.64	0.63
1:A:7:THR:HG22	1:A:119:PRO:HB2	1.80	0.63
1:A:324:ASP:O	1:A:326:ILE:HD12	1.98	0.63
1:A:537:PRO:HB2	1:A:541:GLY:HA3	1.81	0.63
2:B:178:ILE:HD11	2:B:201:LYS:HG2	1.81	0.63
2:B:373:GLN:HE22	2:B:407:GLN:H	1.45	0.63
1:A:276:VAL:HG12	1:A:276:VAL:O	1.98	0.63
1:A:96:HIS:CE1	1:A:350:LYS:HD2	2.34	0.62
1:A:430:GLU:CD	1:A:530:LYS:HE3	2.20	0.62
1:A:277:ARG:HD2	1:A:334:GLN:HB2	1.81	0.62
1:A:509:GLN:N	1:A:510:PRO:HD3	2.14	0.62
2:B:66:LYS:O	2:B:68:SER:N	2.33	0.62
2:B:1:PRO:HD2	2:B:117:SER:HA	1.82	0.62
2:B:393:ILE:HD13	2:B:398:TRP:HB2	1.81	0.62
1:A:17:ASP:O	1:A:83:ARG:HD3	1.98	0.62
2:B:17:ASP:O	2:B:83:ARG:NH1	2.33	0.62
2:B:146:TYR:CG	2:B:150:PRO:HG3	2.35	0.62
2:B:1:PRO:CD	2:B:117:SER:HA	2.29	0.61
2:B:104:LYS:HB2	2:B:192:ASP:HA	1.82	0.61
1:A:235:HIS:CD2	1:A:238:LYS:HG3	2.35	0.61
1:A:286:THR:HG21	1:A:291:GLU:OE1	2.00	0.61
1:A:434:ILE:H	1:A:494:ASN:HD21	1.48	0.61
1:A:38:CYS:HB3	1:A:144:TYR:CE1	2.35	0.61
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.35	0.61
2:B:335:GLY:O	2:B:355:ALA:HA	2.01	0.61
1:A:58:THR:HG22	1:A:59:PRO:HD2	1.81	0.61
1:A:503:LEU:HD11	1:A:507:GLN:OE1	2.00	0.61
2:B:421:PRO:HG2	2:B:422:LEU:H	1.65	0.60
1:A:126:LYS:NZ	1:A:126:LYS:HB3	2.16	0.60
1:A:329:ILE:HD11	1:A:375:ILE:HD12	1.83	0.60
1:A:108:VAL:HG23	1:A:108:VAL:O	2.00	0.60
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.83	0.60
1:A:518:VAL:O	1:A:522:ILE:HG13	2.01	0.60
1:A:219:LYS:HD2	1:A:219:LYS:N	2.16	0.60



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:441:TYR:O	1:A:548:VAL:HG11	2.01	0.60
1:A:49:LYS:HA	1:A:143:ARG:O	2.01	0.60
1:A:495:ILE:HB	1:A:533:LEU:HD22	1.83	0.60
2:B:213:GLY:C	2:B:215:THR:H	2.05	0.60
1:A:97:PRO:HG2	1:A:232:TYR:CD2	2.37	0.60
1:A:170:PRO:HB2	1:A:174:GLN:NE2	2.16	0.60
1:A:340:GLN:HB3	1:A:351:THR:HG22	1.84	0.60
1:A:7:THR:CG2	1:A:119:PRO:HB2	2.32	0.60
2:B:100:LEU:HD11	2:B:106:VAL:CG1	2.32	0.60
1:A:132:ILE:HG13	1:A:142:ILE:CB	2.20	0.59
2:B:371:ALA:O	2:B:375:ILE:HG13	2.02	0.59
1:A:19:PRO:O	1:A:56:TYR:HB2	2.02	0.59
2:B:281:LYS:HG2	2:B:284:ARG:CZ	2.32	0.59
2:B:365:VAL:HG12	2:B:366:LYS:N	2.17	0.59
2:B:275:LYS:O	2:B:302:GLU:CD	2.41	0.59
2:B:277:ARG:N	2:B:277:ARG:HD2	2.17	0.59
2:B:326:ILE:HG21	2:B:342:TYR:CE1	2.37	0.59
1:A:5:ILE:CD1	1:A:167:ILE:HD11	2.32	0.59
1:A:124:PHE:CD2	1:A:124:PHE:O	2.55	0.59
1:A:426:TRP:O	1:A:427:TYR:HB3	2.03	0.59
1:A:451:LYS:HE3	1:A:471:ASN:ND2	2.17	0.59
1:A:460:ASN:HD22	1:A:460:ASN:N	2.00	0.59
1:A:540:LYS:HE3	2:B:265:ASN:HD21	1.68	0.59
1:A:238:LYS:HE2	1:A:315:HIS:HB2	1.85	0.58
2:B:154:LYS:HG2	2:B:184:MET:HG2	1.83	0.58
1:A:57:ASN:ND2	1:A:58:THR:H	2.01	0.58
1:A:499:SER:OG	1:A:502:ALA:HB3	2.02	0.58
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.04	0.58
1:A:201:LYS:HA	1:A:204:GLU:HG3	1.85	0.58
1:A:244:ILE:HD13	1:A:310:LEU:HD22	1.86	0.58
1:A:12:LEU:HD11	1:A:127:TYR:CE2	2.39	0.58
1:A:46:LYS:HE2	1:A:116:PHE:O	2.03	0.58
2:B:166:LYS:HE2	2:B:212:TRP:CH2	2.38	0.58
1:A:19:PRO:O	1:A:56:TYR:CB	2.52	0.58
2:B:114:ALA:HB1	2:B:160:PHE:CZ	2.39	0.58
2:B:206:ARG:NE	2:B:217:PRO:HB2	2.19	0.58
1:A:420:PRO:HA	1:A:421:PRO:C	2.24	0.57
1:A:483:TYR:CE1	1:A:520:GLN:HB3	2.39	0.57
1:A:34:LEU:CD1	1:A:132:ILE:HG22	2.35	0.57
1:A:188:TYR:CD2	4:A:562:357:H6'	2.39	0.57
1:A:517:LEU:O	1:A:520:GLN:HB2	2.04	0.57



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:B:66:LYS:C	2:B:68:SER:N	2.57	0.57
1:A:34:LEU:HD12	1:A:132:ILE:HG22	1.86	0.57
1:A:242:GLN:O	1:A:244:ILE:N	2.35	0.57
1:A:33:ALA:O	1:A:36:GLU:HB3	2.04	0.57
1:A:545:ASN:HA	1:A:548:VAL:HG23	1.85	0.57
1:A:164:MET:CE	1:A:187:LEU:HD11	2.32	0.57
2:B:91:GLN:HE21	2:B:91:GLN:C	2.07	0.57
2:B:266:TRP:HH2	2:B:426:TRP:CZ3	2.22	0.57
1:A:490:GLY:O	1:A:492:GLU:N	2.37	0.57
1:A:296:THR:HG22	1:A:298:GLU:OE1	2.05	0.57
1:A:460:ASN:HD22	1:A:461:LYS:N	1.92	0.57
2:B:297:GLU:HA	2:B:297:GLU:OE1	2.04	0.56
2:B:373:GLN:NE2	2:B:407:GLN:H	2.02	0.56
1:A:108:VAL:CG1	1:A:188:TYR:CD2	2.86	0.56
1:A:94:ILE:HD13	1:A:230:MET:HG3	1.87	0.56
1:A:284:ARG:HG3	1:A:285:GLY:N	2.19	0.56
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.39	0.56
1:A:394:GLN:HG2	1:A:397:THR:OG1	2.04	0.56
2:B:156:SER:N	2:B:157:PRO:CD	2.68	0.56
2:B:423:VAL:HG12	2:B:423:VAL:O	2.06	0.56
1:A:350:LYS:NZ	1:A:350:LYS:HB3	2.21	0.56
1:A:457:TYR:C	1:A:457:TYR:CD2	2.79	0.56
2:B:279:LEU:HA	2:B:299:ALA:HB1	1.88	0.56
2:B:385:LYS:O	2:B:385:LYS:HG3	2.05	0.56
1:A:131:THR:OG1	1:A:143:ARG:NE	2.35	0.56
1:A:254:VAL:O	1:A:258:GLN:HG3	2.05	0.56
1:A:406:TRP:CZ2	2:B:418:ASN:O	2.59	0.56
1:A:537:PRO:O	1:A:541:GLY:O	2.24	0.56
2:B:85:GLN:HG3	2:B:154:LYS:CB	2.36	0.56
2:B:248:GLU:HA	2:B:307:ARG:NH2	2.20	0.56
1:A:223:LYS:O	1:A:223:LYS:HG3	2.06	0.56
1:A:542:ILE:CG1	1:A:546:GLU:HA	2.36	0.56
2:B:419:THR:O	2:B:421:PRO:HD3	2.06	0.56
1:A:219:LYS:C	1:A:221:HIS:H	2.09	0.55
1:A:487:GLN:HG3	1:A:524:GLN:NE2	2.21	0.55
2:B:201:LYS:O	2:B:204:GLU:HB3	2.06	0.55
2:B:259:LYS:O	2:B:263:LYS:HD3	2.06	0.55
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.88	0.55
2:B:419:THR:O	2:B:419:THR:HG23	2.06	0.55
2:B:252:TRP:O	2:B:292:VAL:HG13	2.07	0.55
2:B:311:LYS:O	2:B:313:PRO:HD3	2.07	0.55



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:376:THR:HG23	1:A:386:THR:HG22	1.88	0.55	
1:A:483:TYR:HB2	1:A:521:ILE:CG1	2.37	0.55	
2:B:60:VAL:HG12	2:B:75:VAL:HG22	1.88	0.55	
2:B:249:LYS:HE2	2:B:252:TRP:CZ3	2.42	0.55	
1:A:41:MET:HB2	1:A:47:ILE:CD1	2.37	0.55	
1:A:210:LEU:O	1:A:210:LEU:HD12	2.06	0.55	
1:A:382:ILE:O	2:B:136:ASN:HB2	2.05	0.55	
1:A:402:TRP:CE3	1:A:403:THR:HA	2.42	0.55	
2:B:278:GLN:HE22	2:B:281:LYS:HD2	1.71	0.55	
2:B:296:THR:O	2:B:300:GLU:HB2	2.07	0.55	
2:B:345:PRO:HB2	2:B:346:PHE:HD1	1.72	0.55	
2:B:348:ASN:C	2:B:349:LEU:HD23	2.26	0.55	
1:A:235:HIS:HD2	1:A:238:LYS:HG3	1.70	0.55	
2:B:282:LEU:HD13	2:B:296:THR:OG1	2.06	0.55	
2:B:23:GLN:NE2	2:B:24:TRP:O	2.40	0.55	
2:B:213:GLY:O	2:B:215:THR:N	2.40	0.55	
1:A:84:THR:HG23	1:A:124:PHE:CZ	2.42	0.54	
1:A:399:GLU:OE1	1:A:402:TRP:NE1	2.39	0.54	
1:A:496:VAL:HG12	1:A:496:VAL:O	2.06	0.54	
1:A:435:VAL:CG2	2:B:290:THR:HG21	2.33	0.54	
1:A:344:GLU:HG3	1:A:345:PRO:HD2	1.88	0.54	
1:A:96:HIS:NE2	1:A:350:LYS:HD2	2.23	0.54	
1:A:277:ARG:HH11	1:A:334:GLN:HB2	1.73	0.54	
1:A:194:GLU:O	1:A:196:GLY:N	2.41	0.54	
1:A:317:VAL:HG13	1:A:349:LEU:HD23	1.90 0.54		
1:A:325:LEU:HD22	1:A:341:ILE:CG2	2.38	0.54	
1:A:501:TYR:CE1	1:A:505:ILE:HD11	2.43	0.54	
1:A:515:SER:O	1:A:517:LEU:N	2.41	0.54	
2:B:66:LYS:NZ	2:B:218:ASP:HB2	2.23	0.54	
2:B:315:HIS:C	2:B:317:VAL:H	2.11	0.54	
1:A:162:SER:O	1:A:166:LYS:HG3	2.08	0.54	
1:A:298:GLU:CD	1:A:298:GLU:N	2.60	0.54	
1:A:368:LEU:O	1:A:372:VAL:HG23	2.07	0.54	
1:A:427:TYR:OH	1:A:509:GLN:HA	2.09	0.54	
2:B:261:VAL:HG21	2:B:283:LEU:HD11	1.90	0.53	
2:B:274:ILE:HG22	2:B:274:ILE:O	2.07	0.53	
1:A:372:VAL:HG11	1:A:411:ILE:HG23	1.90	0.53	
1:A:73:LYS:HG2	1:A:74:LEU:N	2.23	0.53	
2:B:80:LEU:HD12	2:B:80:LEU:O	2.08	0.53	
2:B:209:LEU:HB3	2:B:215:THR:OG1	2.08	0.53	
2:B:241:VAL:CG2	2:B:242:GLN:H	2.19	0.53	



Interatomic Clash				
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:B:337:TRP:HE1	2:B:367:GLN:HG2	1.73	0.53	
1:A:23:GLN:HE21	1:A:24:TRP:H	1.57	0.53	
1:A:234:LEU:HD22	4:A:562:357:H111	1.90	0.53	
1:A:301:LEU:O	1:A:305:GLU:HG3	2.09	0.53	
1:A:362:THR:CG2	1:A:363:ASN:N	2.49	0.53	
1:A:398:TRP:CZ3	1:A:411:ILE:HD11	2.43	0.53	
2:B:22:LYS:HD3	2:B:24:TRP:CZ3	2.42	0.53	
2:B:343:GLN:O	2:B:344:GLU:HG2	2.08	0.53	
2:B:329:ILE:HD11	2:B:375:ILE:HD12	1.91	0.53	
1:A:94:ILE:HG23	1:A:229:TRP:CH2	2.44	0.52	
2:B:277:ARG:H	2:B:277:ARG:HD2	1.67	0.52	
1:A:115:TYR:HD1	1:A:115:TYR:H	1.57	0.52	
1:A:54:ASN:CB	1:A:55:PRO:CD	2.77	0.52	
1:A:112:GLY:C	1:A:114:ALA:H	2.13	0.52	
2:B:10:VAL:HG13	2:B:88:TRP:CZ2	2.43	0.52	
2:B:249:LYS:HG2	2:B:252:TRP:CE2	2.44	0.52	
1:A:277:ARG:HH11	1:A:334:GLN:CB	2.22	0.52	
2:B:183:TYR:HE2	2:B:184:MET:SD	2.32	0.52	
1:A:260:LEU:HD21	1:A:303:LEU:HD13	1.92	0.52	
1:A:269:GLN:O	1:A:351:THR:N	2.31	0.52	
1:A:425:LEU:HD13	1:A:428:GLN:OE1	2.10	0.52	
2:B:282:LEU:HG	2:B:293:ILE:CD1	2.39	0.52	
2:B:388:LYS:NZ	2:B:415:GLU:OE1	2.43	0.52	
2:B:168:LEU:HD13	2:B:180:ILE:HD12	1.91	0.52	
2:B:395:LYS:O	2:B:399:GLU:HG3	2.10	0.52	
1:A:130:PHE:CZ	1:A:144:TYR:HB2	2.44	0.52	
1:A:233:GLU:OE1	1:A:235:HIS:NE2	2.41	0.52	
1:A:517:LEU:O	1:A:520:GLN:N	2.43	0.52	
2:B:326:ILE:CG2	2:B:342:TYR:CE1	2.93	0.52	
1:A:296:THR:CG2	1:A:297:GLU:N	2.73	0.51	
2:B:125:ARG:C	2:B:127:TYR:H	2.13	0.51	
2:B:276:VAL:HG22	2:B:276:VAL:O	2.09	0.51	
2:B:90:VAL:HG12	2:B:91:GLN:N	2.25	0.51	
2:B:194:GLU:O	2:B:195:ILE:C	2.48	0.51	
2:B:50:ILE:HG21	2:B:54:ASN:HD22	1.75	0.51	
2:B:314:VAL:HB	2:B:317:VAL:HG21	1.92	0.51	
1:A:516:GLU:HA	1:A:519:ASN:HD22	1.74	0.51	
1:A:62:ALA:O	1:A:63:ILE:HD13	2.10	0.51	
1:A:411:ILE:O	1:A:412:PRO:O	2.27	0.51	
1:A:164:MET:HE3	1:A:187:LEU:HD21	1.93	0.51	
2:B:115:TYR:O	2:B:117:SER:N	2.43	0.51	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:B:183:TYR:CD2	2:B:184:MET:HG3	2.46	0.51	
2:B:278:GLN:HE21	2:B:278:GLN:HA	1.75	0.51	
1:A:542:ILE:HG12	1:A:546:GLU:HA	1.93	0.51	
1:A:54:ASN:CB	1:A:55:PRO:HD3	2.19	0.51	
1:A:424:LYS:HD3	1:A:426:TRP:CH2	2.46	0.51	
2:B:320:ASP:OD1	2:B:322:SER:OG	2.20	0.51	
1:A:134:SER:CB	1:A:140:PRO:HD3	2.41	0.51	
2:B:276:VAL:N	2:B:277:ARG:NH1	2.48	0.51	
1:A:153:TRP:O	1:A:156:SER:HB2	2.11	0.50	
1:A:358:ARG:O	1:A:360:ALA:N	2.43	0.50	
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.93	0.50	
1:A:116:PHE:O	1:A:148:VAL:HG11	2.11	0.50	
1:A:233:GLU:OE2	1:A:242:GLN:HG3	2.11	0.50	
1:A:483:TYR:HB2	1:A:521:ILE:HG12	1.92	0.50	
2:B:245:VAL:HG22	2:B:246:LEU:O	2.11	0.50	
1:A:3:SER:CB	1:A:5:ILE:HG13	2.37	0.50	
1:A:276:VAL:O	1:A:276:VAL:CG1	2.60	0.50	
1:A:460:ASN:C	1:A:462:GLY:H	2.14	0.50	
2:B:174:GLN:O	2:B:176:PRO:CD	2.57	0.50	
2:B:332:GLN:HB3	2:B:336:GLN:O	2.11	0.50	
2:B:94:ILE:HD11	2:B:158:ALA:HA	1.92	0.50	
2:B:314:VAL:HB	2:B:317:VAL:CG2	2.42	0.50	
1:A:279:LEU:HD12	1:A:279:LEU:N	2.24 0.50		
2:B:151:GLN:O	2:B:153:TRP:N	2.45	0.50	
1:A:77:PHE:O	1:A:80:LEU:HB3	2.12	0.50	
1:A:108:VAL:HG13	1:A:227:PHE:CE1	2.47	0.50	
1:A:113:ASP:O	1:A:114:ALA:C	2.50	0.50	
1:A:167:ILE:O	1:A:170:PRO:HD2	2.12	0.50	
1:A:183:TYR:C	1:A:183:TYR:CD2	2.85	0.50	
1:A:240:THR:CG2	1:A:241:VAL:H	2.08	0.50	
2:B:376:THR:O	2:B:379:SER:N	2.45	0.50	
1:A:275:LYS:O	1:A:276:VAL:HG23	2.12	0.50	
2:B:249:LYS:HB3	2:B:249:LYS:NZ	2.27	0.50	
2:B:66:LYS:NZ	2:B:218:ASP:CB	2.75	0.50	
2:B:274:ILE:HG23	2:B:306:ASN:OD1	2.11	0.50	
2:B:406:TRP:CZ2	2:B:412:PRO:HD2	2.47	0.50	
1:A:434:ILE:HG21	1:A:492:GLU:CG	2.41	0.49	
2:B:132:ILE:HB	2:B:142:ILE:HG13	1.94	0.49	
2:B:252:TRP:CZ3	2:B:260:LEU:HD22	2.47	0.49	
2:B:315:HIS:O	2:B:317:VAL:N	2.45	0.49	
2:B:345:PRO:HB2	2:B:346:PHE:CD1	2.46	0.49	



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:57:ASN:CG	1:A:58:THR:H	2.13	0.49
1:A:98:ALA:HB2	1:A:350:LYS:HG3	1.93	0.49
2:B:118:VAL:HB	2:B:149:LEU:HD13	1.93	0.49
1:A:2:ILE:HG22	1:A:3:SER:N	2.27	0.49
1:A:65:LYS:HE2	1:A:66:LYS:N	2.28	0.49
1:A:195:ILE:O	1:A:199:ARG:HD3	2.11	0.49
1:A:226:PRO:HB3	1:A:235:HIS:ND1	2.27	0.49
1:A:238:LYS:HE2	1:A:315:HIS:CB	2.43	0.49
1:A:286:THR:HG22	1:A:287:LYS:N	2.28	0.49
2:B:115:TYR:C	2:B:117:SER:H	2.15	0.49
1:A:138:GLU:O	1:A:140:PRO:HD3	2.13	0.49
1:A:92:LEU:CG	1:A:93:GLY:N	2.70	0.49
2:B:198:HIS:O	2:B:201:LYS:N	2.46	0.49
2:B:235:HIS:O	2:B:238:LYS:HG2	2.13	0.49
2:B:28:GLU:HA	2:B:31:ILE:HD12	1.94	0.49
1:A:58:THR:HG22	1:A:76:ASP:O	2.12	0.49
1:A:460:ASN:HA	2:B:286:THR:O	2.13	0.49
1:A:246:LEU:HD23	1:A:246:LEU:H	1.78	0.49
2:B:282:LEU:HG	2:B:293:ILE:HD11	1.94	0.49
1:A:175:ASN:N	1:A:176:PRO:HD3	2.27	0.48
1:A:317:VAL:HG22	1:A:318:TYR:H	1.77	0.48
1:A:233:GLU:CD	1:A:242:GLN:NE2	2.61	0.48
1:A:413:GLU:OE2	1:A:413:GLU:HA	2.12	0.48
1:A:482:ILE:O	1:A:483:TYR:C	2.50	0.48
1:A:542:ILE:O	1:A:543:GLY:O	2.31	0.48
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.95	0.48
1:A:542:ILE:O	1:A:542:ILE:HG23	2.13	0.48
2:B:84:THR:O	2:B:86:ASP:N	2.46	0.48
2:B:139:THR:HB	2:B:140:PRO:CD	2.34	0.48
1:A:242:GLN:CB	1:A:243:PRO:CD	2.87	0.48
2:B:100:LEU:HD11	2:B:106:VAL:HG13	1.93	0.48
1:A:223:LYS:C	1:A:225:PRO:HD3	2.34	0.48
1:A:366:LYS:O	1:A:370:GLU:HG3	2.13	0.48
2:B:65:LYS:HD2	2:B:72:ARG:HG3	1.95	0.48
2:B:279:LEU:HA	2:B:299:ALA:CB	2.42	0.48
1:A:249:LYS:HG3	1:A:250:ASP:OD2	2.14	0.48
1:A:253:THR:HG23	1:A:256:ASP:H	1.79	0.48
1:A:340:GLN:HA	1:A:351:THR:HA	1.96	0.48
1:A:402:TRP:CD2	1:A:403:THR:N	2.81	0.48
1:A:457:TYR:C	1:A:457:TYR:HD2	2.15	0.48
1:A:58:THR:CG2	1:A:59:PRO:HD2	2.44	0.48



		Interatomic	
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:296:THR:HG22	1:A:297:GLU:H	1.76	0.48
2:B:279:LEU:CD1	2:B:299:ALA:HB1	2.43	0.48
1:A:90:VAL:HG23	1:A:91:GLN:N	2.22	0.48
1:A:442:VAL:HG12	1:A:457:TYR:HB3	1.95	0.48
2:B:260:LEU:HG	2:B:264:LEU:HD12	1.94	0.48
1:A:163:SER:HA	1:A:166:LYS:CE	2.42	0.48
2:B:28:GLU:O	2:B:32:LYS:HG3	2.13	0.48
2:B:425:LEU:HA	2:B:427:TYR:HD1	1.79	0.48
1:A:178:ILE:HD11	1:A:201:LYS:HG3	1.96	0.47
1:A:345:PRO:HB2	1:A:346:PHE:CD1	2.49	0.47
1:A:451:LYS:HE3	1:A:471:ASN:HD22	1.78	0.47
1:A:501:TYR:CZ	1:A:505:ILE:HD11	2.49	0.47
2:B:284:ARG:NH1	2:B:284:ARG:CG	2.67	0.47
1:A:234:LEU:HB3	4:A:562:357:H111	1.96	0.47
1:A:270:ILE:O	1:A:270:ILE:HG13	2.14	0.47
1:A:521:ILE:O	1:A:521:ILE:HG22	2.14	0.47
2:B:213:GLY:C	2:B:215:THR:N	2.67	0.47
2:B:281:LYS:HG2	2:B:284:ARG:NH2	2.29	0.47
1:A:179:VAL:HG23	1:A:179:VAL:O	2.15	0.47
1:A:384:GLY:O	2:B:27:THR:HG23	2.14	0.47
2:B:167:ILE:O	2:B:170:PRO:HD2	2.14	0.47
1:A:17:ASP:OD2	1:A:56:TYR:HE2	1.96	0.47
1:A:178:ILE:CG2	1:A:189:VAL:HG13	2.44	0.47
1:A:278:GLN:HG3	1:A:298:GLU:HB3	1.96	0.47
1:A:406:TRP:CZ2	2:B:419:THR:HB	2.49	0.47
2:B:210:LEU:HA	2:B:215:THR:O	2.15	0.47
1:A:10:VAL:HG12	1:A:11:LYS:N	2.29	0.47
1:A:95:PRO:HA	2:B:136:ASN:O	2.13	0.47
1:A:108:VAL:CG1	1:A:227:PHE:CE1	2.98	0.47
1:A:335:GLY:HA2	1:A:367:GLN:HE22	1.80	0.47
1:A:493:VAL:CG2	1:A:494:ASN:N	2.77	0.47
2:B:194:GLU:O	2:B:197:GLN:N	2.47	0.47
2:B:131:THR:CG2	2:B:141:GLY:HA3	2.45	0.47
1:A:46:LYS:HD2	1:A:46:LYS:N	2.29	0.47
1:A:56:TYR:CD1	1:A:56:TYR:N	2.72	0.47
1:A:88:TRP:HA	1:A:88:TRP:CE3	2.50	0.47
1:A:130:PHE:HE1	1:A:144:TYR:HB2	1.74	0.47
1:A:455:ALA:HB2	1:A:469:LEU:HD11	1.96	0.47
1:A:92:LEU:HG	1:A:93:GLY:H	1.80	0.47
1:A:218:ASP:O	1:A:220:LYS:N	2.47	0.47
2:B:108:VAL:HG22	2:B:188:TYR:CD2	2.50	0.47



		Interatomic	Clash	
Atom-1	Atom-1 Atom-2		overlap (Å)	
1:A:277:ARG:O	1:A:281:LYS:HB2	2.14	0.46	
1:A:296:THR:CG2	1:A:297:GLU:H	2.27	0.46	
1:A:326:ILE:HD12	1:A:326:ILE:N	2.30	0.46	
2:B:296:THR:HG23	2:B:297:GLU:H	1.80	0.46	
1:A:2:ILE:CG2	1:A:3:SER:N	2.78	0.46	
1:A:235:HIS:HB3	1:A:236:PRO:HD2	1.97	0.46	
1:A:12:LEU:O	1:A:13:LYS:C	2.54	0.46	
1:A:115:TYR:HE2	1:A:156:SER:HB3	1.80	0.46	
1:A:294:PRO:O	1:A:296:THR:N	2.48	0.46	
2:B:261:VAL:HG21	2:B:283:LEU:CD1	2.45	0.46	
2:B:314:VAL:CG1	2:B:315:HIS:N	2.78	0.46	
1:A:59:PRO:HB2	1:A:61:PHE:HE1	1.80	0.46	
1:A:79:GLU:O	1:A:83:ARG:NH1	2.49	0.46	
1:A:161:GLN:NE2	1:A:161:GLN:C	2.69	0.46	
1:A:3:SER:OG	1:A:212:TRP:O	2.34	0.46	
1:A:175:ASN:O	1:A:177:ASP:N	2.46	0.46	
1:A:270:ILE:HD11	1:A:315:HIS:O	2.16	0.46	
1:A:547:GLN:CA	1:A:547:GLN:HE21	2.28	0.46	
2:B:11:LYS:N	2:B:11:LYS:CD	2.75	0.46	
2:B:326:ILE:HG21	2:B:342:TYR:HE1	1.81	0.46	
1:A:83:ARG:HG3	1:A:83:ARG:NH1	2.28	0.46	
1:A:206:ARG:HG3	1:A:216:THR:OG1	2.16	0.46	
1:A:381:VAL:O	2:B:136:ASN:HA	2.16	0.46	
1:A:277:ARG:NH2	1:A:281:LYS:HE2	2.31 0.46		
1:A:354:TYR:CD1	1:A:374:LYS:HD2	2.39 0.46		
2:B:149:LEU:HB3	2:B:156:SER:HB3	1.98	0.46	
1:A:27:THR:O	1:A:31:ILE:N	2.47	0.46	
1:A:283:LEU:O	1:A:284:ARG:C	2.54	0.46	
1:A:498:ASP:HA	1:A:536:VAL:O	2.15	0.46	
2:B:30:LYS:HB3	2:B:62:ALA:HB3	1.98	0.46	
1:A:279:LEU:HD21	1:A:303:LEU:HD13	1.98	0.46	
1:A:369:THR:HG1	1:A:398:TRP:HZ3	1.63	0.46	
2:B:365:VAL:O	2:B:367:GLN:N	2.49	0.46	
1:A:253:THR:O	1:A:257:ILE:HG13	2.16	0.45	
2:B:314:VAL:CG1	2:B:315:HIS:H	2.24	0.45	
2:B:330:GLN:HG2	2:B:338:THR:OG1	2.16	0.45	
1:A:170:PRO:HG2	1:A:171:PHE:H	1.80	0.45	
1:A:435:VAL:HG22	2:B:290:THR:CG2	2.34	0.45	
2:B:160:PHE:O	2:B:161:GLN:C	2.54	0.45	
1:A:5:ILE:HD11	1:A:167:ILE:HD11	1.97	0.45	
1:A:175:ASN:C	1:A:177:ASP:H	2.20	0.45	



	louo pugom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.80	0.45
2:B:100:LEU:HD11	2:B:106:VAL:HG11	1.98	0.45
2:B:271:TYR:HA	2:B:272:PRO:HD3	1.79	0.45
2:B:295:LEU:CB	2:B:300:GLU:HG2	2.46	0.45
2:B:374:LYS:HE2	2:B:378:GLU:OE2	2.15	0.45
1:A:12:LEU:O	1:A:13:LYS:O	2.34	0.45
1:A:164:MET:HB3	1:A:182:GLN:HE22	1.82	0.45
1:A:246:LEU:HD12	1:A:303:LEU:HD11	1.99	0.45
1:A:398:TRP:CD1	1:A:399:GLU:N	2.84	0.45
1:A:493:VAL:HG22	1:A:494:ASN:H	1.80	0.45
1:A:3:SER:HB3	1:A:4:PRO:HD2	1.98	0.45
2:B:94:ILE:HA	2:B:95:PRO:HD2	1.75	0.45
2:B:183:TYR:CE2	2:B:184:MET:HG3	2.51	0.45
1:A:189:VAL:HG21	1:A:205:LEU:HD23	1.98	0.45
1:A:511:ASP:CG	1:A:512:LYS:HG2	2.37	0.45
2:B:128:THR:CB	2:B:146:TYR:HB2	2.47	0.45
2:B:193:LEU:HD12	2:B:198:HIS:HA	1.99	0.45
1:A:5:ILE:HD13	1:A:167:ILE:HD11	1.99	0.45
1:A:34:LEU:CB	1:A:132:ILE:HG21	2.47	0.45
1:A:155:GLY:O	1:A:159:ILE:HD12	2.17	0.45
2:B:39:THR:O	2:B:43:LYS:HG3	2.16	0.45
1:A:458:VAL:HG22	1:A:464:GLN:HG2	1.97	0.45
2:B:23:GLN:HG3	2:B:131:THR:O	2.17	0.45
1:A:19:PRO:O	1:A:56:TYR:HB3	2.17	0.45
1:A:216:THR:HB	1:A:217:PRO:HD2	1.99	0.45
1:A:249:LYS:HG3	1:A:250:ASP:N	2.21	0.45
1:A:250:ASP:OD2	1:A:250:ASP:N	2.50	0.45
1:A:394:GLN:O	1:A:396:GLU:N	2.50	0.45
1:A:100:LEU:HD21	4:A:562:357:H8'1	1.99	0.44
2:B:162:SER:O	2:B:164:MET:N	2.49	0.44
1:A:12:LEU:CD1	1:A:127:TYR:CE2	3.01	0.44
1:A:358:ARG:C	1:A:360:ALA:N	2.67	0.44
1:A:17:ASP:CG	1:A:18:GLY:N	2.70	0.44
1:A:122:GLU:O	1:A:125:ARG:HG3	2.18	0.44
2:B:130:PHE:CZ	2:B:144:TYR:HB2	2.52	0.44
1:A:134:SER:CB	1:A:140:PRO:CD	2.96	0.44
1:A:151:GLN:HA	1:A:151:GLN:HE21	1.82	0.44
1:A:405:TYR:O	2:B:331:LYS:HD3	2.18	0.44
1:A:468:PRO:C	1:A:469:LEU:HG	2.37	0.44
2:B:401:TRP:O	2:B:402:TRP:C	2.56	0.44
1:A:130:PHE:CD1	1:A:130:PHE:N	2.86	0.44



		Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
1:A:350:LYS:HB3	1:A:350:LYS:HZ2	1.81	0.44	
1:A:537:PRO:O	1:A:541:GLY:HA3	2.18	0.44	
2:B:124:PHE:O	2:B:125:ARG:C	2.56	0.44	
2:B:369:THR:HA	2:B:398:TRP:HH2	1.83	0.44	
1:A:94:ILE:CG2	1:A:229:TRP:CH2	3.01	0.44	
1:A:189:VAL:HG21	1:A:205:LEU:CD2	2.48	0.44	
1:A:522:ILE:O	1:A:525:LEU:N	2.50	0.44	
2:B:183:TYR:CD2	2:B:183:TYR:C	2.91	0.44	
1:A:12:LEU:HD11	1:A:127:TYR:CD2	2.53	0.44	
2:B:125:ARG:C	2:B:127:TYR:N	2.66	0.44	
1:A:543:GLY:C	1:A:545:ASN:H	2.19	0.44	
2:B:1:PRO:HB2	2:B:2:ILE:H	1.62	0.44	
2:B:164:MET:C	2:B:166:LYS:N	2.70	0.44	
1:A:273:GLY:O	1:A:274:ILE:C	2.55	0.43	
1:A:303:LEU:O	1:A:307:ARG:HG3	2.19	0.43	
1:A:430:GLU:OE1	1:A:530:LYS:HE3	2.18	0.43	
2:B:66:LYS:HZ2	2:B:218:ASP:HB3	1.82	0.43	
2:B:295:LEU:HB2	2:B:300:GLU:HG2	2.00	0.43	
2:B:363:ASN:HB3	2:B:366:LYS:HB3	2.00	0.43	
2:B:214:LEU:HG	2:B:214:LEU:O	2.18	0.43	
2:B:249:LYS:HE2	2:B:252:TRP:CE3	2.53	0.43	
2:B:1:PRO:C	2:B:2:ILE:HG13	2.38	0.43	
2:B:96:HIS:HE1	2:B:381:VAL:O	2.01	0.43	
2:B:423:VAL:HG13	2:B:426:TRP:HE3	1.83 0.43		
1:A:83:ARG:HH11	1:A:83:ARG:CG	2.28 0.43		
1:A:116:PHE:HA	1:A:148:VAL:HG21	2.00	0.43	
1:A:350:LYS:HE3	1:A:378:GLU:OE2	2.18	0.43	
1:A:438:GLU:OE1	1:A:463:ARG:NH2	2.52	0.43	
2:B:91:GLN:HE21	2:B:91:GLN:CA	2.32	0.43	
2:B:257:ILE:O	2:B:260:LEU:HB3	2.18	0.43	
2:B:305:GLU:OE2	2:B:309:ILE:HD11	2.18	0.43	
1:A:193:LEU:HB3	1:A:197:GLN:HG3	2.01	0.43	
1:A:399:GLU:HG3	1:A:402:TRP:HE1	1.83	0.43	
1:A:170:PRO:HG2	1:A:208:HIS:CE1	2.53	0.43	
2:B:241:VAL:CG2	2:B:242:GLN:N	2.76	0.43	
2:B:331:LYS:HA	2:B:337:TRP:CE3	2.54	0.43	
1:A:402:TRP:CZ3	1:A:403:THR:HA	2.54	0.43	
2:B:151:GLN:C	2:B:153:TRP:N	2.71	0.43	
2:B:153:TRP:O	2:B:155:GLY:N	2.43	0.43	
2:B:358:ARG:O	2:B:362:THR:CB	2.67	0.43	
2:B:379:SER:OG	2:B:387:PRO:HD3	2.19	0.43	



		Interatomic	Clash
Atom-1	tom-1 Atom-2		overlap (Å)
1:A:86:ASP:HA	1:A:154:LYS:HZ1	1.84	0.43
1:A:100:LEU:HD11	4:A:562:357:C8'	2.49	0.43
1:A:115:TYR:CE2	1:A:156:SER:HB3	2.54	0.43
1:A:154:LYS:O	1:A:156:SER:N	2.50	0.43
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.54	0.43
1:A:334:GLN:HE21	1:A:334:GLN:HB3	1.68	0.43
2:B:349:LEU:O	2:B:350:LYS:HB2	2.19	0.43
1:A:22:LYS:HD2	1:A:22:LYS:HA	1.69	0.43
1:A:116:PHE:HA	1:A:148:VAL:CG2	2.49	0.43
1:A:257:ILE:O	1:A:261:VAL:HG23	2.19	0.43
1:A:277:ARG:HH21	1:A:281:LYS:HE2	1.84	0.43
2:B:426:TRP:O	2:B:426:TRP:HD1	2.01	0.43
1:A:514:GLU:OE1	1:A:514:GLU:N	2.51	0.42
1:A:543:GLY:C	1:A:545:ASN:N	2.73	0.42
2:B:219:LYS:HB3	2:B:219:LYS:HZ3	1.84	0.42
1:A:248:GLU:HB3	1:A:307:ARG:NH2	2.34	0.42
2:B:398:TRP:O	2:B:402:TRP:HD1	2.01	0.42
1:A:138:GLU:O	1:A:138:GLU:CG	2.64	0.42
2:B:18:GLY:HA3	2:B:127:TYR:CD1	2.54	0.42
2:B:305:GLU:O	2:B:309:ILE:HG13	2.19	0.42
1:A:69:THR:O	1:A:69:THR:HG22	2.19	0.42
1:A:201:LYS:CA	1:A:204:GLU:HG3	2.50	0.42
2:B:249:LYS:HG2	2:B:252:TRP:CZ2	2.54	0.42
2:B:376:THR:O	2:B:377:THR:C	2.57	0.42
2:B:418:ASN:O	2:B:419:THR:HB	2.18 0.42	
1:A:540:LYS:HE3	2:B:265:ASN:ND2	2.32	0.42
2:B:306:ASN:HD22	2:B:309:ILE:CD1	2.28	0.42
2:B:332:GLN:CB	2:B:336:GLN:O	2.67	0.42
2:B:346:PHE:CD1	2:B:346:PHE:N	2.87	0.42
1:A:3:SER:HB2	1:A:5:ILE:HD12	2.00	0.42
1:A:34:LEU:HB2	1:A:132:ILE:HG21	2.01	0.42
1:A:507:GLN:O	1:A:509:GLN:HG3	2.19	0.42
2:B:353:LYS:O	2:B:353:LYS:HG2	2.20	0.42
1:A:114:ALA:HB1	1:A:160:PHE:CE1	2.55	0.42
1:A:171:PHE:C	1:A:173:LYS:N	2.73	0.42
1:A:441:TYR:CD2	1:A:544:GLY:HA3	2.53	0.42
2:B:388:LYS:HA	2:B:413:GLU:O	2.19	0.42
1:A:94:ILE:HG23	1:A:229:TRP:CZ2	2.55	0.42
2:B:43:LYS:C	2:B:45:GLY:H	2.20	0.42
2:B:236:PRO:HA	2:B:239:TRP:CE2	2.55	0.42
1:A:233:GLU:OE2	1:A:242:GLN:CG	2.68	0.42



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:91:GLN:O	1:A:92:LEU:C	2.58	0.41	
1:A:122:GLU:CD	1:A:125:ARG:HH11	2.24	0.41	
1:A:325:LEU:HD22	1:A:341:ILE:HG21	2.02	0.41	
2:B:181:TYR:CD1	2:B:182:GLN:N	2.88	0.41	
1:A:126:LYS:HB3	1:A:126:LYS:HZ3	1.82	0.41	
2:B:278:GLN:HE21	2:B:278:GLN:CA	2.32	0.41	
2:B:340:GLN:CG	2:B:426:TRP:CZ2	3.00	0.41	
1:A:120:LEU:O	1:A:121:ASP:C	2.58	0.41	
1:A:260:LEU:HD11	1:A:303:LEU:HD11	2.01	0.41	
1:A:277:ARG:NH1	1:A:334:GLN:HB2	2.35	0.41	
1:A:515:SER:O	1:A:516:GLU:C	2.59	0.41	
2:B:28:GLU:HG3	2:B:135:ILE:HD11	2.02	0.41	
2:B:118:VAL:O	2:B:149:LEU:HD12	2.19	0.41	
2:B:206:ARG:HG3	2:B:206:ARG:HH11	1.85	0.41	
2:B:275:LYS:HG2	2:B:277:ARG:HD3	2.02	0.41	
1:A:50:ILE:O	1:A:143:ARG:HB3	2.21	0.41	
1:A:83:ARG:NH1	1:A:83:ARG:CG	2.83	0.41	
1:A:334:GLN:H	1:A:334:GLN:HG2	1.65	0.41	
2:B:165:THR:O	2:B:169:GLU:HB2	2.20	0.41	
2:B:178:ILE:HD11	2:B:201:LYS:CG	2.50	0.41	
2:B:254:VAL:O	2:B:258:GLN:HG3	2.20	0.41	
1:A:88:TRP:O	1:A:89:GLU:C	2.59	0.41	
1:A:249:LYS:HG2	1:A:251:SER:OG	2.21	0.41	
2:B:44:GLU:OE1	2:B:46:LYS:HE3	2.20	0.41	
2:B:149:LEU:HA	2:B:150:PRO:HD3	1.87 0.41		
2:B:241:VAL:CG1	2:B:243:PRO:HD3	2.43	0.41	
2:B:253:THR:OG1	2:B:256:ASP:OD2	2.24	0.41	
1:A:55:PRO:HB2	1:A:56:TYR:H	1.54	0.41	
1:A:271:TYR:HA	1:A:272:PRO:HD3	1.88	0.41	
2:B:392:PRO:HA	2:B:417:VAL:HG22	2.03	0.41	
1:A:66:LYS:O	1:A:68:SER:N	2.54	0.41	
1:A:183:TYR:CD2	1:A:184:MET:HG3	2.55	0.41	
1:A:183:TYR:CE1	1:A:229:TRP:NE1	2.89	0.41	
1:A:261:VAL:O	1:A:262:GLY:C	2.59	0.41	
2:B:188:TYR:CD1	2:B:188:TYR:N	2.88	0.41	
2:B:339:TYR:C	2:B:340:GLN:OE1	2.59	0.41	
2:B:164:MET:O	2:B:166:LYS:N	2.53	0.41	
2:B:206:ARG:CZ	2:B:206:ARG:HB3	2.51	0.41	
1:A:10:VAL:HG11	1:A:153:TRP:HZ2	1.84	0.41	
1:A:509:GLN:N	1:A:510:PRO:CD	2.81	0.41	
1:A:516:GLU:HG2	1:A:517:LEU:N	2.35	0.41	



A + a 1	A 4 ama 2	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:B:246:LEU:HD12	2:B:307:ARG:HG2	2.02	0.41	
2:B:345:PRO:C	2:B:346:PHE:CD1	2.95	0.41	
1:A:132:ILE:HD11	1:A:142:ILE:HG21	2.02	0.41	
1:A:280:SER:C	1:A:282:LEU:N	2.74	0.41	
1:A:402:TRP:CE3	1:A:402:TRP:C	2.94	0.41	
1:A:416:PHE:CZ	1:A:418:ASN:HA	2.56	0.41	
2:B:160:PHE:O	2:B:162:SER:N	2.54	0.41	
1:A:56:TYR:O	1:A:143:ARG:NH2	2.53	0.40	
1:A:173:LYS:O	1:A:176:PRO:HD3	2.20	0.40	
2:B:319:TYR:O	2:B:321:PRO:HD3	2.22	0.40	
1:A:60:VAL:O	1:A:61:PHE:HD1	2.02	0.40	
1:A:126:LYS:HB3	1:A:126:LYS:HZ2	1.85	0.40	
1:A:197:GLN:HA	1:A:200:THR:OG1	2.21	0.40	
1:A:402:TRP:CE3	1:A:403:THR:N	2.89	0.40	
2:B:2:ILE:O	2:B:2:ILE:HG22	2.21	0.40	
2:B:183:TYR:CD1	2:B:380:ILE:HG23	2.57	0.40	
1:A:27:THR:HG23	1:A:27:THR:O	2.21	0.40	
1:A:263:LYS:HB2	1:A:263:LYS:HE3	1.80	0.40	
1:A:275:LYS:O	1:A:276:VAL:CG2	2.69	0.40	
1:A:317:VAL:HG22	1:A:318:TYR:N	2.36	0.40	
2:B:151:GLN:C	2:B:153:TRP:H	2.24	0.40	
2:B:205:LEU:O	2:B:206:ARG:C	2.58	0.40	
2:B:221:HIS:HD2	2:B:229:TRP:CB	2.34	0.40	
2:B:253:THR:CG2	2:B:292:VAL:HG22	2.44	0.40	
2:B:255:ASN:O	2:B:259:LYS:HG3	2.21	0.40	
2:B:426:TRP:O	2:B:426:TRP:CD1	2.74	0.40	
1:A:103:LYS:HE2	1:A:179:VAL:HG21	2.02	0.40	
1:A:344:GLU:HG3	1:A:345:PRO:CD	2.51	0.40	
2:B:155:GLY:O	2:B:159:ILE:HG13	2.21	0.40	
2:B:340:GLN:HB3	2:B:348:ASN:HD22	1.87	0.40	
2:B:423:VAL:HG13	2:B:426:TRP:CE3	2.55	0.40	
1:A:458:VAL:HG13	1:A:464:GLN:HG2	2.02	0.40	
2:B:167:ILE:HA	2:B:212:TRP:CE3	2.57	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	А	550/560~(98%)	414 (75%)	100 (18%)	36~(6%)	1 5
2	В	425/430 (99%)	313 (74%)	75 (18%)	37 (9%)	1 3
All	All	975/990 (98%)	727 (75%)	175 (18%)	73 (8%)	1 4

All (73) Ramachandran outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	28	GLU
1	А	90	VAL
1	А	114	ALA
1	А	242	GLN
1	А	357	MET
1	А	491	LEU
1	А	516	GLU
2	В	116	PHE
2	В	126	LYS
2	В	195	ILE
2	В	220	LYS
2	В	421	PRO
1	А	66	LYS
1	А	195	ILE
1	А	276	VAL
1	А	295	LEU
1	А	296	THR
1	А	412	PRO
1	A	543	GLY
2	В	12	LEU
2	В	18	GLY
2	В	67	ASP
2	В	85	GLN
2	В	103	LYS
2	В	154	LYS



\mathbf{Mol}	Chain	Res	Type
2	В	163	SER
2	В	174	GLN
2	В	214	LEU
2	В	284	ARG
2	В	296	THR
2	В	314	VAL
2	В	316	GLY
2	В	366	LYS
2	В	376	THR
2	В	377	THR
1	А	92	LEU
1	А	151	GLN
1	А	220	LYS
1	А	289	LEU
1	А	395	LYS
1	А	528	LYS
2	В	161	GLN
2	В	240	THR
2	В	272	PRO
2	В	355	ALA
1	А	16	MET
1	А	54	ASN
1	А	70	LYS
1	А	503	LEU
1	А	538	ALA
2	В	2	ILE
2	В	68	SER
1	А	140	PRO
1	А	241	VAL
1	А	359	GLY
2	В	176	PRO
2	В	345	PRO
1	А	176	PRO
1	А	309	ILE
2	В	111	VAL
2	В	313	PRO
2	В	412	PRO
2	В	419	THR
1	А	52	PRO
1	А	155	GLY
1	А	243	PRO
1	А	274	ILE



Continued from previous page...

Mol	Chain	Res	Type
2	В	231	GLY
1	А	4	PRO
1	А	13	LYS
2	В	217	PRO
2	В	225	PRO
2	В	241	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	477/500~(95%)	418 (88%)	59~(12%)	4	18	
2	В	375/392~(96%)	337~(90%)	38 (10%)	7	26	
All	All	852/892~(96%)	755~(89%)	97 (11%)	5	21	

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	6	GLU
1	А	39	THR
1	А	46	LYS
1	А	55	PRO
1	А	56	TYR
1	А	65	LYS
1	А	76	ASP
1	А	84	THR
1	А	92	LEU
1	А	126	LYS
1	А	130	PHE
1	А	131	THR
1	А	132	ILE
1	А	143	ARG
1	А	156	SER
1	А	161	GLN
1	А	164	MET



Mol	Chain	Res	Type
1	А	177	ASP
1	А	183	TYR
1	А	184	MET
1	А	199	ARG
1	А	203	GLU
1	А	217	PRO
1	А	218	ASP
1	А	246	LEU
1	А	250	ASP
1	А	253	THR
1	А	277	ARG
1	А	297	GLU
1	А	334	GLN
1	А	344	GLU
1	А	350	LYS
1	А	361	HIS
1	А	364	ASP
1	А	367	GLN
1	А	387	PRO
1	А	397	THR
1	А	399	GLU
1	А	403	THR
1	А	409	THR
1	А	414	TRP
1	А	418	ASN
1	А	457	TYR
1	А	460	ASN
1	А	492	GLU
1	А	496	VAL
1	А	497	THR
1	A	500	GLN
1	А	507	GLN
1	A	511	ASP
1	А	516	GLU
1	A	523	GLU
1	A	533	LEU
1	А	537	PRO
1	A	545	ASN
1	A	547	GLN
1	A	548	VAL
1	А	549	ASP
1	А	551	LEU



Mol	Chain	Res	Type
2	В	11	LYS
2	В	23	GLN
2	В	50	ILE
2	В	67	ASP
2	В	86	ASP
2	В	91	GLN
2	В	113	ASP
2	В	126	LYS
2	В	142	ILE
2	В	149	LEU
2	В	164	MET
2	В	169	GLU
2	В	176	PRO
2	В	201	LYS
2	В	207	GLN
2	В	211	ARG
2	В	212	TRP
2	В	218	ASP
2	В	219	LYS
2	В	221	HIS
2	В	232	TYR
2	В	249	LYS
2	В	250	ASP
2	В	284	ARG
2	В	290	THR
2	В	297	GLU
2	В	298	GLU
2	В	300	GLU
2	В	307	ARG
2	В	310	LEU
2	В	315	HIS
2	В	324	ASP
2	В	334	GLN
2	В	342	TYR
2	В	348	ASN
2	В	367	GLN
2	В	369	THR
2	В	386	THR

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such side chains are listed below:



Mol	Chain	\mathbf{Res}	Type
1	А	91	GLN
1	А	151	GLN
1	А	161	GLN
1	А	174	GLN
1	А	182	GLN
1	А	197	GLN
1	А	242	GLN
1	А	278	GLN
1	А	332	GLN
1	А	334	GLN
1	А	340	GLN
1	А	367	GLN
1	А	418	ASN
1	А	460	ASN
1	А	471	ASN
1	А	494	ASN
1	А	509	GLN
1	А	519	ASN
1	А	545	ASN
1	А	547	GLN
2	В	54	ASN
2	В	91	GLN
2	В	96	HIS
2	В	161	GLN
2	В	207	GLN
2	В	258	GLN
2	В	278	GLN
2	В	306	ASN
2	В	373	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)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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).

Mal	Type	Chain Bog		Chain	Tink	Bo	ond leng	ths	B	ond ang	les
Moi Type	Unain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2		
4	357	А	562	-	$25,\!25,\!25$	1.64	5 (20%)	26,34,34	1.54	5 (19%)	

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
4	357	А	562	-	-	2/14/14/14	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	А	562	357	C5-C6	2.84	1.43	1.39
4	А	562	357	C2B-C1'	2.68	1.43	1.39
4	А	562	357	C5-C4	2.38	1.44	1.40
4	А	562	357	C3-C4	2.31	1.44	1.40
4	А	562	357	C2B-C3B	2.29	1.42	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	562	357	C6-N1-C2	4.09	123.04	117.92
4	А	562	357	C6'-N1'-C2'	-3.92	104.74	115.42
4	А	562	357	C5'-O4'-C3'	2.81	130.44	112.96
4	А	562	357	C7'-C4-C5	2.36	121.94	119.87
4	А	562	357	C7'-C4-C3	-2.12	118.33	121.76

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	А	562	357	C3'-C2'-N1'-C6'
4	А	562	357	C3'-C2'-N1'-C3

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	562	357	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 then 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, 95^{th} 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	А	552/560~(98%)	-0.00	12 (2%)	62	45	46, 94, 118, 126	0
2	В	427/430~(99%)	0.10	25~(5%)	22	13	38, 80, 120, 127	0
All	All	979/990~(98%)	0.04	37(3%)	40	26	38, 90, 119, 127	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	2	ILE	10.2
2	В	231	GLY	6.6
2	В	3	SER	6.5
1	А	133	PRO	5.7
2	В	225	PRO	5.6
1	А	547	GLN	5.4
2	В	227	PHE	4.2
1	А	551	LEU	4.2
1	А	552	VAL	4.1
2	В	230	MET	4.0
2	В	229	TRP	3.9
2	В	226	PRO	3.7
2	В	360	ALA	3.3
2	В	1	PRO	3.2
2	В	409	THR	3.1
2	В	228	LEU	3.1
2	В	310	LEU	3.1
1	А	68	SER	3.0
2	В	410	TRP	2.9
1	А	134	SER	2.8
1	А	128	THR	2.6
2	В	224	GLU	2.6
2	В	223	LYS	2.6
2	В	408	ALA	2.5



		1	1 0	
Mol	Chain	Res	Type	RSRZ
1	А	548	VAL	2.4
1	А	62	ALA	2.3
1	А	142	ILE	2.3
2	В	299	ALA	2.3
2	В	222	GLN	2.3
2	В	357	MET	2.2
2	В	279	LEU	2.2
1	А	1	PRO	2.2
2	В	359	GLY	2.2
1	А	89	GLU	2.2
2	В	186	ASP	2.1
2	В	295	LEU	2.1
2	В	252	TRP	2.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	MN	А	561	1/1	0.92	0.15	85,85,85,85	0
4	357	А	562	24/24	0.96	0.37	72,79,87,89	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.

