



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 06:01 am BST

PDB ID : 1HNI  
Title : STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN A COMPLEX  
WITH THE NONNUCLEOSIDE INHIBITOR ALPHA-APA R 95845 AT 2.8  
ANGSTROMS RESOLUTION  
Authors : Ding, J.; Das, K.; Arnold, E.  
Deposited on : 1995-02-28  
Resolution : 2.80 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

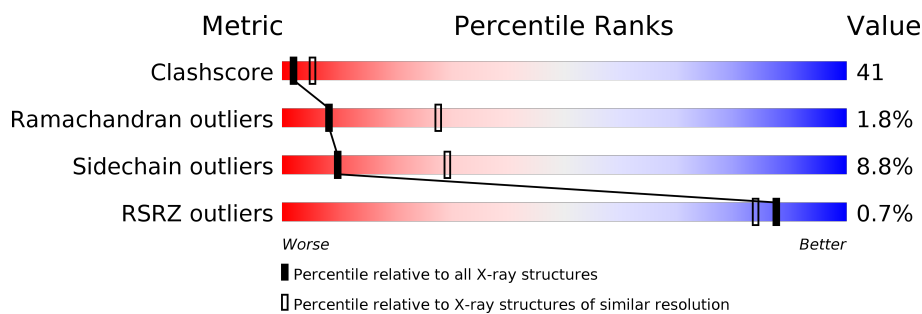
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	558	<div> <div>%</div> <div> <div></div> <div>39%</div> <div>53%</div> <div>7%</div> </div> </div>
2	B	427	<div> <div>%</div> <div> <div></div> <div>41%</div> <div>54%</div> <div>5%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	AAA	A	559	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7819 atoms, of which 4 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 HIV-1 REVERSE TRANSCRIPTASE (SUBUNIT P66).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	558	Total	C	N	O	S	0	0	0
			4368	2825	724	813	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	280	SER	CYS	CONFLICT	UNP P03366

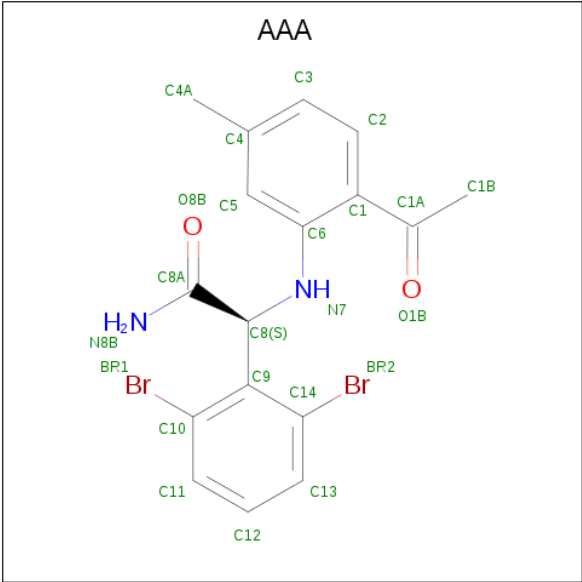
- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE (SUBUNIT P51).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	427	Total	C	N	O	S	0	0	0
			3424	2231	564	624	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	172	ARG	LYS	CONFLICT	UNP P03367
B	280	SER	CYS	CONFLICT	UNP P03367
B	357	THR	MET	CONFLICT	UNP P03367

- Molecule 3 is (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE (three-letter code: AAA) (formula: C<sub>17</sub>H<sub>16</sub>Br<sub>2</sub>N<sub>2</sub>O<sub>2</sub>).

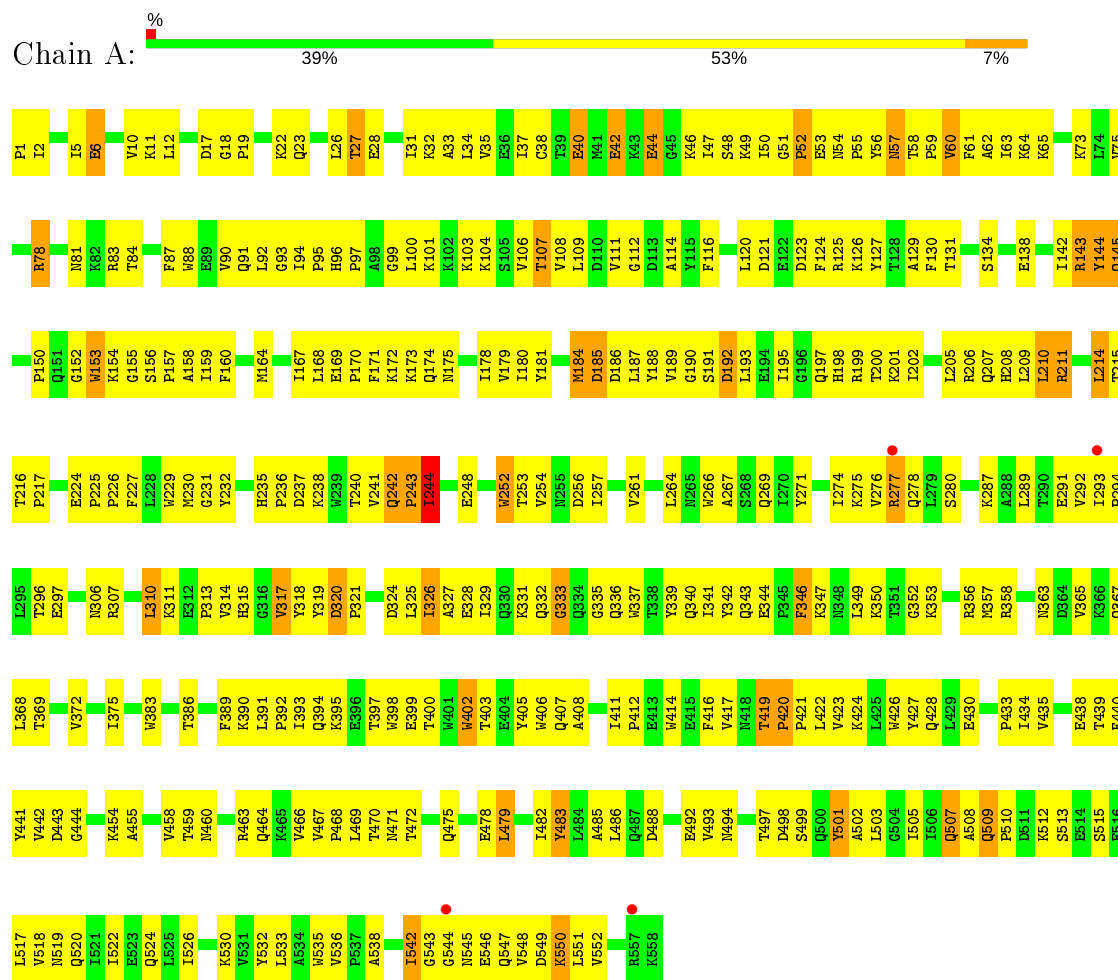


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	Br	C	H	N	O	0	0
			27	2	17	4	2	2		

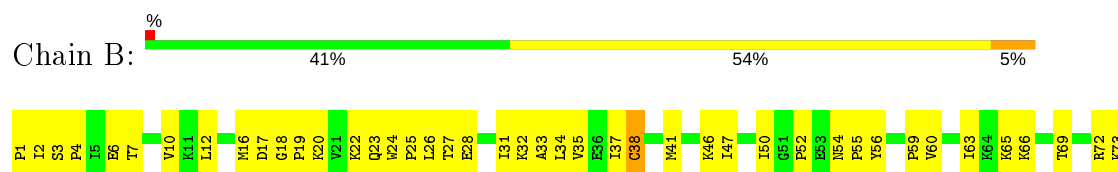
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). 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: HIV-1 REVERSE TRANSCRIPTASE (SUBUNIT P66)



- Molecule 2: HIV-1 REVERSE TRANSCRIPTASE (SUBUNIT P51)



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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	223.30 Å 69.90 Å 106.50 Å 90.00° 105.40° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.80 36.66 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80) 75.7 (36.66-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.61 Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.255 , (Not available) 0.272 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.3	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 596.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.80	EDS
Total number of atoms	7819	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: AAA

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	0.67	0/4483	0.50	1/6115 (0.0%)
2	B	1.41	4/3523 (0.1%)	1.25	8/4800 (0.2%)
All	All	1.06	4/8006 (0.0%)	0.91	9/10915 (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
1	A	0	2
2	B	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	172	ARG	CD-NE	60.74	2.49	1.46
2	B	22	LYS	CE-NZ	28.75	2.21	1.49
2	B	172	ARG	NE-CZ	12.94	1.49	1.33
2	B	22	LYS	CD-CE	-10.15	1.25	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	172	ARG	CD-NE-CZ	-63.77	34.32	123.60
2	B	22	LYS	CD-CE-NZ	-36.13	28.59	111.70
2	B	172	ARG	CG-CD-NE	15.56	144.48	111.80
2	B	78	ARG	NE-CZ-NH2	7.46	124.03	120.30
2	B	83	ARG	NE-CZ-NH2	7.32	123.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	211	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	A	184	MET	CG-SD-CE	5.96	109.74	100.20
2	B	225	PRO	N-CA-CB	5.86	110.34	103.30
2	B	226	PRO	N-CA-CB	5.80	110.25	103.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	483	TYR	Sidechain
1	A	501	TYR	Sidechain
2	B	127	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	A	4368	0	4256	388	0
2	B	3424	0	3372	267	0
3	A	23	4	16	12	0
All	All	7815	4	7644	631	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 41.

All (631) 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:85:GLN:HG3	2:B:154:LYS:CB	1.67	1.25
1:A:420:PRO:HB2	1:A:421:PRO:HD3	1.27	1.11
1:A:112:GLY:HA2	1:A:185:ASP:OD2	1.56	1.04
2:B:59:PRO:HG2	2:B:76:ASP:HB3	1.35	1.02
1:A:536:VAL:HG21	1:A:542:ILE:HG12	1.41	1.01
2:B:85:GLN:CG	2:B:154:LYS:HB3	1.88	1.01
1:A:419:THR:HB	1:A:420:PRO:HD2	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:206:ARG:HG2	2:B:217:PRO:HG2	1.49	0.93
2:B:85:GLN:HG3	2:B:154:LYS:HB3	0.95	0.93
2:B:319:TYR:HA	2:B:343:GLN:HE22	1.33	0.93
1:A:252:TRP:HA	1:A:252:TRP:CE3	2.05	0.91
1:A:420:PRO:CB	1:A:421:PRO:HD3	1.99	0.90
1:A:393:ILE:HB	1:A:423:VAL:HB	1.53	0.90
1:A:252:TRP:HE3	1:A:252:TRP:HA	1.36	0.89
2:B:257:ILE:HG12	2:B:283:LEU:HD23	1.57	0.87
2:B:242:GLN:H	2:B:243:PRO:HD3	1.40	0.87
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.58	0.86
2:B:319:TYR:HA	2:B:343:GLN:NE2	1.90	0.86
1:A:19:PRO:HA	1:A:83:ARG:NH1	1.91	0.86
2:B:120:LEU:HD21	2:B:124:PHE:HD2	1.39	0.86
1:A:242:GLN:H	1:A:243:PRO:HD2	1.41	0.85
1:A:125:ARG:O	1:A:145:GLN:HG3	1.77	0.85
2:B:250:ASP:OD2	2:B:303:LEU:HD22	1.76	0.85
1:A:34:LEU:HD21	1:A:62:ALA:HB2	1.57	0.85
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.58	0.84
1:A:60:VAL:HG22	1:A:130:PHE:HB2	1.56	0.84
1:A:542:ILE:HG23	1:A:545:ASN:HB3	1.59	0.84
1:A:411:ILE:HD13	1:A:414:TRP:HE1	1.38	0.84
1:A:498:ASP:HB2	1:A:538:ALA:HB2	1.60	0.83
2:B:242:GLN:N	2:B:243:PRO:CD	2.42	0.83
1:A:104:LYS:HD2	1:A:192:ASP:HB3	1.61	0.83
1:A:547:GLN:O	1:A:550:LYS:HB3	1.79	0.83
2:B:80:LEU:HD11	2:B:84:THR:HG21	1.59	0.82
1:A:498:ASP:HB3	1:A:545:ASN:HD21	1.45	0.81
1:A:420:PRO:HB2	1:A:421:PRO:CD	2.09	0.81
1:A:186:ASP:HB3	1:A:188:TYR:HE1	1.47	0.80
1:A:459:THR:OG1	1:A:463:ARG:HB3	1.82	0.80
2:B:50:ILE:HG21	2:B:145:GLN:HB2	1.64	0.80
1:A:408:ALA:HB3	2:B:393:ILE:HD12	1.63	0.80
2:B:74:LEU:HD21	2:B:411:ILE:HD11	1.63	0.80
1:A:411:ILE:HD13	1:A:414:TRP:NE1	1.96	0.80
2:B:250:ASP:HB2	2:B:260:LEU:HD22	1.63	0.79
2:B:277:ARG:O	2:B:280:SER:OG	2.00	0.78
2:B:279:LEU:HD13	2:B:299:ALA:HB1	1.67	0.77
2:B:325:LEU:H	2:B:325:LEU:HD23	1.50	0.77
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.65	0.77
1:A:458:VAL:HG22	1:A:464:GLN:HG2	1.67	0.76
1:A:443:ASP:HB3	1:A:548:VAL:HG12	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:THR:HA	1:A:292:VAL:HA	1.68	0.75
2:B:34:LEU:HB3	2:B:132:ILE:HD12	1.69	0.75
1:A:49:LYS:HB3	1:A:144:TYR:HE1	1.51	0.74
1:A:395:LYS:HD2	1:A:414:TRP:CH2	2.20	0.74
2:B:380:ILE:O	2:B:384:GLY:HA2	1.86	0.74
2:B:241:VAL:CG2	2:B:351:THR:OG1	2.35	0.74
1:A:195:ILE:HG22	1:A:199:ARG:HH12	1.53	0.74
2:B:242:GLN:H	2:B:243:PRO:CD	2.00	0.74
2:B:319:TYR:HD1	2:B:343:GLN:HE22	1.35	0.74
1:A:22:LYS:HE2	1:A:143:ARG:HH22	1.53	0.73
2:B:59:PRO:HG2	2:B:76:ASP:CB	2.14	0.73
1:A:483:TYR:CE1	1:A:520:GLN:HB3	2.24	0.73
2:B:369:THR:HG21	2:B:405:TYR:HB2	1.68	0.73
1:A:443:ASP:CB	1:A:548:VAL:HG12	2.18	0.73
2:B:66:LYS:HB2	2:B:69:THR:HG21	1.69	0.73
1:A:398:TRP:CZ2	1:A:411:ILE:HG12	2.24	0.73
2:B:264:LEU:HD22	2:B:274:ILE:CD1	2.19	0.72
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.23	0.72
1:A:275:LYS:HA	1:A:336:GLN:HE22	1.53	0.72
1:A:23:GLN:HB2	1:A:59:PRO:HA	1.71	0.72
1:A:111:VAL:O	1:A:114:ALA:HB2	1.89	0.72
1:A:486:LEU:HD13	1:A:524:GLN:HB2	1.71	0.72
1:A:229:TRP:CD2	3:A:559:AAA:H4A2	2.23	0.71
1:A:240:THR:HG22	1:A:241:VAL:H	1.53	0.71
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.25	0.71
2:B:115:TYR:CE2	2:B:185:ASP:HB3	2.24	0.71
2:B:18:GLY:HA3	2:B:56:TYR:CE1	2.26	0.71
2:B:337:TRP:HB2	2:B:354:TYR:HB3	1.73	0.71
2:B:281:LYS:HA	2:B:284:ARG:HG3	1.71	0.71
1:A:390:LYS:HB3	1:A:417:VAL:HG21	1.71	0.70
1:A:103:LYS:HE3	1:A:179:VAL:HG21	1.73	0.70
2:B:214:LEU:O	2:B:214:LEU:HG	1.92	0.70
1:A:252:TRP:CE3	1:A:256:ASP:OD2	2.44	0.70
3:A:559:AAA:BR2	3:A:559:AAA:O8B	2.65	0.70
2:B:130:PHE:CE1	2:B:144:TYR:HB3	2.28	0.69
2:B:78:ARG:NH1	2:B:411:ILE:HG22	2.07	0.69
1:A:337:TRP:HE1	1:A:367:GLN:NE2	1.90	0.69
1:A:123:ASP:O	1:A:126:LYS:HG2	1.92	0.69
1:A:19:PRO:HA	1:A:83:ARG:HH11	1.56	0.69
1:A:261:VAL:HG13	1:A:276:VAL:CG1	2.21	0.69
1:A:224:GLU:HG2	1:A:226:PRO:HD2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:GLN:H	1:A:243:PRO:CD	2.05	0.69
1:A:229:TRP:CZ2	3:A:559:AAA:H3	2.28	0.68
1:A:275:LYS:HG3	1:A:336:GLN:OE1	1.93	0.68
2:B:264:LEU:HD22	2:B:274:ILE:HD11	1.75	0.68
2:B:3:SER:N	2:B:4:PRO:HD3	2.09	0.68
1:A:34:LEU:CD2	1:A:62:ALA:HB2	2.24	0.68
1:A:5:ILE:HG13	1:A:6:GLU:N	2.09	0.68
1:A:326:ILE:HD12	1:A:342:TYR:CE1	2.29	0.67
2:B:82:LYS:O	2:B:86:ASP:HB2	1.93	0.67
2:B:85:GLN:HG3	2:B:154:LYS:HB2	1.75	0.67
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.76	0.67
2:B:295:LEU:HD12	2:B:300:GLU:CD	2.15	0.67
1:A:543:GLY:HA2	2:B:284:ARG:C	2.15	0.67
1:A:549:ASP:OD1	1:A:550:LYS:N	2.27	0.67
1:A:520:GLN:O	1:A:524:GLN:HG2	1.93	0.67
1:A:99:GLY:HA3	2:B:136:ASN:ND2	2.10	0.67
2:B:103:LYS:HD3	2:B:191:SER:HA	1.76	0.67
2:B:264:LEU:HD13	2:B:274:ILE:HD11	1.77	0.67
2:B:66:LYS:HA	2:B:407:GLN:HE21	1.60	0.67
2:B:368:LEU:O	2:B:372:VAL:HG23	1.94	0.67
2:B:250:ASP:OD2	2:B:303:LEU:HD13	1.95	0.66
2:B:27:THR:O	2:B:31:ILE:HG13	1.96	0.66
1:A:95:PRO:HG2	1:A:181:TYR:OH	1.95	0.66
1:A:101:LYS:HE2	1:A:321:PRO:HG2	1.77	0.66
1:A:328:GLU:HG3	1:A:390:LYS:HB2	1.78	0.66
2:B:80:LEU:O	2:B:84:THR:OG1	2.11	0.66
1:A:60:VAL:CG2	1:A:130:PHE:HB2	2.25	0.66
1:A:168:LEU:HD21	1:A:209:LEU:HD21	1.77	0.65
2:B:50:ILE:HD11	2:B:143:ARG:HB3	1.78	0.65
1:A:90:VAL:HG12	1:A:158:ALA:HA	1.77	0.65
2:B:332:GLN:OE1	2:B:332:GLN:HA	1.96	0.65
1:A:543:GLY:HA2	2:B:284:ARG:O	1.97	0.65
1:A:399:GLU:O	1:A:403:THR:HG23	1.97	0.65
2:B:402:TRP:O	2:B:406:TRP:HB2	1.97	0.65
2:B:120:LEU:HD21	2:B:124:PHE:CD2	2.29	0.65
1:A:51:GLY:HA2	1:A:143:ARG:HB3	1.79	0.64
1:A:408:ALA:HB3	2:B:393:ILE:CD1	2.27	0.64
2:B:297:GLU:O	2:B:301:LEU:HG	1.96	0.64
1:A:368:LEU:HD11	1:A:391:LEU:HD22	1.79	0.64
2:B:343:GLN:HE21	2:B:349:LEU:HD11	1.61	0.64
2:B:180:ILE:HG12	2:B:189:VAL:HG22	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:LEU:N	1:A:214:LEU:HD23	2.11	0.64
1:A:224:GLU:OE2	1:A:226:PRO:HG2	1.98	0.64
1:A:497:THR:HG22	1:A:499:SER:H	1.63	0.64
2:B:24:TRP:CG	2:B:25:PRO:HD2	2.33	0.64
1:A:274:ILE:HA	1:A:306:ASN:ND2	2.13	0.64
2:B:109:LEU:HD13	2:B:187:LEU:HD23	1.80	0.64
1:A:193:LEU:HD13	1:A:197:GLN:HG2	1.80	0.64
1:A:202:ILE:O	1:A:206:ARG:HG3	1.97	0.64
2:B:274:ILE:HG13	2:B:306:ASN:CG	2.17	0.64
1:A:78:ARG:HA	1:A:81:ASN:HB2	1.80	0.64
1:A:26:LEU:HG	1:A:27:THR:H	1.62	0.63
1:A:240:THR:HG22	1:A:241:VAL:N	2.13	0.63
1:A:40:GLU:O	1:A:44:GLU:HG2	1.97	0.63
1:A:411:ILE:O	1:A:411:ILE:HD12	1.98	0.63
2:B:282:LEU:HD11	2:B:293:ILE:HG22	1.79	0.63
1:A:264:LEU:O	1:A:274:ILE:HG21	1.98	0.63
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.79	0.63
2:B:178:ILE:HD11	2:B:201:LYS:HD3	1.80	0.63
2:B:354:TYR:CD2	2:B:371:ALA:HB2	2.34	0.63
1:A:271:TYR:HE1	1:A:314:VAL:N	1.96	0.63
2:B:115:TYR:CD1	2:B:115:TYR:N	2.62	0.63
2:B:34:LEU:HB3	2:B:132:ILE:CD1	2.29	0.62
1:A:368:LEU:O	1:A:372:VAL:HG23	1.99	0.62
2:B:104:LYS:O	2:B:236:PRO:HD2	1.98	0.62
1:A:326:ILE:HD12	1:A:342:TYR:HE1	1.63	0.62
1:A:11:LYS:HG2	1:A:12:LEU:H	1.64	0.62
2:B:115:TYR:HD1	2:B:115:TYR:N	1.97	0.62
1:A:498:ASP:HB3	1:A:545:ASN:ND2	2.13	0.62
2:B:254:VAL:O	2:B:257:ILE:HG23	2.00	0.62
2:B:60:VAL:HG11	2:B:130:PHE:HD2	1.63	0.62
1:A:442:VAL:CG1	1:A:485:ALA:HB2	2.30	0.61
2:B:33:ALA:O	2:B:37:ILE:HG13	2.00	0.61
1:A:419:THR:HB	1:A:420:PRO:CD	2.24	0.61
1:A:522:ILE:O	1:A:526:ILE:HG13	2.00	0.61
1:A:33:ALA:O	1:A:37:ILE:HG13	2.00	0.61
1:A:341:ILE:HD11	1:A:375:ILE:HG23	1.83	0.61
1:A:318:TYR:HE2	3:A:559:AAA:C12	2.14	0.61
1:A:18:GLY:HA3	1:A:56:TYR:CD2	2.35	0.61
1:A:58:THR:HB	1:A:59:PRO:HD2	1.81	0.61
2:B:319:TYR:HD1	2:B:343:GLN:NE2	1.97	0.61
2:B:241:VAL:HG21	2:B:351:THR:OG1	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:230:MET:O	2:B:233:GLU:HG3	2.00	0.60
1:A:408:ALA:HB1	2:B:364:ASP:HB3	1.83	0.60
1:A:406:TRP:CH2	2:B:419:THR:N	2.69	0.60
2:B:77:PHE:HD2	2:B:152:GLY:HA3	1.67	0.60
2:B:343:GLN:NE2	2:B:349:LEU:HD11	2.17	0.60
1:A:326:ILE:O	1:A:341:ILE:HG23	2.01	0.60
2:B:50:ILE:CG2	2:B:145:GLN:HB2	2.30	0.60
2:B:114:ALA:HB1	2:B:160:PHE:CZ	2.37	0.60
2:B:254:VAL:HG23	2:B:291:GLU:O	2.01	0.60
1:A:121:ASP:O	1:A:125:ARG:HG3	2.02	0.60
1:A:28:GLU:HA	1:A:31:ILE:HD12	1.84	0.59
2:B:80:LEU:HD11	2:B:84:THR:CG2	2.30	0.59
1:A:271:TYR:OH	1:A:313:PRO:HA	2.02	0.59
1:A:544:GLY:O	1:A:548:VAL:HG23	2.02	0.59
1:A:443:ASP:HB3	1:A:552:VAL:HG21	1.84	0.59
1:A:78:ARG:HD3	1:A:81:ASN:HD22	1.67	0.59
2:B:325:LEU:H	2:B:325:LEU:CD2	2.15	0.59
1:A:443:ASP:HB2	1:A:548:VAL:CG1	2.32	0.59
2:B:156:SER:N	2:B:157:PRO:HD2	2.18	0.59
1:A:17:ASP:O	1:A:83:ARG:HD3	2.02	0.59
2:B:250:ASP:OD2	2:B:303:LEU:CD2	2.49	0.59
2:B:315:HIS:CD2	2:B:316:GLY:H	2.21	0.59
2:B:175:ASN:OD1	2:B:201:LYS:HE2	2.02	0.59
1:A:397:THR:O	1:A:400:THR:OG1	2.18	0.59
1:A:398:TRP:CE2	1:A:411:ILE:HG12	2.38	0.59
1:A:544:GLY:C	1:A:548:VAL:HG23	2.23	0.59
1:A:156:SER:HB2	1:A:157:PRO:CD	2.32	0.58
2:B:113:ASP:O	2:B:116:PHE:HB2	2.03	0.58
1:A:38:CYS:HB3	1:A:144:TYR:HE2	1.67	0.58
2:B:73:LYS:HZ3	2:B:146:TYR:HE1	1.51	0.58
1:A:224:GLU:HG2	1:A:226:PRO:HG2	1.86	0.58
2:B:241:VAL:HG23	2:B:351:THR:OG1	2.03	0.58
2:B:87:PHE:O	2:B:90:VAL:HG12	2.04	0.58
1:A:59:PRO:HB2	1:A:61:PHE:CZ	2.40	0.57
1:A:363:ASN:OD1	1:A:365:VAL:HB	2.04	0.57
1:A:542:ILE:HD12	2:B:283:LEU:HD13	1.84	0.57
2:B:325:LEU:HD23	2:B:325:LEU:N	2.18	0.57
1:A:199:ARG:HA	1:A:202:ILE:HG12	1.86	0.57
1:A:46:LYS:HD3	1:A:116:PHE:HD1	1.68	0.57
2:B:274:ILE:HG13	2:B:306:ASN:OD1	2.04	0.57
1:A:235:HIS:HB3	1:A:236:PRO:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:GLY:O	1:A:241:VAL:HG13	2.05	0.57
1:A:90:VAL:CG1	1:A:158:ALA:HA	2.35	0.57
1:A:254:VAL:HG23	1:A:291:GLU:O	2.05	0.57
1:A:505:ILE:O	1:A:508:ALA:HB3	2.05	0.56
2:B:81:ASN:O	2:B:85:GLN:N	2.37	0.56
1:A:31:ILE:O	1:A:35:VAL:HG23	2.04	0.56
1:A:90:VAL:HG23	1:A:91:GLN:N	2.20	0.56
1:A:73:LYS:NZ	1:A:75:VAL:HG21	2.20	0.56
1:A:130:PHE:CZ	1:A:144:TYR:HB3	2.40	0.56
1:A:241:VAL:HG12	1:A:243:PRO:HD2	1.86	0.56
2:B:7:THR:HG22	2:B:119:PRO:O	2.05	0.56
2:B:60:VAL:HG11	2:B:130:PHE:CD2	2.39	0.56
1:A:104:LYS:CD	1:A:192:ASP:HB3	2.34	0.56
2:B:306:ASN:HA	2:B:309:ILE:HG22	1.88	0.56
1:A:104:LYS:HD2	1:A:192:ASP:CB	2.33	0.56
1:A:248:GLU:HB2	1:A:307:ARG:HH12	1.70	0.56
2:B:399:GLU:HA	2:B:402:TRP:CD1	2.41	0.56
2:B:406:TRP:CE2	2:B:408:ALA:HB3	2.41	0.56
1:A:224:GLU:HG2	1:A:226:PRO:CD	2.35	0.56
1:A:10:VAL:HG22	1:A:87:PHE:HE1	1.69	0.56
1:A:90:VAL:O	1:A:91:GLN:NE2	2.39	0.56
2:B:78:ARG:HD3	2:B:411:ILE:O	2.06	0.56
1:A:186:ASP:HB3	1:A:188:TYR:CE1	2.35	0.55
1:A:244:ILE:HG21	1:A:267:ALA:HB2	1.88	0.55
1:A:271:TYR:CD1	1:A:314:VAL:HB	2.40	0.55
2:B:261:VAL:HG13	2:B:276:VAL:HG21	1.88	0.55
2:B:306:ASN:O	2:B:309:ILE:HG22	2.06	0.55
1:A:193:LEU:O	1:A:198:HIS:HB2	2.06	0.55
2:B:242:GLN:N	2:B:243:PRO:HD2	2.19	0.55
1:A:229:TRP:CE3	3:A:559:AAA:H4A2	2.42	0.55
1:A:26:LEU:HG	1:A:27:THR:N	2.21	0.55
2:B:103:LYS:HD3	2:B:191:SER:CA	2.36	0.55
2:B:66:LYS:HB2	2:B:69:THR:CG2	2.36	0.55
2:B:17:ASP:H	2:B:83:ARG:HH21	1.54	0.55
1:A:503:LEU:HD11	1:A:507:GLN:NE2	2.22	0.55
1:A:178:ILE:O	1:A:180:ILE:HG13	2.07	0.55
2:B:319:TYR:O	2:B:321:PRO:HD3	2.07	0.55
2:B:66:LYS:HA	2:B:407:GLN:NE2	2.22	0.55
1:A:208:HIS:HA	1:A:211:ARG:NH1	2.21	0.55
1:A:509:GLN:N	1:A:510:PRO:CD	2.70	0.55
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:SER:OG	1:A:518:VAL:HG23	2.07	0.54
2:B:241:VAL:O	2:B:241:VAL:HG22	2.06	0.54
2:B:255:ASN:HB2	2:B:289:LEU:HB3	1.88	0.54
1:A:543:GLY:N	2:B:283:LEU:O	2.40	0.54
2:B:354:TYR:OH	2:B:370:GLU:HB3	2.07	0.54
1:A:383:TRP:O	2:B:135:ILE:HG21	2.07	0.54
1:A:402:TRP:CD1	1:A:402:TRP:C	2.79	0.54
1:A:547:GLN:O	1:A:550:LYS:CB	2.53	0.54
1:A:318:TYR:CE2	3:A:559:AAA:H12	2.42	0.54
2:B:80:LEU:CD1	2:B:84:THR:CG2	2.86	0.54
2:B:295:LEU:H	2:B:295:LEU:HD23	1.72	0.54
2:B:373:GLN:HG2	2:B:406:TRP:CZ3	2.42	0.54
1:A:18:GLY:HA3	1:A:56:TYR:CG	2.43	0.54
1:A:242:GLN:N	1:A:243:PRO:HD2	2.17	0.54
1:A:439:THR:O	1:A:459:THR:HA	2.07	0.54
1:A:443:ASP:CB	1:A:548:VAL:CG1	2.85	0.54
2:B:315:HIS:CG	2:B:316:GLY:N	2.75	0.54
1:A:438:GLU:HG3	1:A:460:ASN:OD1	2.08	0.54
2:B:10:VAL:HG21	2:B:153:TRP:HH2	1.73	0.54
1:A:215:THR:O	1:A:217:PRO:HD3	2.08	0.54
2:B:3:SER:N	2:B:4:PRO:CD	2.71	0.54
1:A:168:LEU:CD2	1:A:209:LEU:HD21	2.37	0.54
1:A:211:ARG:HG3	1:A:211:ARG:NH1	2.23	0.53
1:A:97:PRO:HG2	1:A:232:TYR:CD1	2.42	0.53
1:A:271:TYR:HE1	1:A:314:VAL:H	1.50	0.53
1:A:63:ILE:HG22	1:A:64:LYS:N	2.23	0.53
1:A:81:ASN:OD1	1:A:154:LYS:HB2	2.09	0.53
2:B:73:LYS:NZ	2:B:130:PHE:CZ	2.72	0.53
1:A:199:ARG:HA	1:A:202:ILE:CG1	2.39	0.53
1:A:90:VAL:HG23	1:A:91:GLN:H	1.73	0.53
2:B:158:ALA:O	2:B:161:GLN:HB2	2.08	0.53
1:A:211:ARG:HG3	1:A:211:ARG:HH11	1.74	0.53
1:A:332:GLN:HG2	1:A:333:GLY:N	2.23	0.53
1:A:325:LEU:HD22	1:A:341:ILE:CG2	2.38	0.53
2:B:339:TYR:C	2:B:340:GLN:HG3	2.29	0.53
1:A:275:LYS:HA	1:A:336:GLN:NE2	2.23	0.53
1:A:277:ARG:NE	1:A:278:GLN:HE21	2.07	0.53
1:A:395:LYS:HD2	1:A:414:TRP:CZ2	2.43	0.53
1:A:548:VAL:O	1:A:551:LEU:HG	2.09	0.53
2:B:250:ASP:HB2	2:B:260:LEU:CD2	2.38	0.53
1:A:63:ILE:CG2	1:A:64:LYS:N	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:PRO:O	1:A:100:LEU:HG	2.09	0.53
2:B:338:THR:OG1	2:B:353:LYS:HE3	2.09	0.53
1:A:22:LYS:CE	1:A:143:ARG:HH22	2.22	0.52
1:A:57:ASN:HA	1:A:129:ALA:HB3	1.91	0.52
2:B:369:THR:O	2:B:373:GLN:HG3	2.09	0.52
1:A:169:GLU:N	1:A:170:PRO:HD2	2.24	0.52
2:B:220:LYS:O	2:B:221:HIS:CG	2.62	0.52
1:A:542:ILE:HD11	2:B:258:GLN:OE1	2.08	0.52
2:B:103:LYS:HB3	2:B:191:SER:O	2.09	0.52
2:B:41:MET:HB3	2:B:47:ILE:HG12	1.91	0.52
1:A:193:LEU:HD22	1:A:197:GLN:NE2	2.25	0.52
1:A:420:PRO:CB	1:A:421:PRO:CD	2.78	0.52
2:B:295:LEU:HD23	2:B:295:LEU:N	2.25	0.52
2:B:393:ILE:HG21	2:B:398:TRP:HB2	1.92	0.52
1:A:405:TYR:O	2:B:331:LYS:HD3	2.09	0.52
2:B:169:GLU:N	2:B:170:PRO:HD2	2.24	0.52
1:A:543:GLY:CA	2:B:283:LEU:O	2.58	0.52
1:A:237:ASP:N	1:A:237:ASP:OD1	2.41	0.52
2:B:152:GLY:O	2:B:184:MET:HE3	2.10	0.52
2:B:241:VAL:HG13	2:B:241:VAL:O	2.10	0.52
1:A:482:ILE:HD12	1:A:502:ALA:HB1	1.91	0.52
1:A:95:PRO:HB2	1:A:229:TRP:HH2	1.75	0.52
2:B:239:TRP:O	2:B:240:THR:HG23	2.08	0.52
1:A:229:TRP:O	1:A:232:TYR:HB2	2.09	0.52
2:B:342:TYR:HA	2:B:348:ASN:HA	1.92	0.52
1:A:225:PRO:HB2	1:A:226:PRO:HD3	1.91	0.51
2:B:10:VAL:HG11	2:B:153:TRP:CZ2	2.46	0.51
1:A:205:LEU:O	1:A:208:HIS:HB3	2.10	0.51
2:B:319:TYR:CE2	2:B:383:TRP:HD1	2.28	0.51
1:A:46:LYS:HD3	1:A:116:PHE:CD1	2.44	0.51
1:A:64:LYS:O	1:A:65:LYS:HG3	2.10	0.51
2:B:111:VAL:HG13	2:B:111:VAL:O	2.10	0.51
2:B:132:ILE:HG22	2:B:142:ILE:O	2.09	0.51
1:A:47:ILE:HG22	1:A:48:SER:N	2.26	0.51
1:A:50:ILE:O	1:A:50:ILE:HG23	2.10	0.51
1:A:479:LEU:HB3	1:A:517:LEU:CD1	2.41	0.51
1:A:229:TRP:CH2	3:A:559:AAA:H3	2.45	0.51
1:A:433:PRO:HG3	1:A:532:TYR:CE2	2.46	0.51
1:A:493:VAL:HG22	1:A:494:ASN:N	2.25	0.51
1:A:49:LYS:HB3	1:A:144:TYR:CE1	2.38	0.51
1:A:512:LYS:O	1:A:513:SER:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:283:LEU:HD12	2:B:283:LEU:C	2.31	0.51
2:B:80:LEU:CD1	2:B:84:THR:HG21	2.36	0.51
2:B:81:ASN:O	2:B:85:GLN:HB3	2.10	0.51
1:A:150:PRO:HB2	1:A:153:TRP:HB2	1.93	0.51
1:A:549:ASP:OD1	1:A:549:ASP:C	2.48	0.51
1:A:433:PRO:HG2	2:B:255:ASN:CG	2.31	0.51
2:B:295:LEU:H	2:B:295:LEU:CD2	2.25	0.51
2:B:32:LYS:O	2:B:35:VAL:HG22	2.11	0.50
1:A:142:ILE:HG22	1:A:142:ILE:O	2.10	0.50
1:A:331:LYS:HE2	1:A:332:GLN:O	2.11	0.50
2:B:319:TYR:CD1	2:B:343:GLN:NE2	2.78	0.50
1:A:392:PRO:O	1:A:423:VAL:HG23	2.10	0.50
2:B:246:LEU:CD2	2:B:263:LYS:HD2	2.41	0.50
2:B:94:ILE:HG23	2:B:161:GLN:NE2	2.27	0.50
2:B:109:LEU:HB2	2:B:187:LEU:HB3	1.94	0.50
1:A:58:THR:N	1:A:129:ALA:O	2.44	0.50
1:A:276:VAL:O	1:A:276:VAL:HG12	2.12	0.50
1:A:238:LYS:HE3	1:A:315:HIS:HB2	1.93	0.50
1:A:109:LEU:HD23	1:A:216:THR:HG21	1.92	0.50
2:B:38:CYS:SG	2:B:144:TYR:CE2	3.04	0.50
1:A:11:LYS:HG2	1:A:12:LEU:N	2.27	0.50
1:A:109:LEU:HD12	1:A:189:VAL:HG23	1.93	0.50
1:A:207:GLN:HA	1:A:210:LEU:HB2	1.94	0.50
1:A:101:LYS:HE2	1:A:321:PRO:CG	2.42	0.50
2:B:118:VAL:HB	2:B:149:LEU:HD12	1.93	0.50
1:A:171:PHE:CE2	1:A:205:LEU:HA	2.47	0.49
1:A:369:THR:OG1	1:A:398:TRP:CH2	2.64	0.49
2:B:132:ILE:CG2	2:B:142:ILE:HB	2.41	0.49
2:B:274:ILE:HG13	2:B:306:ASN:ND2	2.28	0.49
2:B:153:TRP:HE3	2:B:156:SER:HG	1.59	0.49
1:A:443:ASP:HB2	1:A:548:VAL:HG12	1.93	0.49
1:A:64:LYS:O	1:A:65:LYS:CG	2.61	0.49
1:A:372:VAL:HG11	1:A:411:ILE:HG22	1.94	0.49
1:A:120:LEU:HD12	1:A:121:ASP:H	1.77	0.49
1:A:28:GLU:O	1:A:31:ILE:HB	2.13	0.49
2:B:170:PRO:O	2:B:173:LYS:HB2	2.13	0.49
2:B:281:LYS:CA	2:B:284:ARG:HG3	2.38	0.49
1:A:325:LEU:HD22	1:A:341:ILE:HG22	1.95	0.49
1:A:241:VAL:HG11	1:A:266:TRP:CD1	2.47	0.49
2:B:17:ASP:CG	2:B:18:GLY:H	2.16	0.49
1:A:191:SER:OG	1:A:192:ASP:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:PHE:CE1	2:B:127:TYR:HD2	2.31	0.48
1:A:416:PHE:CD1	1:A:417:VAL:N	2.81	0.48
1:A:468:PRO:O	1:A:469:LEU:HD23	2.12	0.48
2:B:162:SER:O	2:B:165:THR:HG22	2.12	0.48
1:A:100:LEU:O	1:A:318:TYR:HB3	2.12	0.48
1:A:106:VAL:HG11	3:A:559:AAA:BR1	2.69	0.48
1:A:22:LYS:NZ	1:A:131:THR:HG21	2.29	0.48
1:A:482:ILE:CD1	1:A:502:ALA:HB1	2.43	0.48
2:B:297:GLU:HA	2:B:297:GLU:OE1	2.14	0.48
1:A:104:LYS:HB2	1:A:192:ASP:CA	2.38	0.48
1:A:393:ILE:CB	1:A:423:VAL:HB	2.33	0.48
2:B:306:ASN:HA	2:B:309:ILE:CG2	2.44	0.48
2:B:19:PRO:C	2:B:20:LYS:HG3	2.35	0.48
1:A:124:PHE:HA	1:A:127:TYR:CD2	2.49	0.48
2:B:426:TRP:HE3	2:B:426:TRP:H	1.61	0.48
2:B:59:PRO:CG	2:B:76:ASP:HB3	2.25	0.48
2:B:124:PHE:CD1	2:B:127:TYR:HD2	2.32	0.47
2:B:319:TYR:CA	2:B:343:GLN:HE22	2.15	0.47
1:A:353:LYS:O	1:A:353:LYS:HG3	2.13	0.47
1:A:441:TYR:HB3	1:A:548:VAL:HG21	1.96	0.47
2:B:16:MET:SD	2:B:16:MET:N	2.88	0.47
1:A:130:PHE:CZ	1:A:144:TYR:CB	2.98	0.47
1:A:106:VAL:HG22	1:A:190:GLY:HA3	1.95	0.47
1:A:150:PRO:HB2	1:A:153:TRP:CB	2.44	0.47
1:A:199:ARG:NH1	1:A:199:ARG:HB2	2.29	0.47
1:A:22:LYS:HZ3	1:A:131:THR:HG21	1.80	0.47
1:A:276:VAL:HG12	1:A:280:SER:HB3	1.96	0.47
1:A:38:CYS:HB3	1:A:144:TYR:CE2	2.48	0.47
1:A:443:ASP:HB2	1:A:548:VAL:HG11	1.95	0.47
2:B:163:SER:O	2:B:167:ILE:HG12	2.14	0.47
2:B:169:GLU:HB3	2:B:170:PRO:CD	2.44	0.47
2:B:223:LYS:HG2	2:B:223:LYS:O	2.14	0.47
2:B:260:LEU:HD21	2:B:303:LEU:HD13	1.96	0.47
1:A:492:GLU:OE1	1:A:530:LYS:HD2	2.15	0.47
1:A:88:TRP:NE1	2:B:143:ARG:HD2	2.30	0.47
1:A:320:ASP:O	1:A:343:GLN:NE2	2.47	0.47
1:A:440:PHE:CD1	1:A:459:THR:HG22	2.49	0.47
2:B:205:LEU:O	2:B:209:LEU:HG	2.15	0.47
1:A:191:SER:HB3	1:A:198:HIS:CD2	2.48	0.47
2:B:261:VAL:O	2:B:265:ASN:HB2	2.15	0.47
2:B:366:LYS:O	2:B:369:THR:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:503:LEU:HD22	1:A:535:TRP:CB	2.45	0.47
1:A:12:LEU:HD23	1:A:84:THR:HA	1.96	0.47
2:B:303:LEU:HD21	2:B:307:ARG:NH2	2.29	0.47
1:A:275:LYS:H	1:A:306:ASN:HD21	1.62	0.47
2:B:81:ASN:OD1	2:B:154:LYS:N	2.35	0.47
1:A:252:TRP:CA	1:A:252:TRP:CE3	2.87	0.47
2:B:118:VAL:HB	2:B:149:LEU:CD1	2.45	0.47
1:A:435:VAL:HG22	2:B:290:THR:HG21	1.97	0.47
2:B:2:ILE:O	2:B:2:ILE:HG22	2.14	0.47
2:B:63:ILE:O	2:B:72:ARG:HB2	2.14	0.47
1:A:152:GLY:O	1:A:153:TRP:C	2.53	0.47
2:B:17:ASP:CG	2:B:18:GLY:N	2.67	0.47
1:A:224:GLU:HG2	1:A:226:PRO:CG	2.44	0.46
2:B:54:ASN:O	2:B:143:ARG:NH2	2.48	0.46
1:A:406:TRP:HH2	2:B:419:THR:N	2.13	0.46
1:A:271:TYR:CE1	1:A:314:VAL:N	2.73	0.46
2:B:178:ILE:HG12	2:B:191:SER:HB3	1.96	0.46
2:B:394:GLN:OE1	2:B:396:GLU:HB2	2.16	0.46
2:B:402:TRP:HH2	2:B:411:ILE:HD13	1.80	0.46
1:A:411:ILE:HD13	1:A:414:TRP:CD1	2.50	0.46
1:A:501:TYR:CE1	1:A:505:ILE:HD11	2.50	0.46
1:A:229:TRP:CG	3:A:559:AAA:H4A2	2.51	0.46
1:A:329:ILE:HD11	1:A:375:ILE:HD12	1.97	0.46
1:A:483:TYR:CZ	1:A:520:GLN:HB3	2.51	0.46
1:A:422:LEU:HB2	1:A:424:LYS:HE2	1.96	0.46
2:B:26:LEU:HD12	2:B:133:PRO:CG	2.46	0.46
2:B:65:LYS:HB2	2:B:72:ARG:HG3	1.96	0.46
1:A:470:THR:HG22	1:A:471:ASN:N	2.31	0.46
1:A:99:GLY:HA3	2:B:136:ASN:HD21	1.79	0.46
2:B:320:ASP:OD1	2:B:322:SER:HB3	2.16	0.46
2:B:419:THR:HG23	2:B:420:PRO:HD2	1.98	0.46
2:B:54:ASN:OD1	2:B:143:ARG:NH2	2.48	0.46
2:B:79:GLU:O	2:B:82:LYS:HB2	2.16	0.46
1:A:253:THR:HB	1:A:289:LEU:O	2.16	0.46
1:A:238:LYS:C	1:A:318:TYR:HE1	2.19	0.46
1:A:434:ILE:HD13	1:A:492:GLU:HB3	1.97	0.46
1:A:64:LYS:C	1:A:65:LYS:HG3	2.36	0.46
2:B:178:ILE:CD1	2:B:201:LYS:HD3	2.45	0.46
2:B:206:ARG:CG	2:B:217:PRO:HG2	2.33	0.46
2:B:356:ARG:O	2:B:367:GLN:NE2	2.49	0.46
2:B:46:LYS:NZ	2:B:116:PHE:HB3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:LEU:CD2	1:A:214:LEU:N	2.78	0.46
2:B:135:ILE:HG22	2:B:136:ASN:N	2.31	0.46
1:A:475:GLN:O	1:A:478:GLU:HB2	2.16	0.45
2:B:241:VAL:CG2	2:B:351:THR:HG1	2.28	0.45
1:A:103:LYS:HE3	1:A:179:VAL:CG2	2.44	0.45
1:A:296:THR:O	1:A:297:GLU:C	2.54	0.45
1:A:344:GLU:HB2	1:A:347:LYS:HB2	1.97	0.45
1:A:38:CYS:O	1:A:42:GLU:N	2.48	0.45
1:A:428:GLN:HG3	1:A:509:GLN:HE22	1.81	0.45
2:B:306:ASN:O	2:B:310:LEU:HG	2.16	0.45
2:B:73:LYS:HE2	2:B:75:VAL:CG2	2.46	0.45
2:B:81:ASN:O	2:B:85:GLN:CB	2.64	0.45
1:A:394:GLN:HB3	1:A:397:THR:OG1	2.16	0.45
1:A:402:TRP:O	2:B:331:LYS:NZ	2.48	0.45
1:A:331:LYS:HE3	1:A:512:LYS:HZ3	1.82	0.45
2:B:164:MET:HG2	2:B:182:GLN:NE2	2.32	0.45
2:B:77:PHE:HE2	2:B:150:PRO:HB2	1.82	0.45
2:B:63:ILE:O	2:B:72:ARG:N	2.49	0.45
1:A:106:VAL:CG1	1:A:107:THR:N	2.80	0.45
1:A:171:PHE:HB2	1:A:208:HIS:CD2	2.52	0.45
2:B:197:GLN:O	2:B:200:THR:HB	2.17	0.45
2:B:250:ASP:OD2	2:B:303:LEU:CD1	2.64	0.45
2:B:257:ILE:HD12	2:B:282:LEU:HD23	1.97	0.45
2:B:80:LEU:HD12	2:B:84:THR:HG23	1.97	0.45
1:A:188:TYR:CE2	3:A:559:AAA:H4A1	2.52	0.45
2:B:399:GLU:HA	2:B:402:TRP:HD1	1.81	0.45
1:A:328:GLU:HG3	1:A:390:LYS:CB	2.47	0.45
1:A:483:TYR:OH	1:A:520:GLN:NE2	2.50	0.45
2:B:208:HIS:O	2:B:211:ARG:HB2	2.17	0.45
1:A:159:ILE:HD12	1:A:159:ILE:N	2.32	0.45
1:A:171:PHE:CD1	1:A:172:LYS:N	2.85	0.45
1:A:170:PRO:O	1:A:173:LYS:HB3	2.16	0.45
1:A:444:GLY:HA2	1:A:454:LYS:O	2.17	0.45
1:A:369:THR:HG1	1:A:398:TRP:HH2	1.57	0.45
1:A:311:LYS:O	1:A:313:PRO:HD3	2.17	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.52	0.44
1:A:99:GLY:CA	2:B:136:ASN:ND2	2.79	0.44
2:B:252:TRP:HB3	2:B:253:THR:H	1.63	0.44
1:A:124:PHE:HA	1:A:127:TYR:HD2	1.83	0.44
1:A:339:TYR:CD2	1:A:375:ILE:HG12	2.52	0.44
1:A:198:HIS:O	1:A:202:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:TYR:CD1	1:A:318:TYR:N	2.85	0.44
1:A:32:LYS:O	1:A:35:VAL:N	2.50	0.44
2:B:281:LYS:HA	2:B:284:ARG:CG	2.43	0.44
1:A:271:TYR:CE1	1:A:314:VAL:HB	2.52	0.44
1:A:242:GLN:N	1:A:243:PRO:CD	2.73	0.44
2:B:376:THR:O	2:B:379:SER:HB2	2.17	0.44
1:A:317:VAL:HG13	1:A:318:TYR:O	2.18	0.44
1:A:332:GLN:CG	1:A:333:GLY:N	2.81	0.44
1:A:130:PHE:CD1	1:A:130:PHE:N	2.84	0.44
1:A:150:PRO:HD2	1:A:153:TRP:CE3	2.53	0.44
1:A:197:GLN:O	1:A:200:THR:HB	2.18	0.44
1:A:271:TYR:CD2	1:A:310:LEU:HD22	2.53	0.44
1:A:95:PRO:HB2	1:A:229:TRP:CH2	2.53	0.44
2:B:74:LEU:O	2:B:74:LEU:HD23	2.17	0.44
1:A:318:TYR:HD1	1:A:318:TYR:N	2.15	0.44
1:A:63:ILE:CG2	1:A:64:LYS:H	2.31	0.44
2:B:52:PRO:C	2:B:54:ASN:H	2.20	0.44
1:A:293:ILE:HA	1:A:294:PRO:HD3	1.81	0.43
2:B:115:TYR:OH	2:B:185:ASP:HA	2.16	0.43
1:A:28:GLU:CD	1:A:28:GLU:H	2.22	0.43
2:B:261:VAL:HG21	2:B:283:LEU:HD21	2.00	0.43
2:B:10:VAL:HG22	2:B:88:TRP:CZ2	2.53	0.43
1:A:10:VAL:HG12	1:A:11:LYS:N	2.31	0.43
1:A:332:GLN:O	1:A:333:GLY:C	2.57	0.43
1:A:271:TYR:HD1	1:A:314:VAL:HB	1.82	0.43
1:A:92:LEU:O	1:A:92:LEU:HG	2.17	0.43
1:A:97:PRO:HA	1:A:100:LEU:HG	2.01	0.43
1:A:52:PRO:O	1:A:54:ASN:N	2.51	0.43
2:B:252:TRP:O	2:B:292:VAL:HG13	2.19	0.43
2:B:91:GLN:O	2:B:91:GLN:NE2	2.52	0.43
1:A:225:PRO:HB2	1:A:226:PRO:CD	2.48	0.43
1:A:306:ASN:HD22	1:A:306:ASN:HA	1.67	0.43
1:A:335:GLY:O	1:A:356:ARG:CB	2.67	0.43
1:A:492:GLU:HA	1:A:530:LYS:O	2.18	0.43
1:A:73:LYS:HZ3	1:A:75:VAL:HG21	1.84	0.43
2:B:419:THR:CG2	2:B:420:PRO:HD2	2.49	0.43
2:B:78:ARG:NH1	2:B:411:ILE:CG2	2.80	0.43
1:A:159:ILE:CD1	1:A:159:ILE:H	2.32	0.43
1:A:201:LYS:HA	1:A:201:LYS:HD3	1.72	0.43
1:A:229:TRP:CD2	3:A:559:AAA:C4A	2.99	0.43
2:B:411:ILE:HA	2:B:412:PRO:HD2	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:ASP:OD1	1:A:192:ASP:N	2.51	0.42
1:A:224:GLU:CG	1:A:226:PRO:HG2	2.48	0.42
1:A:393:ILE:HD12	1:A:423:VAL:HG11	2.01	0.42
1:A:479:LEU:HB3	1:A:517:LEU:HD11	2.01	0.42
2:B:174:GLN:C	2:B:176:PRO:HD3	2.39	0.42
2:B:244:ILE:HG13	2:B:244:ILE:H	1.59	0.42
1:A:310:LEU:HA	1:A:310:LEU:HD22	1.86	0.42
1:A:96:HIS:CE1	1:A:350:LYS:HG3	2.54	0.42
1:A:357:MET:O	1:A:358:ARG:C	2.57	0.42
1:A:501:TYR:CZ	1:A:505:ILE:HD11	2.55	0.42
2:B:120:LEU:HD12	2:B:121:ASP:H	1.84	0.42
1:A:327:ALA:HB3	1:A:389:PHE:CD1	2.54	0.42
2:B:50:ILE:CD1	2:B:143:ARG:HB3	2.48	0.42
2:B:193:LEU:CD2	2:B:201:LYS:HD2	2.49	0.42
2:B:143:ARG:HH11	2:B:143:ARG:HG2	1.84	0.42
2:B:345:PRO:O	2:B:346:PHE:HB2	2.19	0.42
2:B:337:TRP:CB	2:B:354:TYR:HB3	2.46	0.42
1:A:155:GLY:O	1:A:159:ILE:HD13	2.19	0.42
1:A:225:PRO:N	1:A:226:PRO:HD2	2.35	0.42
2:B:23:GLN:OE1	2:B:59:PRO:HA	2.20	0.42
1:A:548:VAL:C	1:A:550:LYS:N	2.72	0.42
1:A:93:GLY:HA3	2:B:137:ASN:CG	2.40	0.42
1:A:229:TRP:CE2	3:A:559:AAA:H3	2.54	0.42
2:B:153:TRP:CE2	2:B:155:GLY:HA3	2.55	0.42
1:A:22:LYS:HE2	1:A:143:ARG:NH2	2.29	0.42
1:A:319:TYR:CG	1:A:320:ASP:N	2.88	0.42
2:B:65:LYS:O	2:B:65:LYS:HD3	2.20	0.42
2:B:12:LEU:HD23	2:B:84:THR:HG22	2.01	0.42
1:A:455:ALA:O	1:A:466:VAL:HA	2.20	0.42
1:A:458:VAL:HG21	1:A:551:LEU:HD21	2.01	0.42
2:B:1:PRO:HB2	2:B:2:ILE:H	1.53	0.42
2:B:329:ILE:HG22	2:B:330:GLN:N	2.35	0.42
2:B:85:GLN:CD	2:B:154:LYS:HD3	2.39	0.42
1:A:339:TYR:CE1	1:A:352:GLY:C	2.93	0.42
1:A:493:VAL:CG2	1:A:494:ASN:N	2.83	0.41
1:A:78:ARG:O	1:A:81:ASN:HB2	2.19	0.41
1:A:171:PHE:HD1	1:A:172:LYS:N	2.18	0.41
1:A:211:ARG:CG	1:A:211:ARG:HH11	2.32	0.41
1:A:339:TYR:CD1	1:A:352:GLY:O	2.73	0.41
1:A:368:LEU:CD2	1:A:393:ILE:HG21	2.50	0.41
2:B:73:LYS:HG2	2:B:74:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLY:C	1:A:100:LEU:HD23	2.41	0.41
1:A:10:VAL:HG11	1:A:153:TRP:HZ2	1.86	0.41
2:B:143:ARG:HG2	2:B:143:ARG:NH1	2.36	0.41
2:B:183:TYR:O	2:B:184:MET:C	2.58	0.41
1:A:230:MET:C	1:A:232:TYR:H	2.24	0.41
1:A:195:ILE:HG23	1:A:199:ARG:HH22	1.86	0.41
2:B:251:SER:OG	2:B:295:LEU:HB3	2.20	0.41
2:B:427:TYR:OXT	2:B:427:TYR:CG	2.74	0.41
1:A:331:LYS:HE3	1:A:512:LYS:NZ	2.35	0.41
1:A:54:ASN:HA	1:A:55:PRO:HD2	1.85	0.41
1:A:134:SER:CB	1:A:138:GLU:O	2.69	0.41
2:B:241:VAL:HG21	2:B:351:THR:HG1	1.84	0.41
2:B:337:TRP:O	2:B:353:LYS:HA	2.21	0.41
1:A:73:LYS:HZ2	1:A:75:VAL:HG21	1.86	0.41
1:A:1:PRO:HB2	1:A:2:ILE:H	1.66	0.41
1:A:393:ILE:HD12	1:A:423:VAL:CG1	2.51	0.41
1:A:406:TRP:HH2	2:B:418:ASN:HA	1.85	0.41
1:A:459:THR:HG1	1:A:463:ARG:HB3	1.82	0.41
1:A:208:HIS:HA	1:A:211:ARG:HH11	1.86	0.41
1:A:339:TYR:CE2	1:A:375:ILE:HG12	2.56	0.41
1:A:545:ASN:O	1:A:546:GLU:C	2.59	0.41
2:B:332:GLN:HE22	2:B:424:LYS:HA	1.85	0.41
1:A:225:PRO:O	1:A:227:PHE:CD2	2.74	0.41
1:A:478:GLU:CD	1:A:499:SER:HB2	2.41	0.41
1:A:492:GLU:HG2	1:A:530:LYS:HB2	2.03	0.41
1:A:519:ASN:O	1:A:522:ILE:HB	2.21	0.41
1:A:542:ILE:HD12	1:A:543:GLY:H	1.85	0.41
1:A:121:ASP:OD2	1:A:123:ASP:HB2	2.21	0.40
1:A:159:ILE:H	1:A:159:ILE:HD12	1.85	0.40
1:A:23:GLN:OE1	1:A:60:VAL:N	2.53	0.40
1:A:164:MET:O	1:A:167:ILE:N	2.54	0.40
1:A:198:HIS:CE1	1:A:202:ILE:HD11	2.56	0.40
1:A:257:ILE:O	1:A:261:VAL:HG23	2.21	0.40
1:A:78:ARG:HD3	1:A:78:ARG:HA	1.74	0.40
2:B:252:TRP:O	2:B:292:VAL:HA	2.22	0.40
1:A:470:THR:O	1:A:471:ASN:C	2.60	0.40
2:B:135:ILE:O	2:B:138:GLU:HG3	2.21	0.40
2:B:169:GLU:HB3	2:B:170:PRO:HD3	2.03	0.40
2:B:103:LYS:CE	2:B:179:VAL:HG23	2.52	0.40
2:B:194:GLU:O	2:B:197:GLN:N	2.53	0.40
2:B:16:MET:HB3	2:B:83:ARG:NH2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:THR:OG1	1:A:108:VAL:N	2.54	0.40
1:A:242:GLN:C	1:A:244:ILE:H	2.24	0.40
1:A:344:GLU:O	1:A:346:PHE:N	2.54	0.40
1:A:433:PRO:HG3	1:A:532:TYR:HE2	1.84	0.40
1:A:99:GLY:CA	2:B:136:ASN:HD21	2.34	0.40
1:A:344:GLU:C	1:A:346:PHE:H	2.25	0.40
1:A:427:TYR:OH	1:A:510:PRO:HD2	2.22	0.40
1:A:56:TYR:O	1:A:57:ASN:HB3	2.21	0.40
1:A:433:PRO:HB3	2:B:289:LEU:HB2	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	556/558 (100%)	443 (80%)	99 (18%)	14 (2%)	5	19
2	B	425/427 (100%)	354 (83%)	67 (16%)	4 (1%)	17	46
All	All	981/985 (100%)	797 (81%)	166 (17%)	18 (2%)	8	28

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	MET
1	A	53	GLU
1	A	153	TRP
1	A	242	GLN
1	A	287	LYS
1	A	412	PRO
2	B	317	VAL
1	A	52	PRO
1	A	244	ILE

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Mol	Chain	Res	Type
1	A	426	TRP
1	A	333	GLY
2	B	242	GLN
2	B	314	VAL
1	A	277	ARG
1	A	420	PRO
1	A	243	PRO
2	B	55	PRO
1	A	419	THR

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	453/498 (91%)	409 (90%)	44 (10%)	8	24
2	B	362/389 (93%)	334 (92%)	28 (8%)	13	35
All	All	815/887 (92%)	743 (91%)	72 (9%)	10	29

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	27	THR
1	A	40	GLU
1	A	42	GLU
1	A	44	GLU
1	A	57	ASN
1	A	60	VAL
1	A	78	ARG
1	A	94	ILE
1	A	107	THR
1	A	143	ARG
1	A	144	TYR
1	A	145	GLN
1	A	174	GLN

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Mol	Chain	Res	Type
1	A	175	ASN
1	A	185	ASP
1	A	187	LEU
1	A	192	ASP
1	A	210	LEU
1	A	211	ARG
1	A	214	LEU
1	A	244	ILE
1	A	252	TRP
1	A	269	GLN
1	A	310	LEU
1	A	317	VAL
1	A	320	ASP
1	A	324	ASP
1	A	326	ILE
1	A	340	GLN
1	A	346	PHE
1	A	349	LEU
1	A	386	THR
1	A	402	TRP
1	A	430	GLU
1	A	467	VAL
1	A	472	THR
1	A	479	LEU
1	A	488	ASP
1	A	507	GLN
1	A	509	GLN
1	A	533	LEU
1	A	542	ILE
1	A	550	LYS
2	B	6	GLU
2	B	28	GLU
2	B	38	CYS
2	B	89	GLU
2	B	91	GLN
2	B	111	VAL
2	B	115	TYR
2	B	123	ASP
2	B	146	TYR
2	B	172	ARG
2	B	203	GLU
2	B	206	ARG

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Mol	Chain	Res	Type
2	B	210	LEU
2	B	215	THR
2	B	240	THR
2	B	244	ILE
2	B	279	LEU
2	B	280	SER
2	B	302	GLU
2	B	317	VAL
2	B	324	ASP
2	B	336	GLN
2	B	340	GLN
2	B	369	THR
2	B	403	THR
2	B	414	TRP
2	B	418	ASN
2	B	427	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	197	GLN
1	A	278	GLN
1	A	306	ASN
1	A	340	GLN
1	A	361	HIS
1	A	367	GLN
1	A	407	GLN
1	A	474	ASN
1	A	507	GLN
1	A	509	GLN
1	A	520	GLN
1	A	545	ASN
2	B	91	GLN
2	B	147	ASN
2	B	161	GLN
2	B	207	GLN
2	B	315	HIS
2	B	343	GLN
2	B	367	GLN
2	B	407	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 carbohydrates 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$
3	AAA	A	559	-	24,24,24	1.35	3 (12%)	29,34,34	1.12	2 (6%)

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	AAA	A	559	-	-	3/16/16/16	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	559	AAA	C5-C6	3.82	1.45	1.39
3	A	559	AAA	C6-N7	2.44	1.43	1.37
3	A	559	AAA	C1-C6	2.43	1.44	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	559	AAA	O1B-C1A-C1	2.35	123.66	120.56
3	A	559	AAA	C10-C9-C8	-2.26	119.76	122.34

There are no chirality outliers.

All (3) torsion outliers are listed below:

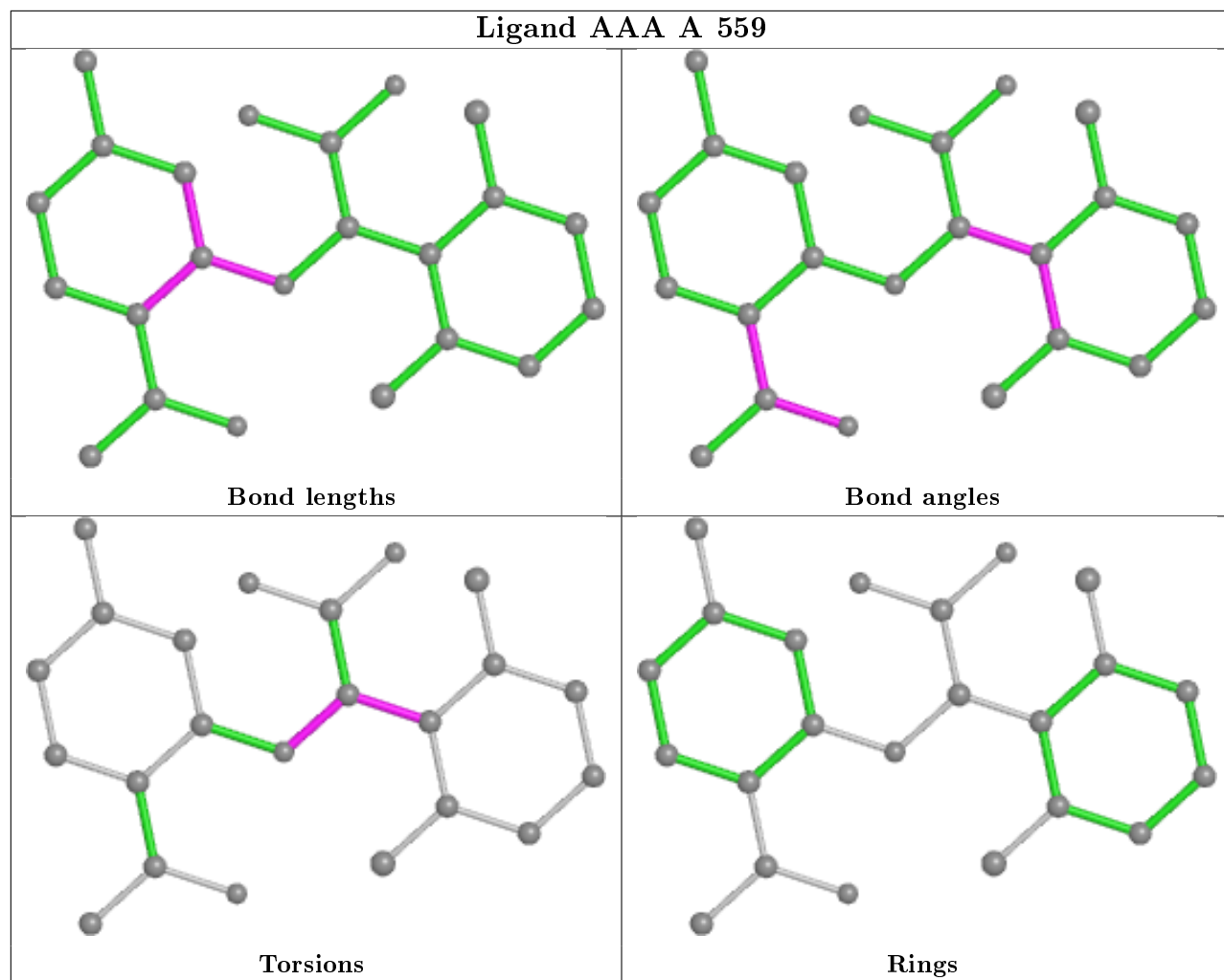
Mol	Chain	Res	Type	Atoms
3	A	559	AAA	C8A-C8-N7-C6
3	A	559	AAA	C9-C8-N7-C6
3	A	559	AAA	C8A-C8-C9-C14

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	559	AAA	12	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	558/558 (100%)	-0.43	4 (0%) 87 84	8, 44, 66, 72	0
2	B	427/427 (100%)	-0.47	3 (0%) 87 84	5, 33, 64, 72	0
All	All	985/985 (100%)	-0.45	7 (0%) 87 84	5, 41, 65, 72	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	231	GLY	3.8
2	B	282	LEU	3.6
1	A	293	ILE	3.2
1	A	557	ARG	3.0
1	A	544	GLY	2.9
2	B	230	MET	2.3
1	A	277	ARG	2.2

### 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 carbohydrates in this entry.

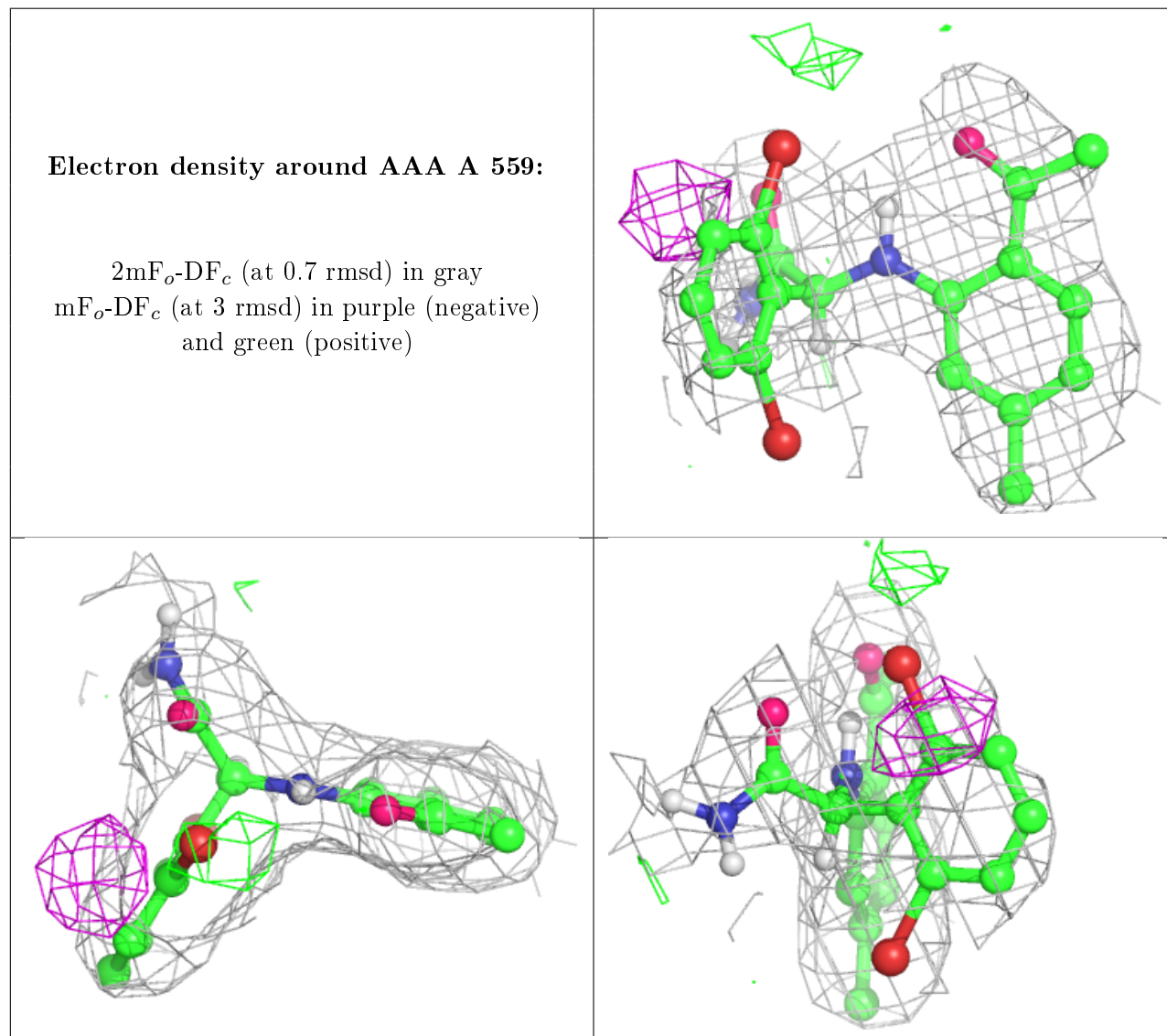
### 6.4 Ligands [i](#)

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<sup>th</sup> 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
3	AAA	A	559	23/23	0.94	0.15	10,20,28,32	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 ⓘ

There are no such residues in this entry.