



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:36 AM GMT

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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

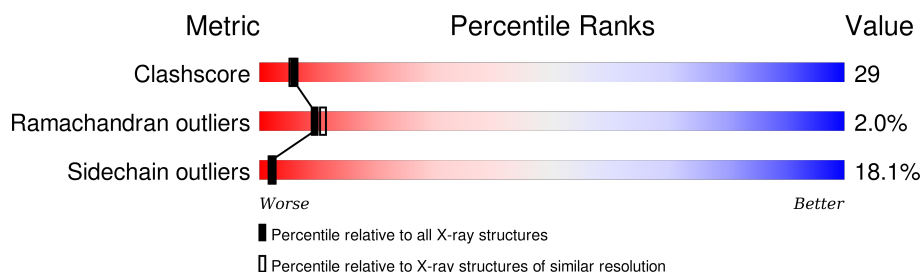
1 Overall quality at a glance ⓘ

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	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

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

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
1	A	554	Total	C	N	O	S	0	0	0
			4510	2915	754	833	8			

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

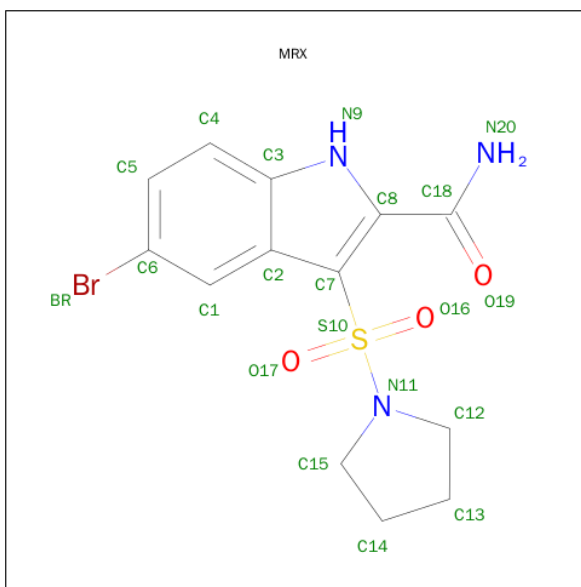
- Molecule 2 is a protein called Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4) (p66 RT).

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

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-CARBOXYAMIDE (three-letter code: MRX) (formula: C₁₃H₁₄BrN₃O₃S).



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

- Molecule 4 is water.

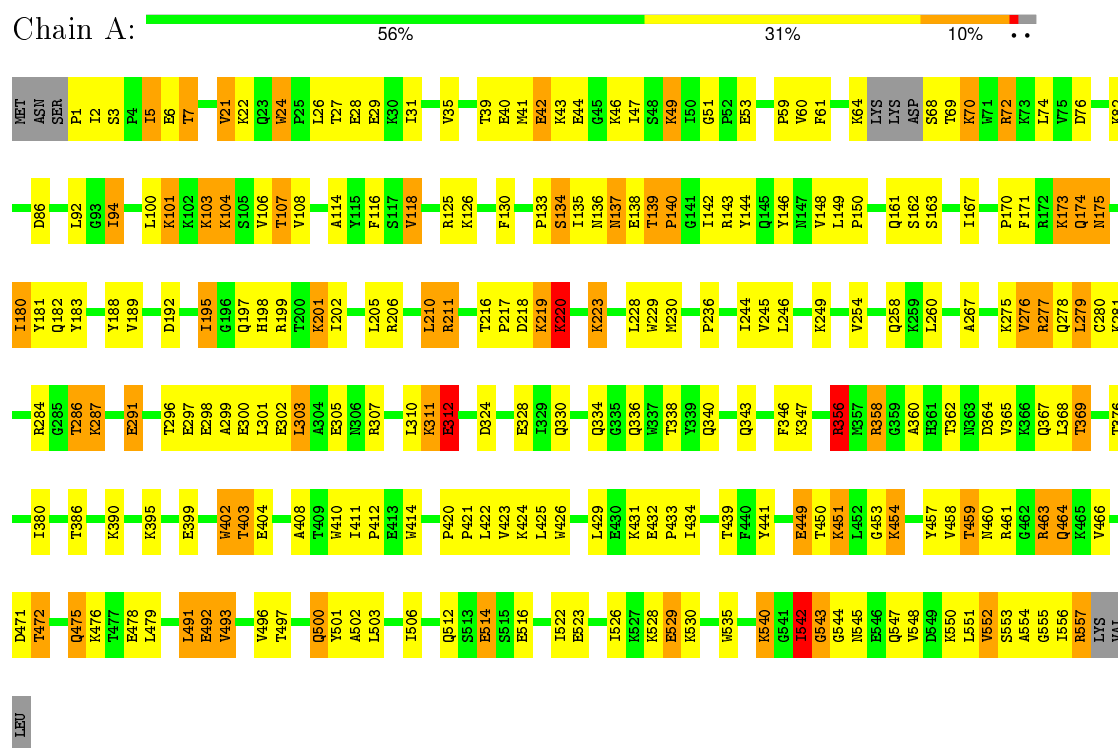
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	413	Total	O	0	0
			413	413		
4	B	297	Total	O	0	0
			297	297		

3 Residue-property plots

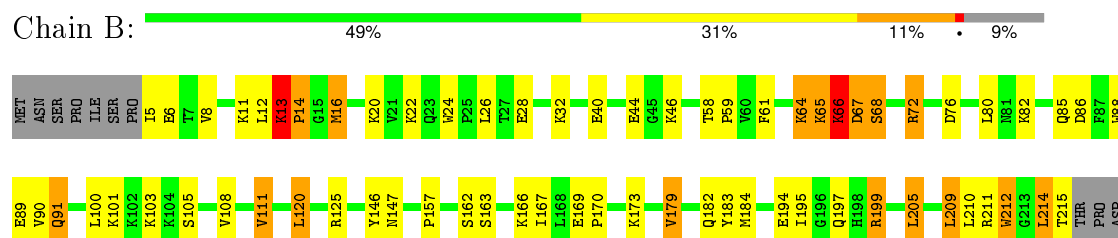
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

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
PHE	A288	GLY	THR
LEU	L289	ALA	PHE
TRP	T290	H361	
MET	L293	T362	
E231	P294	N363	
Y232	L295	D364	
E233	T296	T365	
	E297	K366	
	E298	Q367	
P236	E299	L368	
D237	E300	T369	
K238	L301	E370	
W239	E302	A371	
T240	L303	V372	
Y241	A304	Q373	
Q242	E305	K374	
P243	N306	L375	
I244		T376	
Y245	I309	T377	
L246	L310	E378	
	K311	K385	
K249	E312		
D250	P313	K388	
S251	V314	F389	
W252	H315	K390	
T253	G316		
V254	V317	E396	
N255	Y318		
D256	Y319	T400	
I257	D320	W401	
Q258	P321		
K259		Y405	
L260	D324	W406	
V261	L325	Q407	
Q262	K263	A408	
K263	L264	T409	
L264	W266	W410	
W266	Q334	E415	
A267	G335		
S268	Q336	P420	
Q269	W337	P421	
I270		L422	
Y271	I341	V423	
P272	Y342	K424	
Q273	Q343	L425	
I274	E344	W426	
K275	P345	Y427	
V276	F346	Q428	
W277	K347	LEU	
K278	N348	GLU	
L279	L349	LYS	
C280			

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	119.29 Å 155.81 Å 155.86 Å 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.	Xtriage
Total number of atoms	8593	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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:HD23	2:B:214:LEU:H	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
2:B:274:ILE:HA	2:B:306:ASN:HD21	1.41	0.85
1:A:297:GLU:O	1:A:298:GLU:N	2.07	0.85
1:A:356:ARG:NE	1:A:358:ARG:HG3	1.92	0.84
1:A:195:ILE:H	1:A:195:ILE:HD12	1.41	0.84
1:A:454:LYS:CD	1:A:556:ILE:HD13	2.08	0.84
1:A:24:TRP:H	1:A:24:TRP:HD1	1.24	0.84
2:B:274:ILE:HA	2:B:306:ASN:ND2	1.93	0.83
1:A:399:GLU:O	1:A:403:THR:HB	1.79	0.83
1:A:478:GLU:HG3	4:A:596:HOH:O	1.80	0.82
1:A:411:ILE:HG22	1:A:412:PRO:O	1.79	0.82
1:A:199:ARG:HH11	1:A:199:ARG:HG2	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
2:B:214:LEU:N	2:B:214:LEU:HD23	2.03	0.73
2:B:125:ARG:HG2	2:B:146:TYR:O	1.88	0.73
1:A:219:LYS:O	1:A:220:LYS:HB3	1.89	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:H	2:B:303:LEU:HD23	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:399:GLU:HA	1:A:402:TRP:HE3	1.52	0.70
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.74	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:296:THR:HG21	4:A:597:HOH:O	1.93	0.68
1:A:223:LYS:CD	1:A:223:LYS:H	2.03	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
2:B:246:LEU:HD11	2:B:310:LEU:CD2	2.19	0.68
1:A:367:GLN:NE2	1:A:512:GLN:OE1	2.27	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
2:B:295:LEU:HD23	2:B:299:ALA:HB3	1.77	0.66
1:A:540:LYS:CB	1:A:542:ILE:HD11	2.26	0.66
1:A:454:LYS:HZ3	1:A:556:ILE:CD1	2.09	0.66
1:A:223:LYS:N	1:A:223:LYS:HD2	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
2:B:282:LEU:HD12	2:B:293:ILE:CD1	2.26	0.65
1:A:139:THR:HG22	1:A:140:PRO:N	2.12	0.65
2:B:363:ASN:HA	4:B:580:HOH:O	1.97	0.65
2:B:345:PRO:O	2:B:346:PHE:HB2	1.96	0.65
2:B:16:MET:HA	2:B:16:MET:HE2	1.78	0.65
1:A:51:GLY:O	1:A:143:ARG:NH1	2.30	0.65
1:A:171:PHE:O	1:A:175:ASN:ND2	2.29	0.64
2:B:377:THR:HG22	2:B:410:TRP:HZ2	1.61	0.64
2:B:276:VAL:HG12	2:B:280:CYS:SG	2.36	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:282:LEU:HD21	2:B:299:ALA:CB	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:GLU:O	2:B:44:GLU:HG3	1.98	0.63
2:B:273:GLY:O	2:B:275:LYS:HG2	1.99	0.63
2:B:103:LYS:HE3	2:B:179:VAL:HG13	1.81	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:NH1	1:A:463:ARG:HG2	1.99	0.62
2:B:195:ILE:O	2:B:199:ARG:HG3	1.98	0.62
2:B:16:MET:CE	2:B:16:MET:HA	2.28	0.62
2:B:253:THR:HG23	2:B:255:ASN:H	1.65	0.61
1:A:472:THR:HG22	1:A:476:LYS:CB	2.30	0.61
1:A:365:VAL:O	1:A:369:THR:HG23	2.01	0.61
2:B:295:LEU:HD22	2:B:300:GLU:HG2	1.82	0.61
1:A:362:THR:CG2	1:A:367:GLN:HE21	2.14	0.60
1:A:94:ILE:HD13	1:A:230:MET:HG3	1.82	0.60
2:B:362:THR:HG23	2:B:366:LYS:HZ2	1.66	0.60
1:A:106:VAL:HG11	3:A:561:MRX:BR	2.56	0.60
1:A:28:GLU:HG2	1:A:135:ILE:HG12	1.82	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
2:B:279:LEU:O	2:B:282:LEU:HB2	2.02	0.60
1:A:3:SER:CB	1:A:5:ILE:HG12	2.31	0.60
1:A:556:ILE:N	1:A:556:ILE:HD12	2.17	0.60
1:A:60:VAL:HG11	1:A:130:PHE:CD2	2.37	0.60
2:B:286:THR:O	2:B:286:THR:HG23	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:N	1:A:24:TRP:CD1	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
2:B:252:TRP:CD1	2:B:295:LEU:HD12	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLU:HB2	1:A:402:TRP:CZ3	2.38	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:1:PRO:HD3	4:A:639:HOH:O	2.03	0.58
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.84	0.58
1:A:432:GLU:OE1	1:A:432:GLU:HA	2.04	0.57
1:A:324:ASP:O	1:A:343:GLN:HG2	2.03	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:500:GLN:HG2	2:B:422:LEU:HD12	1.87	0.57
1:A:199:ARG:NH1	1:A:199:ARG:HG2	2.17	0.57
2:B:317:VAL:HG13	2:B:347:LYS:HB3	1.87	0.57
1:A:556:ILE:O	1:A:556:ILE:HG22	2.05	0.57
1:A:441:TYR:O	1:A:548:VAL:HG21	2.05	0.56
1:A:303:LEU:HD13	1:A:307:ARG:NH1	2.20	0.56
1:A:246:LEU:HD11	1:A:310:LEU:CD1	2.34	0.56
2:B:282:LEU:CD2	2:B:299:ALA:HB2	2.34	0.56
2:B:266:TRP:CH2	2:B:427:TYR:CZ	2.92	0.56
2:B:86:ASP:O	2:B:90:VAL:HG22	2.04	0.56
1:A:211:ARG:O	1:A:211:ARG:NH1	2.28	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:422:LEU:O	2:B:425:LEU:HG	2.05	0.55
2:B:278:GLN:NE2	2:B:281:LYS:NZ	2.54	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
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:466:VAL:HG21	1:A:551:LEU:CD1	2.37	0.54
2:B:297:GLU:HA	2:B:300:GLU:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:377:THR:HG22	2:B:410:TRP:CZ2	2.42	0.54
1:A:138:GLU:O	1:A:139:THR:HB	2.08	0.54
1:A:555:GLY:C	1:A:556:ILE:HD12	2.27	0.54
1:A:3:SER:HB3	1:A:5:ILE:HG12	1.89	0.54
2:B:240:THR:O	2:B:241:VAL:O	2.26	0.54
1:A:311:LYS:O	1:A:312:GLU:HB3	2.08	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
2:B:362:THR:HG22	2:B:367:GLN:HG3	1.89	0.53
1:A:502:ALA:O	1:A:506:ILE:HD12	2.08	0.53
1:A:278:GLN:OE1	1:A:281:LYS:NZ	2.31	0.53
1:A:47:ILE:HD12	1:A:144:TYR:CD1	2.43	0.53
1:A:64:LYS:HE2	1:A:69:THR:CG2	2.14	0.53
1:A:69:THR:HG22	1:A:69:THR:O	2.08	0.53
1:A:180:ILE:HG22	1:A:189:VAL:HG13	1.91	0.53
2:B:334:GLN:HG3	2:B:334:GLN:O	2.09	0.53
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.09	0.53
2:B:300:GLU:HA	2:B:303:LEU:HD21	1.90	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
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:409:THR:HG21	4:B:451:HOH:O	2.09	0.52
2:B:157:PRO:HG3	2:B:184:MET:HA	1.91	0.52
1:A:296:THR:HG22	1:A:299:ALA:HB2	1.90	0.52
1:A:134:SER:HB2	1:A:140:PRO:O	2.10	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:408:ALA:HB1	2:B:364:ASP:HB3	1.91	0.52
1:A:41:MET:HE2	1:A:47:ILE:HG23	1.91	0.52
1:A:40:GLU:O	1:A:44:GLU:HG3	2.08	0.52
1:A:356:ARG:HH21	1:A:358:ARG:HD2	1.74	0.52
1:A:298:GLU:OE2	1:A:298:GLU:N	2.42	0.52
1:A:312:GLU:HB2	4:A:922:HOH:O	2.08	0.52
2:B:301:LEU:O	2:B:304:ALA:HB3	2.10	0.52
2:B:241:VAL:HB	2:B:243:PRO:HD3	1.91	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
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: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
1:A:31:ILE:HD13	1:A:133:PRO:O	2.10	0.51
2:B:297:GLU:OE1	2:B:300:GLU:OE2	2.29	0.51
2:B:261:VAL:HB	2:B:276:VAL:HG13	1.92	0.51
1:A:466:VAL:CG2	1:A:551:LEU:HD11	2.40	0.51
2:B:24:TRP:CZ3	2:B:59:PRO:CG	2.94	0.51
1:A:500:GLN:HG2	2:B:422:LEU:CD1	2.41	0.51
1:A:458:VAL:CG1	1:A:548:VAL:HG22	2.33	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
2:B:86:ASP:OD2	2:B:90:VAL:HG21	2.11	0.50
1:A:395:LYS:HD3	4:A:853:HOH:O	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:548:VAL:O	1:A:552:VAL:HB	2.11	0.50
1:A:466:VAL:CG2	1:A:551:LEU:HG	2.42	0.50
2:B:242:GLN:HG2	2:B:352:GLY:CA	2.42	0.50
2:B:266:TRP:O	2:B:268:SER:O	2.29	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
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:236:PRO:HA	2:B:239:TRP:CD2	2.46	0.49
2:B:233:GLU:HB2	4:B:510:HOH:O	2.12	0.49
2:B:108:VAL:HB	2:B:232:TYR:HB3	1.94	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:HG13	2:B:111:VAL:O	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)
2:B:303:LEU:HD23	2:B:303:LEU:N	2.25	0.49
2:B:101:LYS:O	2:B:236:PRO:HB2	2.13	0.49
1:A:137:ASN:OD1	1:A:137:ASN:O	2.30	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:CD	1:A:219:LYS:H	2.21	0.48
1:A:276:VAL:HG13	1:A:280:CYS:SG	2.53	0.48
1:A:330:GLN:HE22	1:A:340:GLN:NE2	1.91	0.48
1:A:118:VAL:HG22	1:A:149:LEU:HG	1.93	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
2:B:44:GLU:OE2	2:B:46:LYS:HE2	2.14	0.48
1:A:424:LYS:NZ	1:A:426:TRP:CZ2	2.81	0.48
1:A:108:VAL:CG1	1:A:188:TYR:CD2	2.96	0.48
1:A:297:GLU:C	1:A:300:GLU:HB2	2.34	0.48
1:A:24:TRP:HE1	1:A:59:PRO:HB3	1.79	0.48
1:A:219:LYS:HD2	1:A:219:LYS:N	2.29	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
2:B:295:LEU:HD23	2:B:299:ALA:CB	2.42	0.47
1:A:116:PHE:HZ	4:A:611:HOH:O	1.97	0.47
1:A:420:PRO:HA	1:A:421:PRO:C	2.33	0.47
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.96	0.47
1:A:410:TRP:CE3	2:B:363:ASN:HB3	2.49	0.47
1:A:380:ILE:HD11	1:A:386:THR:CG2	2.44	0.47
1:A:206:ARG:HG2	1:A:216:THR:OG1	2.14	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
2:B:266:TRP:CD1	2:B:426:TRP:CE3	3.02	0.47
1:A:451:LYS:N	1:A:451:LYS:HD3	2.29	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
2:B:268:SER:HA	2:B:271:TYR:O	2.15	0.47
1:A:402:TRP:CD1	1:A:402:TRP:C	2.87	0.47
2:B:396:GLU:O	2:B:400:THR:CG2	2.63	0.47
2:B:396:GLU:O	2:B:400:THR:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HA	1:A:210:LEU:HD23	1.77	0.47
1:A:101:LYS:N	1:A:101:LYS:HD3	2.29	0.47
1:A:5:ILE:HG21	1:A:167:ILE:HD11	1.97	0.47
1:A:108:VAL:HG21	1:A:223:LYS:HD3	1.96	0.46
1:A:72:ARG:HD3	4:A:899:HOH:O	2.15	0.46
2:B:261:VAL:O	2:B:265:ASN:HB3	2.15	0.46
2:B:64:LYS:HG3	2:B:68:SER:O	2.14	0.46
2:B:354:TYR:OH	2:B:370:GLU:OE2	2.31	0.46
1:A:449:GLU:H	1:A:449:GLU:HG2	1.52	0.46
1:A:219:LYS:N	1:A:219:LYS:CD	2.79	0.46
1:A:211:ARG:C	1:A:211:ARG:HD3	2.36	0.46
2:B:24:TRP:CZ3	2:B:59:PRO:HG2	2.51	0.46
1:A:450:THR:O	1:A:451:LYS:HB2	2.14	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:CG	1:A:463:ARG:HH11	2.03	0.46
2:B:13:LYS:CE	2:B:86:ASP:N	2.79	0.46
1:A:466:VAL:CG2	1:A:551:LEU:CG	2.93	0.46
2:B:337:TRP:HE1	2:B:367:GLN:NE2	2.09	0.46
2:B:103:LYS:O	2:B:236:PRO:HD2	2.16	0.46
2:B:275:LYS:H	2:B:306:ASN:HD21	1.64	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
1:A:279:LEU:HD22	1:A:302:GLU:OE1	2.15	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
2:B:244:ILE:CD1	2:B:266:TRP:CZ3	3.00	0.45
1:A:219:LYS:O	1:A:220:LYS:CB	2.63	0.45
2:B:100:LEU:HD13	2:B:179:VAL:HG22	1.99	0.45
1:A:543:GLY:O	1:A:545:ASN:N	2.50	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:275:LYS:HE3	1:A:305:GLU:OE2	2.17	0.45
2:B:205:LEU:HD22	2:B:209:LEU:HD22	1.99	0.45
2:B:305:GLU:HG2	2:B:305:GLU:O	2.17	0.45
1:A:125:ARG:HG2	1:A:146:TYR:O	2.16	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:H	1:A:174:GLN:HG2	1.60	0.45
2:B:242:GLN:HG2	2:B:352:GLY:C	2.38	0.45
2:B:257:ILE:HB	2:B:283:LEU:HD21	1.99	0.45
1:A:199:ARG:NH1	1:A:199:ARG:CG	2.77	0.45
2:B:353:LYS:O	2:B:374:LYS:NZ	2.50	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:371:ALA:O	2:B:375:ILE:HD12	2.17	0.45
2:B:169:GLU:HB3	2:B:170:PRO:HD3	1.99	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
2:B:271:TYR:CD1	2:B:310:LEU:CD1	3.00	0.44
1:A:107:THR:CG2	1:A:198:HIS:CE1	2.90	0.44
1:A:100:LEU:HD22	3:A:561:MRX:H151	1.99	0.44
1:A:60:VAL:HG13	1:A:130:PHE:HB2	1.99	0.44
2:B:194:GLU:OE1	2:B:197:GLN:HG3	2.18	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
2:B:299:ALA:O	2:B:302:GLU:N	2.40	0.44
2:B:214:LEU:N	2:B:214:LEU:CD2	2.76	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
1:A:60:VAL:HG11	1:A:130:PHE:HD2	1.83	0.44
1:A:136:ASN:O	1:A:138:GLU:N	2.50	0.43
1:A:51:GLY:N	1:A:53:GLU:OE1	2.46	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
2:B:125:ARG:HD3	2:B:147:ASN:HD22	1.82	0.43
1:A:2:ILE:HD11	1:A:46:LYS:HD3	2.00	0.43
2:B:24:TRP:HZ3	2:B:59:PRO:HG2	1.84	0.43
1:A:173:LYS:HD2	1:A:173:LYS:HA	1.49	0.43
2:B:13:LYS:HE3	2:B:85:GLN:CA	2.49	0.43
1:A:542:ILE:H	1:A:542:ILE:HG12	1.37	0.43
1:A:287:LYS:HB2	1:A:291:GLU:CD	2.38	0.43
1:A:206:ARG:NH1	1:A:218:ASP:HB3	2.34	0.43
2:B:264:LEU:HD22	2:B:274:ILE:HG23	2.01	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)
1:A:457:TYR:C	1:A:457:TYR:CD1	2.92	0.43
2:B:320:ASP:HA	2:B:321:PRO:HD2	1.87	0.43
2:B:362:THR:CG2	2:B:367:GLN:HG3	2.49	0.43
1:A:346:PHE:CD1	1:A:346:PHE:N	2.82	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:HD13	1:A:180:ILE:HG23	1.79	0.42
1:A:542:ILE:HG13	4:A:578:HOH:O	2.19	0.42
1:A:236:PRO:HA	3:A:561:MRX:H5	2.01	0.42
1:A:134:SER:OG	1:A:139:THR:HB	2.20	0.42
2:B:72:ARG:HH22	2:B:409:THR:HG21	1.81	0.42
2:B:24:TRP:CE3	2:B:61:PHE:HZ	2.37	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
2:B:354:TYR:CD2	2:B:374:LYS:HD2	2.54	0.42
1:A:540:LYS:CB	1:A:542:ILE:CD1	2.97	0.42
2:B:388:LYS:HG2	4:B:535:HOH:O	2.18	0.42
2:B:324:ASP:O	2:B:343:GLN:HG2	2.19	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
2:B:293:ILE:HG13	2:B:293:ILE:O	2.20	0.42
1:A:395:LYS:HG3	1:A:414:TRP:CH2	2.55	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: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:439:THR:O	1:A:459:THR:HA	2.21	0.41
1:A:59:PRO:HB2	1:A:61:PHE:CZ	2.55	0.41
2:B:317:VAL:CG1	2:B:347:LYS:HB3	2.49	0.41
2:B:312:GLU:CB	2:B:313:PRO:CD	2.97	0.41
1:A:399:GLU:HB2	1:A:402:TRP:HZ3	1.83	0.41
1:A:47:ILE:HD12	1:A:144:TYR:CG	2.56	0.41
1:A:493:VAL:CG2	1:A:528:LYS:HE3	2.51	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:254:VAL:O	1:A:258:GLN:HG3	2.21	0.41
2:B:244:ILE:HD11	2:B:266:TRP:CZ3	2.55	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
1:A:434:ILE:HG21	1:A:492:GLU:OE2	2.20	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:253:THR:CG2	2:B:255:ASN:HB3	2.52	0.40
2:B:88:TRP:CZ3	2:B:89:GLU:HB2	2.57	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

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	548/563 (97%)	510 (93%)	27 (5%)	11 (2%)	9	11
2	B	399/443 (90%)	372 (93%)	19 (5%)	8 (2%)	9	11
All	All	947/1006 (94%)	882 (93%)	46 (5%)	19 (2%)	9	11

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 ⓘ

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%)	2	2
2	B	369/403 (92%)	305 (83%)	64 (17%)	2	2
All	All	863/906 (95%)	707 (82%)	156 (18%)	2	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

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	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 ⓘ

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	MRX	A	561	-	20,23,23	3.00	8 (40%)	27,35,35	3.84	15 (55%)

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	C8-C18	-3.18	1.42	1.51
3	A	561	MRX	C5-C6	2.04	1.42	1.38
3	A	561	MRX	O19-C18	2.19	1.28	1.24
3	A	561	MRX	BR-C6	2.47	1.95	1.90
3	A	561	MRX	C1-C6	3.04	1.41	1.36
3	A	561	MRX	O16-S10	3.87	1.48	1.43
3	A	561	MRX	C18-N20	5.13	1.43	1.33
3	A	561	MRX	S10-N11	9.61	1.77	1.63

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	561	MRX	C1-C2-C3	-7.78	117.27	120.34
3	A	561	MRX	O17-S10-N11	-6.58	100.19	106.69
3	A	561	MRX	C5-C6-C1	-5.48	117.06	121.93
3	A	561	MRX	O19-C18-N20	-5.17	115.31	122.59
3	A	561	MRX	O16-S10-N11	-4.86	101.89	106.69
3	A	561	MRX	C12-N11-C15	-4.02	101.00	110.17
3	A	561	MRX	O17-S10-C7	-3.00	103.04	108.80
3	A	561	MRX	C13-C12-N11	-2.10	99.15	103.35
3	A	561	MRX	C4-C5-C6	2.44	121.72	119.25
3	A	561	MRX	C14-C15-N11	2.95	109.24	103.35
3	A	561	MRX	C7-S10-N11	3.04	108.98	102.61
3	A	561	MRX	BR-C6-C1	3.68	124.40	119.83
3	A	561	MRX	C8-N9-C3	5.20	114.50	103.94
3	A	561	MRX	C8-C18-N20	6.99	127.86	115.90
3	A	561	MRX	O17-S10-O16	7.78	132.88	119.47

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

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.