



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2023 – 11:32 AM EDT

PDB ID : 2RF2
Title : HIV reverse transcriptase in complex with inhibitor 7e (NNRTI)
Authors : Yan, Y.; Prasad, S.
Deposited on : 2007-09-27
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

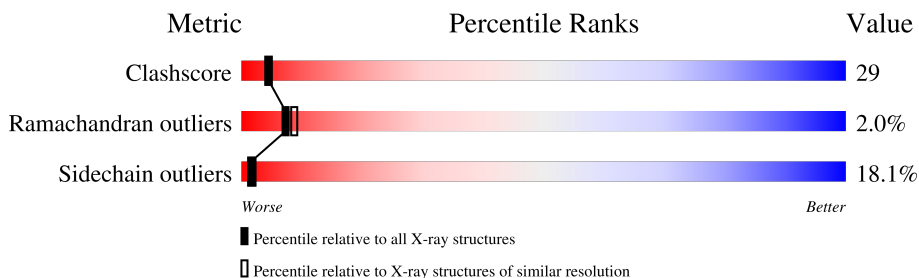
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	563	 56% 31% 10% ..
2	B	443	 49% 31% 11% . 9%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 8593 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/ribonuclease H (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4) (p66 RT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	554	4510	2915	754	833	8	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	expression tag	UNP P04585
A	-1	ASN	-	expression tag	UNP P04585
A	0	SER	-	expression tag	UNP P04585

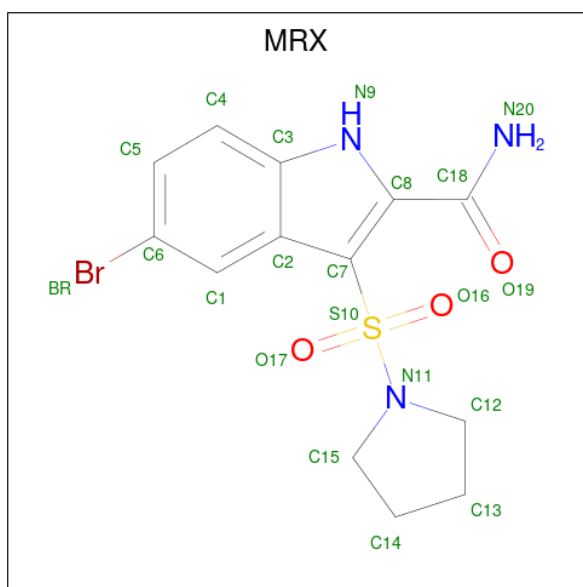
- Molecule 2 is a protein called Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4) (p66 RT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	405	3352	2182	555	609	6	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	MET	-	expression tag	UNP P04585
B	-1	ASN	-	expression tag	UNP P04585
B	0	SER	-	expression tag	UNP P04585

- Molecule 3 is 5-bromo-3-(pyrrolidin-1-ylsulfonyl)-1H-indole-2-carboxamide (three-letter code: MRX) (formula: C₁₃H₁₄BrN₃O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	Br	C	N	O			S
3	A	1	21	1	13	3	3	1	0	0

- Molecule 4 is water.

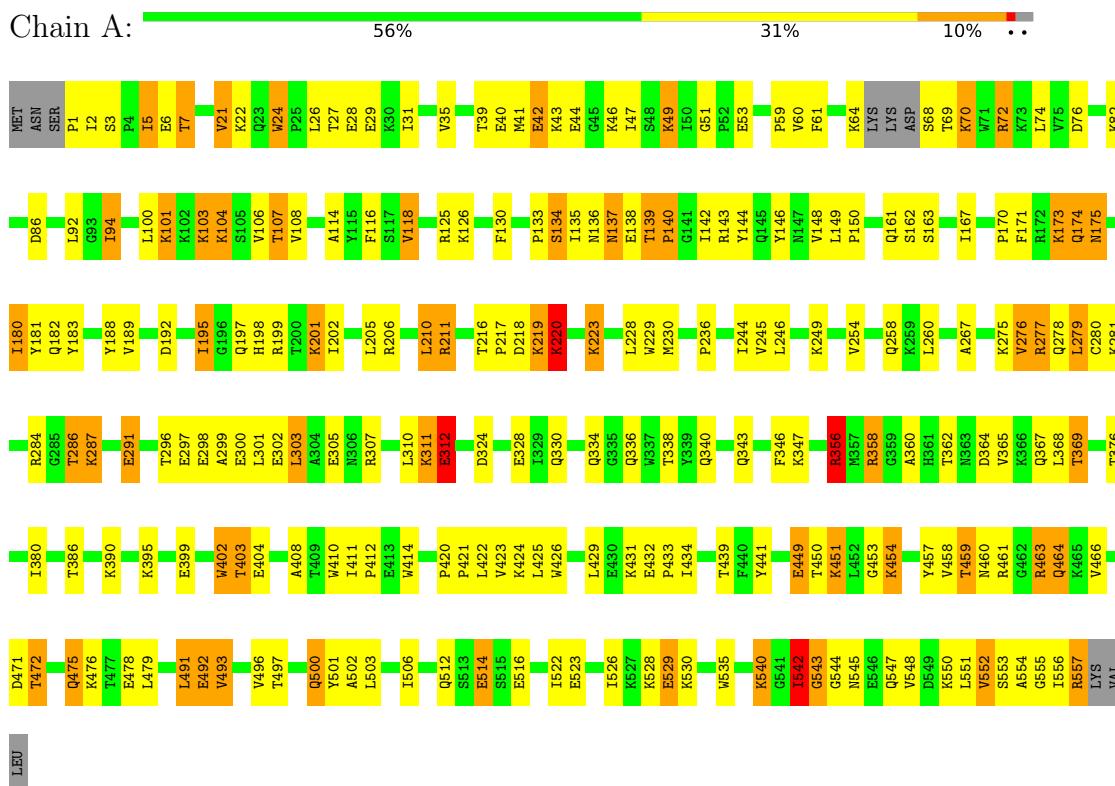
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	413	Total	O	0	0
			413	413		
4	B	297	Total	O	0	0
			297	297		

3 Residue-property plots [i](#)

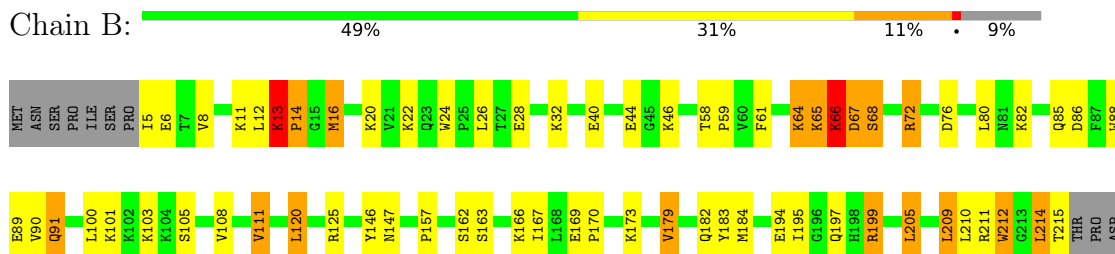
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

- Molecule 1: Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4) (p66 RT)



- Molecule 2: Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4) (p66 RT)



LYS	K281	G352	GLU
LYS	L282	K353	PRO
HIS	L283	Y354	ILE
GLN	R284	A355	VAL
LYS	G285	R356	GLY
GLU	T286	MET	ALA
PRO	K287	ARG	GLU
PRO	A288	GLY	THR
PHE	L289	ALA	PHE
LEU	T290	H361	
TRP		T362	
MET		N363	
G231	I293	D364	
Y232	P294	V365	
E233	L295	K366	
	T296	Q367	
	E297	L368	
P236	E298	T369	
D237	A299	E370	
K238	E300	A371	
W239	L301	V372	
T240	E302	Q373	
V241	L303	K374	
Q242	A304	I375	
P243	E305	T376	
I244	N306	T377	
V245		E378	
L246	I309	K385	
	L310	K388	
K249	K311	F389	
D250	E312	K390	
S251	P313	E396	
W252	Y314	T400	
T253	H315	W401	
V254	Q316	Y405	
N255	V317	W406	
D256	Y318	Q407	
I257	Y319	A408	
Q258	D320	T409	
K259	P321	W410	
L260		E415	
V261	D324	P420	
G262	L325	F421	
K263	L326	L422	
L264	E328	V423	
N265	Q334	K424	
W266	G335	L425	
A267	Q336	W426	
S268	W337	Y427	
Q269	W337	Q428	
I270		LEU	
I271	I341	GLU	
Y272	Y342	LYS	
P273	Q343		
I274	E344		
K275	P345		
V276	F346		
R277	K347		
Q278	N348		
L279	L349		
C280			

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	119.29Å 155.81Å 155.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.77 – 2.40	Depositor
% Data completeness (in resolution range)	99.2 (15.77-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, R_{free}	0.185 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8593	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

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: MRX

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	0.62	0/4625	0.79	1/6282 (0.0%)
2	B	0.62	0/3446	0.82	4/4682 (0.1%)
All	All	0.62	0/8071	0.80	5/10964 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	13	LYS	C-N-CD	-16.25	84.85	120.60
2	B	271	TYR	C-N-CD	-7.60	103.88	120.60
2	B	120	LEU	CA-CB-CG	5.89	128.84	115.30
2	B	244	ILE	N-CA-C	-5.33	96.60	111.00
1	A	86	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts i

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4510	0	4558	258	0
2	B	3352	0	3380	204	0
3	A	21	0	14	3	0
4	A	413	0	0	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	297	0	0	12	0
All	All	8593	0	7952	452	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 29.

All (452) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:LYS:HE2	1:A:69:THR:HG23	1.21	1.17
2:B:253:THR:HG22	2:B:256:ASP:H	1.07	1.10
2:B:422:LEU:HA	2:B:425:LEU:HD21	1.35	1.08
1:A:463:ARG:HG2	1:A:463:ARG:HH11	1.19	1.06
2:B:246:LEU:HD11	2:B:310:LEU:HD23	1.39	1.03
2:B:344:GLU:HB3	2:B:347:LYS:HD3	1.44	0.97
1:A:330:GLN:HE22	1:A:340:GLN:HE22	1.06	0.97
1:A:475:GLN:HG2	1:A:501:TYR:CE2	2.04	0.93
1:A:296:THR:HG23	1:A:299:ALA:H	1.33	0.92
1:A:399:GLU:HA	1:A:402:TRP:CE3	2.04	0.92
1:A:107:THR:HG22	1:A:198:HIS:CE1	2.04	0.92
2:B:214:LEU:H	2:B:214:LEU:HD23	1.33	0.92
1:A:107:THR:HG22	1:A:198:HIS:HE1	1.33	0.91
1:A:356:ARG:HE	1:A:358:ARG:HG3	1.35	0.90
2:B:422:LEU:HA	2:B:425:LEU:CD2	2.02	0.89
1:A:223:LYS:H	1:A:223:LYS:HD2	1.36	0.88
2:B:344:GLU:CB	2:B:347:LYS:HD3	2.03	0.87
1:A:458:VAL:HG13	1:A:548:VAL:HG22	1.55	0.87
2:B:253:THR:HG22	2:B:256:ASP:N	1.89	0.87
2:B:268:SER:O	2:B:269:GLN:HB2	1.75	0.86
1:A:297:GLU:O	1:A:298:GLU:N	2.07	0.85
2:B:274:ILE:HA	2:B:306:ASN:HD21	1.41	0.85
1:A:356:ARG:NE	1:A:358:ARG:HG3	1.92	0.84
1:A:195:ILE:HD12	1:A:195:ILE:H	1.41	0.84
1:A:454:LYS:CD	1:A:556:ILE:HD13	2.08	0.84
1:A:24:TRP:HD1	1:A:24:TRP:H	1.24	0.84
1:A:399:GLU:O	1:A:403:THR:HB	1.79	0.83
2:B:274:ILE:HA	2:B:306:ASN:ND2	1.93	0.83
1:A:411:ILE:HG22	1:A:412:PRO:O	1.79	0.82
1:A:478:GLU:HG3	4:A:596:HOH:O	1.80	0.82
1:A:199:ARG:HG2	1:A:199:ARG:HH11	1.44	0.81
1:A:21:VAL:HG22	1:A:59:PRO:HD3	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:163:SER:HA	2:B:166:LYS:HE2	1.60	0.81
2:B:215:THR:HA	4:B:496:HOH:O	1.80	0.80
1:A:175:ASN:OD1	1:A:201:LYS:NZ	2.15	0.80
1:A:458:VAL:HG22	1:A:548:VAL:CG2	2.12	0.80
1:A:35:VAL:O	1:A:39:THR:HG23	1.82	0.79
1:A:64:LYS:CE	1:A:69:THR:HG23	2.08	0.79
1:A:296:THR:CG2	1:A:299:ALA:H	1.94	0.79
1:A:161:GLN:HG3	4:A:960:HOH:O	1.82	0.78
2:B:373:GLN:O	2:B:377:THR:HG23	1.83	0.78
1:A:277:ARG:HD3	1:A:336:GLN:NE2	1.99	0.77
1:A:475:GLN:HG2	1:A:501:TYR:CD2	2.19	0.77
2:B:373:GLN:HE22	2:B:407:GLN:H	1.30	0.77
2:B:369:THR:HG21	2:B:405:TYR:HB2	1.66	0.77
1:A:107:THR:HG21	1:A:202:ILE:HG13	1.66	0.76
1:A:42:GLU:OE1	1:A:49:LYS:HE3	1.85	0.76
1:A:454:LYS:HZ3	1:A:556:ILE:HD11	1.50	0.76
1:A:70:LYS:HE3	1:A:72:ARG:HG3	1.67	0.75
1:A:244:ILE:HD13	1:A:267:ALA:HB2	1.68	0.75
2:B:13:LYS:HE3	2:B:85:GLN:N	2.01	0.75
2:B:253:THR:O	2:B:257:ILE:HG12	1.88	0.74
1:A:139:THR:HG23	1:A:140:PRO:HD2	1.70	0.74
1:A:360:ALA:HA	1:A:514:GLU:OE1	1.87	0.74
1:A:330:GLN:NE2	1:A:340:GLN:HE22	1.85	0.74
1:A:219:LYS:O	1:A:220:LYS:HB3	1.89	0.73
2:B:125:ARG:HG2	2:B:146:TYR:O	1.88	0.73
2:B:214:LEU:HD23	2:B:214:LEU:N	2.03	0.73
2:B:14:PRO:HB3	4:B:571:HOH:O	1.88	0.73
1:A:108:VAL:CG2	1:A:223:LYS:HD3	2.19	0.72
1:A:61:PHE:HE2	1:A:76:ASP:HB2	1.54	0.72
2:B:373:GLN:NE2	2:B:407:GLN:H	1.87	0.72
1:A:458:VAL:HG22	1:A:548:VAL:HG23	1.72	0.71
2:B:337:TRP:HE1	2:B:367:GLN:HE21	1.35	0.71
2:B:366:LYS:O	2:B:370:GLU:HG3	1.90	0.71
2:B:303:LEU:HD23	2:B:303:LEU:H	1.56	0.71
2:B:312:GLU:OE2	2:B:313:PRO:HD3	1.91	0.71
2:B:300:GLU:O	2:B:304:ALA:HB2	1.91	0.71
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.74	0.70
1:A:399:GLU:HA	1:A:402:TRP:HE3	1.52	0.70
1:A:29:GLU:HG2	4:A:689:HOH:O	1.92	0.70
1:A:246:LEU:HD11	1:A:310:LEU:HD12	1.74	0.70
2:B:282:LEU:HD21	2:B:299:ALA:HB2	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:SER:OG	1:A:5:ILE:HG12	1.91	0.69
2:B:105:SER:HB2	4:B:465:HOH:O	1.91	0.69
1:A:69:THR:HG21	4:A:869:HOH:O	1.92	0.69
2:B:266:TRP:HH2	2:B:427:TYR:CZ	2.11	0.69
2:B:254:VAL:O	2:B:258:GLN:HG3	1.93	0.69
2:B:253:THR:CG2	2:B:256:ASP:H	1.96	0.69
1:A:223:LYS:H	1:A:223:LYS:CD	2.03	0.68
1:A:296:THR:HG21	4:A:597:HOH:O	1.93	0.68
2:B:297:GLU:O	2:B:301:LEU:HG	1.92	0.68
1:A:195:ILE:HD12	1:A:195:ILE:N	2.07	0.68
2:B:103:LYS:HE3	2:B:179:VAL:CG1	2.24	0.68
1:A:540:LYS:HB2	1:A:542:ILE:HD11	1.73	0.68
1:A:454:LYS:HD2	1:A:556:ILE:HD13	1.76	0.68
2:B:72:ARG:NH2	2:B:409:THR:HG21	2.09	0.68
1:A:367:GLN:NE2	1:A:512:GLN:OE1	2.27	0.68
2:B:246:LEU:HD11	2:B:310:LEU:CD2	2.19	0.68
1:A:454:LYS:HE2	1:A:554:ALA:O	1.92	0.68
1:A:556:ILE:O	1:A:557:ARG:HB3	1.92	0.68
1:A:297:GLU:HB3	1:A:298:GLU:N	2.09	0.67
1:A:540:LYS:CB	1:A:542:ILE:HD11	2.26	0.66
2:B:295:LEU:HD23	2:B:299:ALA:HB3	1.77	0.66
1:A:454:LYS:HZ3	1:A:556:ILE:CD1	2.09	0.66
1:A:223:LYS:HD2	1:A:223:LYS:N	2.09	0.66
1:A:108:VAL:HG12	1:A:188:TYR:CD2	2.30	0.66
1:A:195:ILE:H	1:A:195:ILE:CD1	2.03	0.66
1:A:296:THR:HG22	1:A:299:ALA:CB	2.24	0.66
1:A:27:THR:O	1:A:31:ILE:HG13	1.97	0.65
1:A:195:ILE:O	1:A:199:ARG:HG3	1.96	0.65
1:A:139:THR:HG22	1:A:140:PRO:N	2.12	0.65
2:B:282:LEU:HD12	2:B:293:ILE:CD1	2.26	0.65
2:B:363:ASN:HA	4:B:580:HOH:O	1.97	0.65
1:A:51:GLY:O	1:A:143:ARG:NH1	2.30	0.65
2:B:16:MET:HE2	2:B:16:MET:HA	1.78	0.65
2:B:345:PRO:O	2:B:346:PHE:HB2	1.96	0.65
1:A:171:PHE:O	1:A:175:ASN:ND2	2.29	0.64
2:B:276:VAL:HG12	2:B:280:CYS:SG	2.36	0.64
2:B:377:THR:HG22	2:B:410:TRP:HZ2	1.61	0.64
2:B:278:GLN:HE22	2:B:281:LYS:NZ	1.96	0.64
1:A:139:THR:CG2	1:A:140:PRO:HD2	2.27	0.64
2:B:253:THR:HG23	2:B:255:ASN:N	2.12	0.63
2:B:40:GLU:O	2:B:44:GLU:HG3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:LEU:HD21	2:B:299:ALA:CB	2.29	0.63
2:B:103:LYS:HE3	2:B:179:VAL:HG13	1.81	0.63
2:B:273:GLY:O	2:B:275:LYS:HG2	1.99	0.63
1:A:21:VAL:CG2	1:A:59:PRO:HD3	2.29	0.63
2:B:85:GLN:O	2:B:89:GLU:HB3	1.99	0.62
1:A:108:VAL:HG23	1:A:223:LYS:HD3	1.79	0.62
1:A:463:ARG:HG2	1:A:463:ARG:NH1	1.99	0.62
2:B:195:ILE:O	2:B:199:ARG:HG3	1.98	0.62
2:B:16:MET:HA	2:B:16:MET:CE	2.28	0.62
1:A:365:VAL:O	1:A:369:THR:HG23	2.01	0.61
1:A:472:THR:HG22	1:A:476:LYS:CB	2.30	0.61
2:B:253:THR:HG23	2:B:255:ASN:H	1.65	0.61
2:B:295:LEU:HD22	2:B:300:GLU:HG2	1.82	0.61
1:A:94:ILE:HD13	1:A:230:MET:HG3	1.82	0.60
1:A:362:THR:CG2	1:A:367:GLN:HE21	2.14	0.60
1:A:28:GLU:HG2	1:A:135:ILE:HG12	1.82	0.60
1:A:106:VAL:HG11	3:A:561:MRX:BR	2.56	0.60
2:B:362:THR:HG23	2:B:366:LYS:HZ2	1.66	0.60
1:A:182:GLN:HB3	4:A:618:HOH:O	2.00	0.60
2:B:210:LEU:O	2:B:210:LEU:HG	2.01	0.60
1:A:3:SER:CB	1:A:5:ILE:HG12	2.31	0.60
2:B:279:LEU:O	2:B:282:LEU:HB2	2.02	0.60
1:A:556:ILE:HD12	1:A:556:ILE:N	2.17	0.60
1:A:60:VAL:HG11	1:A:130:PHE:CD2	2.37	0.60
2:B:286:THR:HG23	2:B:286:THR:O	2.02	0.60
2:B:312:GLU:HB3	2:B:313:PRO:CD	2.31	0.60
1:A:380:ILE:HD11	1:A:386:THR:HG23	1.84	0.60
1:A:211:ARG:HB2	4:A:832:HOH:O	2.01	0.59
1:A:454:LYS:CE	1:A:556:ILE:HD13	2.32	0.59
1:A:170:PRO:O	1:A:174:GLN:HG2	2.03	0.59
2:B:28:GLU:CG	2:B:32:LYS:HE2	2.33	0.59
1:A:454:LYS:CG	1:A:556:ILE:HD13	2.33	0.59
2:B:163:SER:O	2:B:167:ILE:HG13	2.03	0.59
2:B:353:LYS:HE2	4:B:730:HOH:O	2.03	0.59
1:A:500:GLN:CG	2:B:422:LEU:HD12	2.33	0.59
1:A:277:ARG:HD3	1:A:336:GLN:CD	2.24	0.58
1:A:432:GLU:OE1	1:A:433:PRO:HD2	2.03	0.58
1:A:24:TRP:CD1	1:A:24:TRP:N	2.65	0.58
2:B:242:GLN:H	2:B:243:PRO:CD	2.16	0.58
2:B:246:LEU:CD1	2:B:310:LEU:HD23	2.26	0.58
1:A:399:GLU:HB2	1:A:402:TRP:CZ3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:252:TRP:CD1	2:B:295:LEU:HD12	2.39	0.58
1:A:1:PRO:HD3	4:A:639:HOH:O	2.03	0.58
2:B:28:GLU:HG3	2:B:32:LYS:HE2	1.84	0.58
2:B:66:LYS:HE2	2:B:67:ASP:HB2	1.85	0.58
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.84	0.58
1:A:324:ASP:O	1:A:343:GLN:HG2	2.03	0.57
1:A:432:GLU:OE1	1:A:432:GLU:HA	2.04	0.57
2:B:303:LEU:HA	2:B:306:ASN:HB2	1.85	0.57
2:B:13:LYS:O	2:B:16:MET:HB2	2.05	0.57
1:A:199:ARG:HG2	1:A:199:ARG:NH1	2.17	0.57
1:A:500:GLN:HG2	2:B:422:LEU:HD12	1.87	0.57
1:A:556:ILE:O	1:A:556:ILE:HG22	2.05	0.57
2:B:317:VAL:HG13	2:B:347:LYS:HB3	1.87	0.57
1:A:303:LEU:HD13	1:A:307:ARG:NH1	2.20	0.56
1:A:441:TYR:O	1:A:548:VAL:HG21	2.05	0.56
1:A:246:LEU:HD11	1:A:310:LEU:CD1	2.34	0.56
1:A:211:ARG:O	1:A:211:ARG:NH1	2.28	0.56
2:B:86:ASP:O	2:B:90:VAL:HG22	2.04	0.56
2:B:266:TRP:CH2	2:B:427:TYR:CZ	2.92	0.56
2:B:282:LEU:CD2	2:B:299:ALA:HB2	2.34	0.56
1:A:460:ASN:HA	2:B:286:THR:HG23	1.88	0.56
1:A:61:PHE:CE2	1:A:76:ASP:HB2	2.37	0.56
1:A:216:THR:HB	1:A:217:PRO:HD2	1.86	0.56
2:B:278:GLN:NE2	2:B:281:LYS:NZ	2.54	0.55
2:B:422:LEU:O	2:B:425:LEU:HG	2.05	0.55
2:B:266:TRP:CG	2:B:426:TRP:CE3	2.95	0.55
2:B:13:LYS:CE	2:B:86:ASP:H	2.19	0.55
2:B:212:TRP:HH2	4:B:576:HOH:O	1.90	0.55
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.87	0.55
1:A:557:ARG:O	1:A:557:ARG:HG2	2.05	0.55
2:B:271:TYR:CD1	2:B:310:LEU:HD12	2.41	0.55
1:A:211:ARG:O	1:A:211:ARG:HD3	2.06	0.55
1:A:472:THR:HG22	1:A:476:LYS:HB2	1.87	0.55
2:B:328:GLU:HG3	2:B:390:LYS:HD3	1.88	0.55
2:B:344:GLU:HB2	2:B:347:LYS:HD3	1.88	0.55
1:A:24:TRP:CE2	1:A:61:PHE:HE1	2.24	0.54
1:A:399:GLU:HB3	4:A:662:HOH:O	2.07	0.54
1:A:466:VAL:HG21	1:A:551:LEU:CD1	2.37	0.54
2:B:183:TYR:CE2	2:B:184:MET:HG3	2.42	0.54
2:B:341:ILE:HD11	2:B:375:ILE:HG23	1.89	0.54
1:A:138:GLU:O	1:A:139:THR:HB	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:297:GLU:HA	2:B:300:GLU:HG3	1.89	0.54
2:B:377:THR:HG22	2:B:410:TRP:CZ2	2.42	0.54
1:A:3:SER:HB3	1:A:5:ILE:HG12	1.89	0.54
1:A:311:LYS:O	1:A:312:GLU:HB3	2.08	0.54
1:A:555:GLY:C	1:A:556:ILE:HD12	2.27	0.54
2:B:240:THR:O	2:B:241:VAL:O	2.26	0.54
2:B:314:VAL:O	2:B:315:HIS:HB3	2.08	0.54
1:A:5:ILE:HD11	1:A:118:VAL:HB	1.89	0.54
1:A:286:THR:HG23	1:A:287:LYS:O	2.07	0.54
1:A:453:GLY:HA2	1:A:556:ILE:HG21	1.90	0.54
1:A:108:VAL:HG23	1:A:223:LYS:CD	2.37	0.53
1:A:47:ILE:HD12	1:A:144:TYR:CD1	2.43	0.53
1:A:278:GLN:OE1	1:A:281:LYS:NZ	2.31	0.53
1:A:502:ALA:O	1:A:506:ILE:HD12	2.08	0.53
2:B:362:THR:HG22	2:B:367:GLN:HG3	1.89	0.53
1:A:64:LYS:HE2	1:A:69:THR:CG2	2.14	0.53
1:A:69:THR:O	1:A:69:THR:HG22	2.08	0.53
1:A:180:ILE:HG22	1:A:189:VAL:HG13	1.91	0.53
2:B:334:GLN:O	2:B:334:GLN:HG3	2.09	0.53
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.09	0.53
1:A:542:ILE:O	1:A:543:GLY:O	2.27	0.53
2:B:241:VAL:O	2:B:242:GLN:HB2	2.08	0.53
2:B:300:GLU:HA	2:B:303:LEU:HD21	1.90	0.53
1:A:296:THR:HG22	1:A:299:ALA:HB3	1.90	0.53
2:B:254:VAL:HG21	2:B:288:ALA:O	2.09	0.53
2:B:157:PRO:HG3	2:B:184:MET:HA	1.91	0.52
2:B:409:THR:HG21	4:B:451:HOH:O	2.09	0.52
1:A:134:SER:HB2	1:A:140:PRO:O	2.10	0.52
1:A:296:THR:HG22	1:A:299:ALA:HB2	1.90	0.52
1:A:408:ALA:HB1	2:B:364:ASP:HB3	1.91	0.52
2:B:244:ILE:CD1	2:B:266:TRP:HZ3	2.23	0.52
2:B:268:SER:HB3	2:B:274:ILE:HB	1.92	0.52
1:A:40:GLU:O	1:A:44:GLU:HG3	2.08	0.52
1:A:41:MET:HE2	1:A:47:ILE:HG23	1.91	0.52
1:A:298:GLU:N	1:A:298:GLU:OE2	2.42	0.52
1:A:312:GLU:HB2	4:A:922:HOH:O	2.08	0.52
1:A:356:ARG:HH21	1:A:358:ARG:HD2	1.74	0.52
2:B:241:VAL:HB	2:B:243:PRO:HD3	1.91	0.52
2:B:301:LEU:O	2:B:304:ALA:HB3	2.10	0.52
2:B:278:GLN:HE22	2:B:281:LYS:HZ2	1.56	0.52
1:A:410:TRP:CZ3	2:B:363:ASN:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:THR:HG22	4:A:888:HOH:O	2.10	0.51
1:A:181:TYR:CE2	1:A:183:TYR:HB2	2.45	0.51
2:B:278:GLN:HE21	2:B:278:GLN:HA	1.75	0.51
2:B:266:TRP:CD1	2:B:426:TRP:CZ3	2.99	0.51
1:A:103:LYS:HE3	4:A:591:HOH:O	2.10	0.51
2:B:242:GLN:HG2	2:B:352:GLY:HA2	1.92	0.51
2:B:257:ILE:HG22	2:B:283:LEU:HD11	1.93	0.51
2:B:278:GLN:HA	2:B:281:LYS:HD3	1.92	0.51
1:A:31:ILE:HD13	1:A:133:PRO:O	2.10	0.51
1:A:466:VAL:CG2	1:A:551:LEU:HD11	2.40	0.51
2:B:261:VAL:HB	2:B:276:VAL:HG13	1.92	0.51
2:B:297:GLU:OE1	2:B:300:GLU:OE2	2.29	0.51
2:B:24:TRP:CZ3	2:B:59:PRO:CG	2.94	0.51
1:A:458:VAL:CG1	1:A:548:VAL:HG22	2.33	0.51
1:A:500:GLN:HG2	2:B:422:LEU:CD1	2.41	0.51
1:A:491:LEU:HB2	1:A:529:GLU:HB2	1.93	0.51
1:A:108:VAL:HG11	1:A:188:TYR:CE2	2.45	0.50
1:A:395:LYS:HD3	4:A:853:HOH:O	2.11	0.50
2:B:86:ASP:OD2	2:B:90:VAL:HG21	2.11	0.50
1:A:108:VAL:CG1	1:A:188:TYR:CE2	2.94	0.50
2:B:281:LYS:O	2:B:284:ARG:HD2	2.10	0.50
1:A:475:GLN:HG2	1:A:501:TYR:CZ	2.46	0.50
1:A:466:VAL:CG2	1:A:551:LEU:HG	2.42	0.50
1:A:548:VAL:O	1:A:552:VAL:HB	2.11	0.50
2:B:242:GLN:HG2	2:B:352:GLY:CA	2.42	0.50
1:A:297:GLU:C	1:A:298:GLU:N	2.65	0.50
1:A:472:THR:HG22	1:A:476:LYS:HB3	1.93	0.50
2:B:242:GLN:H	2:B:243:PRO:HD3	1.76	0.50
2:B:266:TRP:O	2:B:268:SER:O	2.29	0.50
1:A:362:THR:HG23	1:A:367:GLN:HE21	1.76	0.50
1:A:180:ILE:HA	1:A:188:TYR:O	2.12	0.50
2:B:5:ILE:HG22	2:B:6:GLU:N	2.27	0.50
2:B:108:VAL:HB	2:B:232:TYR:HB3	1.94	0.49
2:B:233:GLU:HB2	4:B:510:HOH:O	2.12	0.49
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.46	0.49
1:A:466:VAL:HG21	1:A:551:LEU:HD11	1.93	0.49
1:A:94:ILE:HD12	1:A:229:TRP:CH2	2.47	0.49
1:A:356:ARG:NH2	1:A:358:ARG:HD2	2.27	0.49
2:B:111:VAL:O	2:B:111:VAL:HG13	2.12	0.49
2:B:278:GLN:NE2	2:B:281:LYS:HZ3	2.09	0.49
1:A:148:VAL:O	1:A:150:PRO:HD3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ASN:OD1	1:A:137:ASN:O	2.30	0.49
2:B:101:LYS:O	2:B:236:PRO:HB2	2.13	0.49
2:B:303:LEU:HD23	2:B:303:LEU:N	2.25	0.49
1:A:139:THR:CG2	1:A:140:PRO:CD	2.90	0.49
1:A:330:GLN:NE2	1:A:338:THR:HG23	2.28	0.48
1:A:139:THR:CG2	1:A:140:PRO:N	2.76	0.48
1:A:219:LYS:H	1:A:219:LYS:CD	2.21	0.48
1:A:276:VAL:HG13	1:A:280:CYS:SG	2.53	0.48
1:A:118:VAL:HG22	1:A:149:LEU:HG	1.93	0.48
1:A:330:GLN:HE22	1:A:340:GLN:NE2	1.91	0.48
1:A:522:ILE:O	1:A:526:ILE:HG13	2.13	0.48
1:A:107:THR:HG21	1:A:202:ILE:CG1	2.39	0.48
2:B:239:TRP:CH2	2:B:378:GLU:HG2	2.49	0.48
1:A:424:LYS:NZ	1:A:426:TRP:CZ2	2.81	0.48
2:B:44:GLU:OE2	2:B:46:LYS:HE2	2.14	0.48
1:A:24:TRP:HE1	1:A:59:PRO:HB3	1.79	0.48
1:A:108:VAL:CG1	1:A:188:TYR:CD2	2.96	0.48
1:A:219:LYS:HD2	1:A:219:LYS:N	2.29	0.48
1:A:297:GLU:C	1:A:300:GLU:HB2	2.34	0.48
1:A:21:VAL:CG2	1:A:59:PRO:HG3	2.44	0.48
2:B:242:GLN:N	2:B:243:PRO:CD	2.77	0.48
2:B:325:LEU:HD12	2:B:385:LYS:HG3	1.95	0.48
1:A:41:MET:HE2	1:A:47:ILE:CG2	2.44	0.47
1:A:116:PHE:HZ	4:A:611:HOH:O	1.97	0.47
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.96	0.47
1:A:420:PRO:HA	1:A:421:PRO:C	2.33	0.47
2:B:295:LEU:HD23	2:B:299:ALA:CB	2.42	0.47
1:A:206:ARG:HG2	1:A:216:THR:OG1	2.14	0.47
1:A:380:ILE:HD11	1:A:386:THR:CG2	2.44	0.47
1:A:410:TRP:CE3	2:B:363:ASN:HB3	2.49	0.47
1:A:424:LYS:NZ	1:A:426:TRP:CE2	2.83	0.47
1:A:492:GLU:HA	1:A:530:LYS:O	2.14	0.47
1:A:451:LYS:HD3	1:A:451:LYS:N	2.29	0.47
2:B:266:TRP:CD1	2:B:426:TRP:CE3	3.02	0.47
1:A:103:LYS:O	1:A:236:PRO:HB2	2.15	0.47
1:A:466:VAL:HG21	1:A:551:LEU:HG	1.94	0.47
2:B:58:THR:HG23	2:B:76:ASP:O	2.15	0.47
1:A:402:TRP:CD1	1:A:402:TRP:C	2.87	0.47
2:B:268:SER:HA	2:B:271:TYR:O	2.15	0.47
2:B:396:GLU:O	2:B:400:THR:CG2	2.63	0.47
1:A:101:LYS:N	1:A:101:LYS:HD3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HD23	1:A:210:LEU:HA	1.77	0.47
2:B:396:GLU:O	2:B:400:THR:HG23	2.15	0.47
1:A:5:ILE:HG21	1:A:167:ILE:HD11	1.97	0.47
1:A:72:ARG:HD3	4:A:899:HOH:O	2.15	0.46
1:A:108:VAL:HG21	1:A:223:LYS:HD3	1.96	0.46
2:B:64:LYS:HG3	2:B:68:SER:O	2.14	0.46
2:B:261:VAL:O	2:B:265:ASN:HB3	2.15	0.46
1:A:449:GLU:H	1:A:449:GLU:HG2	1.52	0.46
2:B:354:TYR:OH	2:B:370:GLU:OE2	2.31	0.46
1:A:211:ARG:HD3	1:A:211:ARG:C	2.36	0.46
1:A:219:LYS:CD	1:A:219:LYS:N	2.79	0.46
1:A:450:THR:O	1:A:451:LYS:HB2	2.14	0.46
2:B:24:TRP:CZ3	2:B:59:PRO:HG2	2.51	0.46
1:A:330:GLN:HE21	1:A:338:THR:HG23	1.81	0.46
2:B:263:LYS:HB2	4:B:736:HOH:O	2.16	0.46
1:A:463:ARG:HH11	1:A:463:ARG:CG	2.03	0.46
1:A:466:VAL:CG2	1:A:551:LEU:CG	2.93	0.46
2:B:13:LYS:CE	2:B:86:ASP:N	2.79	0.46
2:B:103:LYS:O	2:B:236:PRO:HD2	2.16	0.46
2:B:337:TRP:HE1	2:B:367:GLN:NE2	2.09	0.46
1:A:279:LEU:HD22	1:A:302:GLU:OE1	2.15	0.46
1:A:362:THR:HG21	1:A:367:GLN:HE21	1.81	0.46
2:B:24:TRP:CZ3	2:B:59:PRO:CB	2.99	0.46
2:B:275:LYS:H	2:B:306:ASN:HD21	1.64	0.46
2:B:271:TYR:HA	2:B:272:PRO:HD2	1.75	0.46
1:A:136:ASN:C	1:A:138:GLU:H	2.19	0.45
1:A:138:GLU:O	1:A:139:THR:CB	2.64	0.45
2:B:72:ARG:NH2	2:B:409:THR:CG2	2.78	0.45
2:B:388:LYS:HE3	2:B:415:GLU:HG3	1.98	0.45
2:B:90:VAL:CG2	2:B:91:GLN:N	2.80	0.45
1:A:410:TRP:CE3	2:B:363:ASN:CB	2.98	0.45
1:A:219:LYS:O	1:A:220:LYS:CB	2.63	0.45
1:A:543:GLY:O	1:A:545:ASN:N	2.50	0.45
2:B:100:LEU:HD13	2:B:179:VAL:HG22	1.99	0.45
2:B:244:ILE:CD1	2:B:266:TRP:CZ3	3.00	0.45
1:A:275:LYS:HE3	1:A:305:GLU:OE2	2.17	0.45
1:A:297:GLU:CA	1:A:298:GLU:N	2.80	0.45
2:B:281:LYS:O	2:B:284:ARG:HG3	2.17	0.45
1:A:125:ARG:HG2	1:A:146:TYR:O	2.16	0.45
2:B:205:LEU:HD22	2:B:209:LEU:HD22	1.99	0.45
2:B:305:GLU:O	2:B:305:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:PRO:HD2	4:A:608:HOH:O	2.16	0.45
1:A:174:GLN:HG2	1:A:174:GLN:H	1.60	0.45
2:B:242:GLN:HG2	2:B:352:GLY:C	2.38	0.45
1:A:199:ARG:NH1	1:A:199:ARG:CG	2.77	0.45
1:A:365:VAL:O	1:A:369:THR:CG2	2.65	0.45
1:A:376:THR:HG23	1:A:386:THR:HG22	1.99	0.45
2:B:169:GLU:HB3	2:B:170:PRO:HD3	1.99	0.45
2:B:257:ILE:HB	2:B:283:LEU:HD21	1.99	0.45
2:B:353:LYS:O	2:B:374:LYS:NZ	2.50	0.45
2:B:371:ALA:O	2:B:375:ILE:HD12	2.17	0.45
1:A:5:ILE:HD13	1:A:163:SER:HB3	1.98	0.44
2:B:270:ILE:HG12	2:B:271:TYR:N	2.32	0.44
2:B:354:TYR:HD2	2:B:374:LYS:HD2	1.82	0.44
1:A:454:LYS:NZ	1:A:556:ILE:CD1	2.80	0.44
1:A:60:VAL:HG13	1:A:130:PHE:HB2	1.99	0.44
1:A:100:LEU:HD22	3:A:561:MRX:H151	1.99	0.44
1:A:107:THR:CG2	1:A:198:HIS:CE1	2.90	0.44
2:B:194:GLU:OE1	2:B:197:GLN:HG3	2.18	0.44
2:B:271:TYR:CD1	2:B:310:LEU:CD1	3.00	0.44
2:B:420:PRO:HB2	2:B:423:VAL:HG23	1.99	0.44
1:A:297:GLU:CB	1:A:298:GLU:N	2.80	0.44
1:A:21:VAL:HG22	1:A:59:PRO:CD	2.38	0.44
1:A:466:VAL:HG21	1:A:551:LEU:CG	2.48	0.44
2:B:214:LEU:N	2:B:214:LEU:CD2	2.76	0.44
2:B:299:ALA:O	2:B:302:GLU:N	2.40	0.44
1:A:60:VAL:HG11	1:A:130:PHE:HD2	1.83	0.44
1:A:51:GLY:N	1:A:53:GLU:OE1	2.46	0.43
1:A:136:ASN:O	1:A:138:GLU:N	2.50	0.43
1:A:457:TYR:O	1:A:464:GLN:HA	2.18	0.43
1:A:107:THR:CG2	1:A:202:ILE:HD11	2.48	0.43
1:A:174:GLN:HB2	4:A:849:HOH:O	2.18	0.43
1:A:2:ILE:HD11	1:A:46:LYS:HD3	2.00	0.43
2:B:125:ARG:HD3	2:B:147:ASN:HD22	1.82	0.43
1:A:173:LYS:HD2	1:A:173:LYS:HA	1.49	0.43
2:B:24:TRP:HZ3	2:B:59:PRO:HG2	1.84	0.43
1:A:287:LYS:HB2	1:A:291:GLU:CD	2.38	0.43
1:A:542:ILE:H	1:A:542:ILE:HG12	1.37	0.43
2:B:13:LYS:HE3	2:B:85:GLN:CA	2.49	0.43
1:A:206:ARG:NH1	1:A:218:ASP:HB3	2.34	0.43
1:A:457:TYR:CD1	1:A:457:TYR:C	2.92	0.43
2:B:169:GLU:HG3	4:B:709:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:264:LEU:HD22	2:B:274:ILE:HG23	2.01	0.43
2:B:320:ASP:HA	2:B:321:PRO:HD2	1.87	0.43
1:A:346:PHE:N	1:A:346:PHE:CD1	2.82	0.43
2:B:362:THR:CG2	2:B:367:GLN:HG3	2.49	0.43
2:B:244:ILE:HD13	2:B:266:TRP:HZ3	1.83	0.42
1:A:356:ARG:NH2	1:A:358:ARG:HH11	2.17	0.42
1:A:180:ILE:HG23	1:A:180:ILE:HD13	1.79	0.42
1:A:236:PRO:HA	3:A:561:MRX:H5	2.01	0.42
1:A:542:ILE:HG13	4:A:578:HOH:O	2.19	0.42
1:A:134:SER:OG	1:A:139:THR:HB	2.20	0.42
2:B:24:TRP:CE3	2:B:61:PHE:HZ	2.37	0.42
2:B:72:ARG:HH22	2:B:409:THR:HG21	1.81	0.42
2:B:250:ASP:O	2:B:251:SER:HB3	2.19	0.42
2:B:237:ASP:OD2	2:B:238:LYS:HD3	2.19	0.42
1:A:540:LYS:CB	1:A:542:ILE:CD1	2.97	0.42
2:B:324:ASP:O	2:B:343:GLN:HG2	2.19	0.42
2:B:354:TYR:CD2	2:B:374:LYS:HD2	2.54	0.42
2:B:388:LYS:HG2	4:B:535:HOH:O	2.18	0.42
1:A:497:THR:O	1:A:535:TRP:HA	2.20	0.42
1:A:311:LYS:O	1:A:312:GLU:CB	2.67	0.42
2:B:182:GLN:NE2	4:B:605:HOH:O	2.24	0.42
1:A:395:LYS:HG3	1:A:414:TRP:CH2	2.55	0.42
2:B:293:ILE:HG13	2:B:293:ILE:O	2.20	0.42
1:A:500:GLN:CG	2:B:422:LEU:CD1	2.97	0.41
2:B:274:ILE:CD1	2:B:309:ILE:HG21	2.50	0.41
2:B:90:VAL:HG23	2:B:91:GLN:N	2.35	0.41
2:B:239:TRP:CZ2	2:B:378:GLU:HG2	2.55	0.41
1:A:439:THR:O	1:A:459:THR:HA	2.21	0.41
1:A:500:GLN:HE21	1:A:500:GLN:HB3	1.67	0.41
1:A:553:SER:OG	1:A:557:ARG:NH1	2.54	0.41
2:B:13:LYS:HE2	2:B:86:ASP:N	2.35	0.41
1:A:59:PRO:HB2	1:A:61:PHE:CZ	2.55	0.41
2:B:312:GLU:CB	2:B:313:PRO:CD	2.97	0.41
2:B:317:VAL:CG1	2:B:347:LYS:HB3	2.49	0.41
1:A:47:ILE:HD12	1:A:144:TYR:CG	2.56	0.41
1:A:399:GLU:HB2	1:A:402:TRP:HZ3	1.83	0.41
1:A:493:VAL:CG2	1:A:528:LYS:HE3	2.51	0.41
1:A:254:VAL:O	1:A:258:GLN:HG3	2.21	0.41
1:A:403:THR:HG22	1:A:404:GLU:N	2.36	0.41
1:A:433:PRO:HB2	2:B:290:THR:HG23	2.03	0.41
1:A:434:ILE:HG21	1:A:492:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:TRP:HZ3	2:B:59:PRO:CG	2.34	0.41
2:B:244:ILE:HD11	2:B:266:TRP:CZ3	2.55	0.41
2:B:346:PHE:HD2	2:B:346:PHE:HA	1.73	0.41
1:A:540:LYS:HB2	1:A:542:ILE:CD1	2.46	0.40
1:A:454:LYS:CG	1:A:556:ILE:CD1	2.98	0.40
2:B:65:LYS:HG2	2:B:407:GLN:O	2.20	0.40
2:B:282:LEU:HD12	2:B:293:ILE:HD12	2.02	0.40
2:B:88:TRP:CZ3	2:B:89:GLU:HB2	2.57	0.40
2:B:253:THR:CG2	2:B:255:ASN:HB3	2.52	0.40
2:B:345:PRO:O	2:B:347:LYS:HD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	548/563 (97%)	510 (93%)	27 (5%)	11 (2%)	7	9
2	B	399/443 (90%)	372 (93%)	19 (5%)	8 (2%)	7	9
All	All	947/1006 (94%)	882 (93%)	46 (5%)	19 (2%)	7	9

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	139	THR
1	A	356	ARG
1	A	543	GLY
2	B	14	PRO
2	B	241	VAL
2	B	242	GLN
2	B	243	PRO
1	A	114	ALA

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Mol	Chain	Res	Type
1	A	140	PRO
1	A	492	GLU
1	A	542	ILE
1	A	544	GLY
2	B	66	LYS
1	A	137	ASN
1	A	312	GLU
2	B	13	LYS
2	B	269	GLN
2	B	251	SER
1	A	220	LYS

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	494/503 (98%)	402 (81%)	92 (19%)	1 2
2	B	369/403 (92%)	305 (83%)	64 (17%)	2 2
All	All	863/906 (95%)	707 (82%)	156 (18%)	1 2

All (156) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	6	GLU
1	A	7	THR
1	A	21	VAL
1	A	22	LYS
1	A	24	TRP
1	A	26	LEU
1	A	42	GLU
1	A	43	LYS
1	A	49	LYS
1	A	68	SER
1	A	70	LYS

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Mol	Chain	Res	Type
1	A	72	ARG
1	A	74	LEU
1	A	82	LYS
1	A	92	LEU
1	A	94	ILE
1	A	101	LYS
1	A	103	LYS
1	A	104	LYS
1	A	107	THR
1	A	118	VAL
1	A	126	LYS
1	A	134	SER
1	A	142	ILE
1	A	162	SER
1	A	173	LYS
1	A	174	GLN
1	A	175	ASN
1	A	180	ILE
1	A	195	ILE
1	A	197	GLN
1	A	201	LYS
1	A	205	LEU
1	A	210	LEU
1	A	211	ARG
1	A	219	LYS
1	A	220	LYS
1	A	223	LYS
1	A	228	LEU
1	A	245	VAL
1	A	249	LYS
1	A	260	LEU
1	A	276	VAL
1	A	277	ARG
1	A	279	LEU
1	A	284	ARG
1	A	286	THR
1	A	287	LYS
1	A	291	GLU
1	A	301	LEU
1	A	303	LEU
1	A	311	LYS
1	A	312	GLU

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Mol	Chain	Res	Type
1	A	334	GLN
1	A	347	LYS
1	A	356	ARG
1	A	358	ARG
1	A	368	LEU
1	A	369	THR
1	A	402	TRP
1	A	403	THR
1	A	422	LEU
1	A	425	LEU
1	A	429	LEU
1	A	431	LYS
1	A	449	GLU
1	A	451	LYS
1	A	454	LYS
1	A	459	THR
1	A	461	ARG
1	A	463	ARG
1	A	464	GLN
1	A	471	ASP
1	A	472	THR
1	A	475	GLN
1	A	479	LEU
1	A	491	LEU
1	A	493	VAL
1	A	496	VAL
1	A	500	GLN
1	A	503	LEU
1	A	514	GLU
1	A	516	GLU
1	A	523	GLU
1	A	529	GLU
1	A	540	LYS
1	A	542	ILE
1	A	547	GLN
1	A	550	LYS
1	A	552	VAL
1	A	557	ARG
2	B	8	VAL
2	B	11	LYS
2	B	12	LEU
2	B	13	LYS

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Mol	Chain	Res	Type
2	B	16	MET
2	B	20	LYS
2	B	22	LYS
2	B	26	LEU
2	B	64	LYS
2	B	65	LYS
2	B	66	LYS
2	B	67	ASP
2	B	68	SER
2	B	72	ARG
2	B	80	LEU
2	B	82	LYS
2	B	91	GLN
2	B	111	VAL
2	B	120	LEU
2	B	162	SER
2	B	173	LYS
2	B	179	VAL
2	B	199	ARG
2	B	205	LEU
2	B	209	LEU
2	B	211	ARG
2	B	212	TRP
2	B	214	LEU
2	B	237	ASP
2	B	238	LYS
2	B	240	THR
2	B	241	VAL
2	B	249	LYS
2	B	253	THR
2	B	259	LYS
2	B	260	LEU
2	B	261	VAL
2	B	265	ASN
2	B	270	ILE
2	B	275	LYS
2	B	277	ARG
2	B	278	GLN
2	B	279	LEU
2	B	282	LEU
2	B	284	ARG
2	B	293	ILE

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Mol	Chain	Res	Type
2	B	295	LEU
2	B	297	GLU
2	B	310	LEU
2	B	311	LYS
2	B	314	VAL
2	B	334	GLN
2	B	336	GLN
2	B	341	ILE
2	B	347	LYS
2	B	349	LEU
2	B	353	LYS
2	B	356	ARG
2	B	362	THR
2	B	369	THR
2	B	400	THR
2	B	405	TYR
2	B	425	LEU
2	B	428	GLN

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

Mol	Chain	Res	Type
1	A	57	ASN
1	A	137	ASN
1	A	147	ASN
1	A	151	GLN
1	A	198	HIS
1	A	258	GLN
1	A	330	GLN
1	A	500	GLN
1	A	507	GLN
1	A	509	GLN
1	A	519	ASN
1	A	547	GLN
2	B	96	HIS
2	B	147	ASN
2	B	175	ASN
2	B	182	GLN
2	B	278	GLN
2	B	306	ASN
2	B	336	GLN
2	B	367	GLN

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Mol	Chain	Res	Type
2	B	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](#)

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	MRX	A	561	-	21,23,23	3.09	8 (38%)	26,35,35	3.59	13 (50%)

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	MRX	A	561	-	-	0/6/23/23	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	561	MRX	S10-N11	9.98	1.77	1.63
3	A	561	MRX	C18-N20	5.45	1.43	1.33
3	A	561	MRX	O16-S10	4.45	1.48	1.43
3	A	561	MRX	C8-C18	-3.20	1.42	1.51
3	A	561	MRX	C1-C6	3.06	1.41	1.36
3	A	561	MRX	BR-C6	2.71	1.95	1.90
3	A	561	MRX	O19-C18	2.45	1.28	1.24
3	A	561	MRX	C5-C6	2.18	1.42	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	561	MRX	O17-S10-O16	8.24	132.88	119.52
3	A	561	MRX	C8-C18-N20	7.67	127.86	115.75
3	A	561	MRX	O17-S10-N11	-7.12	100.19	106.69
3	A	561	MRX	O16-S10-N11	-5.26	101.89	106.69
3	A	561	MRX	C8-N9-C3	5.16	114.50	103.90
3	A	561	MRX	O19-C18-N20	-5.11	115.31	122.58
3	A	561	MRX	C14-C15-N11	3.95	109.24	103.43
3	A	561	MRX	C5-C6-C1	-3.54	117.06	121.99
3	A	561	MRX	BR-C6-C1	3.19	124.40	119.72
3	A	561	MRX	C13-C12-N11	-2.92	99.15	103.43
3	A	561	MRX	C7-S10-N11	2.67	108.98	103.46
3	A	561	MRX	O17-S10-C7	-2.67	103.04	108.18
3	A	561	MRX	C6-C1-C2	2.27	122.61	119.79

There are no chirality outliers.

There are no torsion outliers.

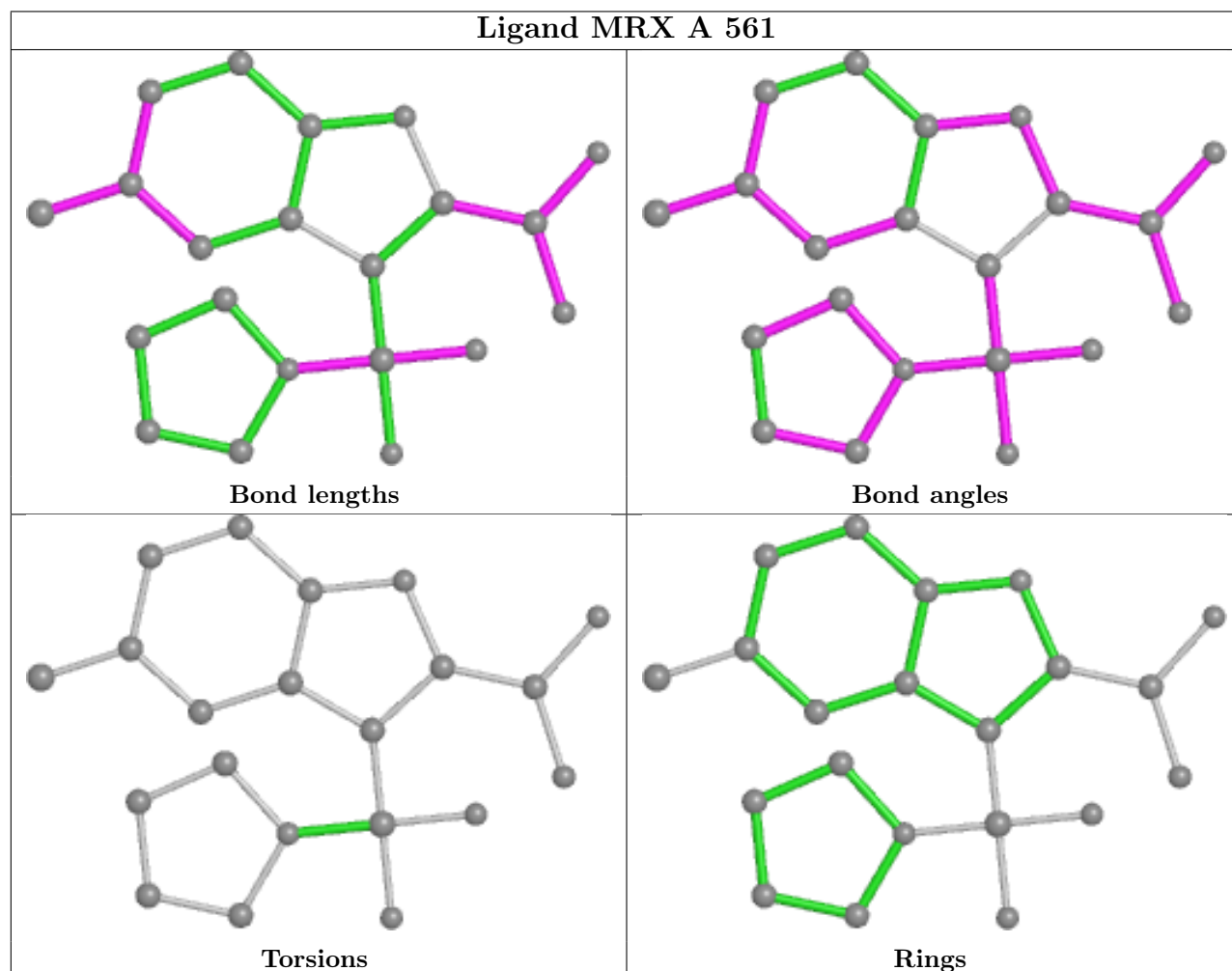
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	561	MRX	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	297:GLU	C	298:GLU	N	2.65

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.