



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 30, 2022 – 12:31 am GMT

PDB ID : 3ZG5
Title : Crystal structure of PBP2a from MRSA in complex with peptidoglycan analogue at allosteric
Authors : Otero, L.H.; Rojas-Altuve, A.; Hermoso, J.A.
Deposited on : 2012-12-14
Resolution : 2.55 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

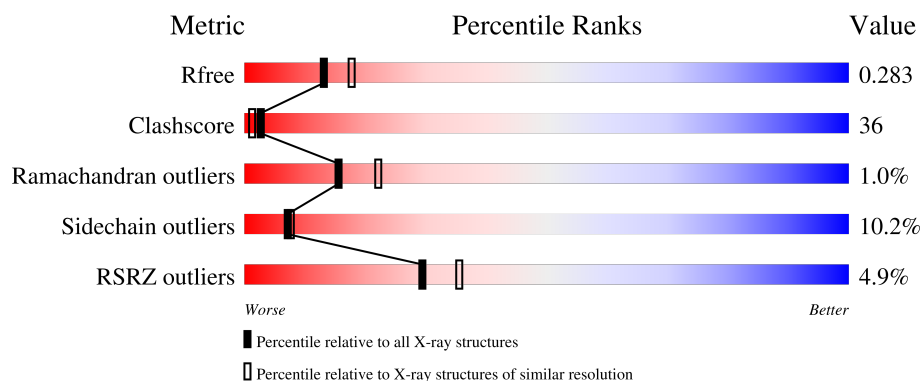
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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

Mol	Chain	Length	Quality of chain
1	A	642	<div> <div>2%</div> <div>57%</div> <div>38%</div> <div>..</div> </div>
1	B	642	<div> <div>7%</div> <div>53%</div> <div>37%</div> <div>9%</div> <div>..</div> </div>
2	C	5	<div> <div>40%</div> <div>20%</div> <div>60%</div> <div>20%</div> </div>
2	D	5	<div> <div>40%</div> <div>20%</div> <div>40%</div> <div>40%</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
2	FGA	C	3	-	-	X	X
2	FGA	D	3	-	-	X	X
2	DAL	D	5	-	-	-	X
2	DAL	D	6	-	-	-	X
5	AMV	C	101	-	-	X	X
5	AMV	D	101	-	-	X	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10542 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 Penicillin binding protein 2 prime.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	636	Total	C	N	O	S	0	0	0
			5105	3219	862	1009	15			
1	B	636	Total	C	N	O	S	0	0	0
			5105	3219	862	1009	15			

- Molecule 2 is a protein called PEPTIDOGLYCAN ANALOGUE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			34	20	6	8			
2	D	5	Total	C	N	O	0	0	0
			34	20	6	8			

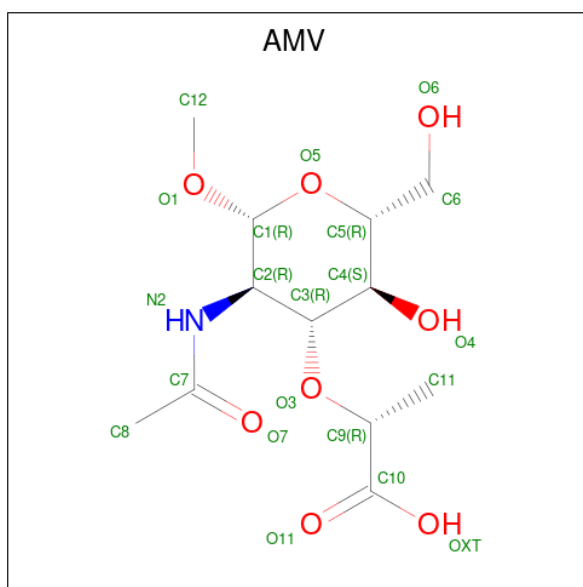
- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Cd	0	0
			2	2		
3	B	2	Total	Cd	0	0
			2	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		
4	B	2	Total	Cl	0	0
			2	2		

- Molecule 5 is methyl 2-acetamido-3-O-[(1R)-1-carboxyethyl]-2-deoxy-beta-D-glucopyranoside (three-letter code: AMV) (formula: C₁₂H₂₁NO₈).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			20	12	1	7		
5	D	1	Total	C	N	O	0	0
			20	12	1	7		

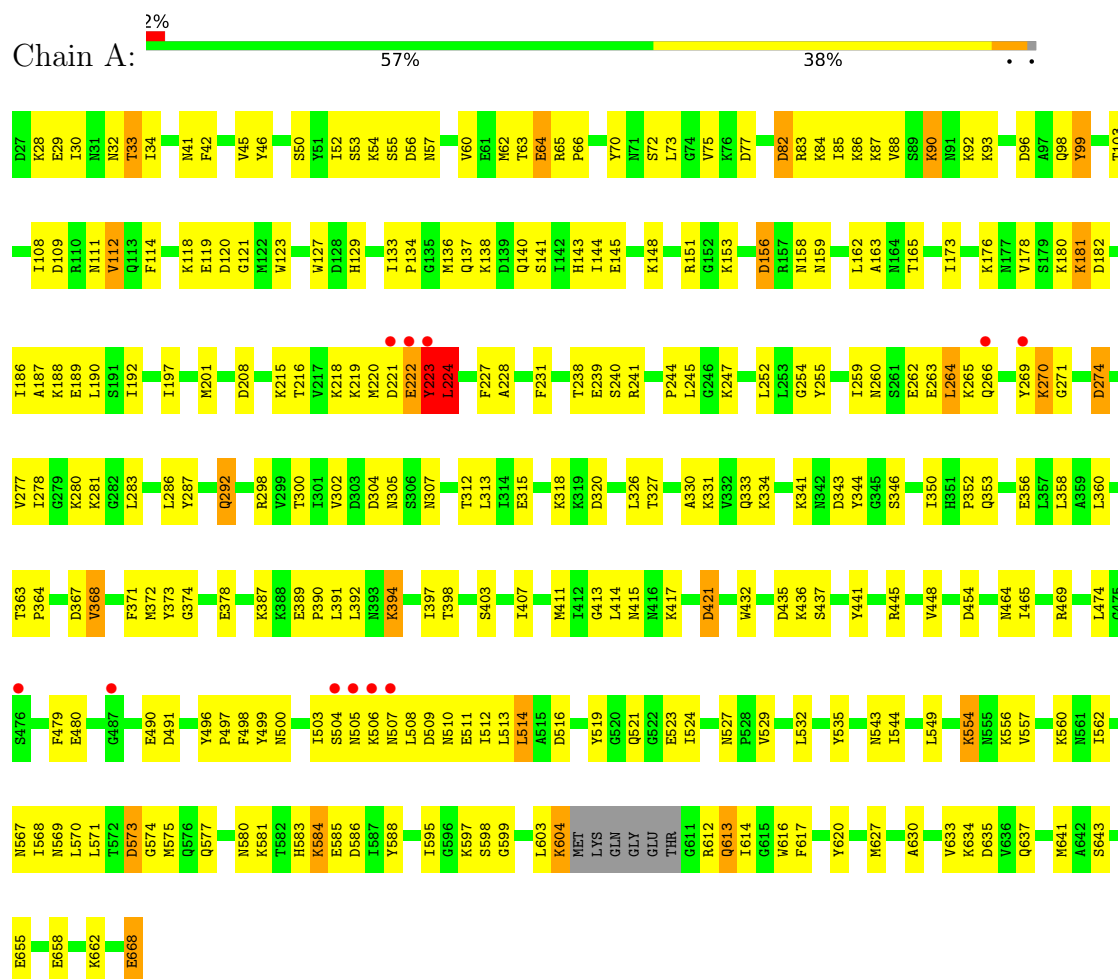
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	116	Total	O	0	0
			116	116		
6	B	97	Total	O	0	0
			97	97		
6	C	1	Total	O	0	0
			1	1		
6	D	2	Total	O	0	0
			2	2		

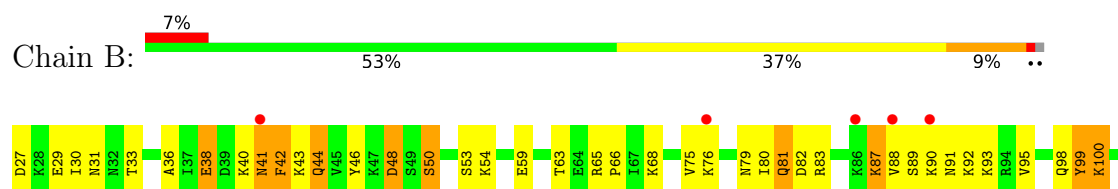
3 Residue-property plots

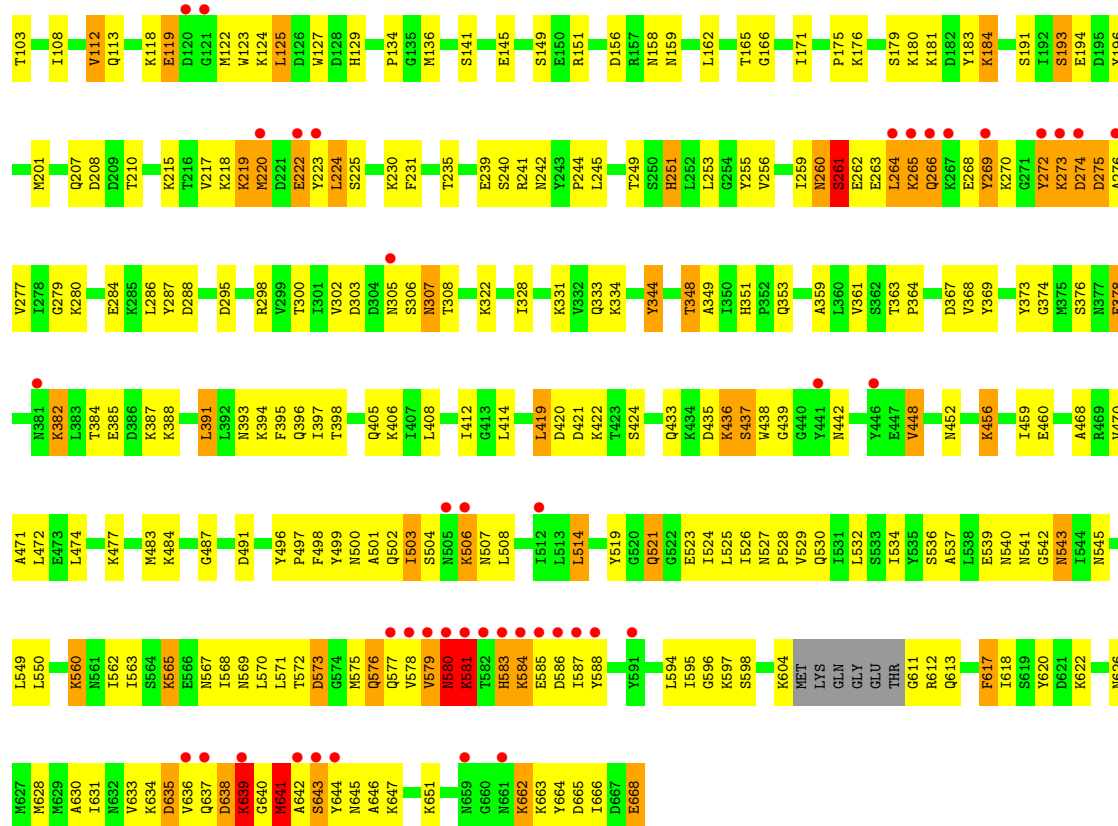
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Penicillin binding protein 2 prime

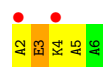


• Molecule 1: Penicillin binding protein 2 prime

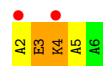
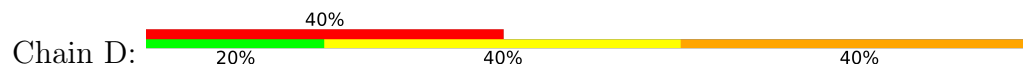




● Molecule 2: PEPTIDOGLYCAN ANALOGUE



● Molecule 2: PEPTIDOGLYCAN ANALOGUE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.54Å 102.02Å 185.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.13 – 2.55 49.13 – 2.55	Depositor EDS
% Data completeness (in resolution range)	93.6 (49.13-2.55) 88.5 (49.13-2.55)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.54Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.2_869)	Depositor
R, R_{free}	0.214 , 0.290 0.212 , 0.283	Depositor DCC
R_{free} test set	2425 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.856	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10542	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AMV, CL, DAL, FGA, CD

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	0.43	0/5189	0.65	3/6975 (0.0%)
1	B	0.52	2/5190 (0.0%)	0.75	11/6978 (0.2%)
2	C	0.16	0/12	0.21	0/12
2	D	0.66	0/12	2.19	0/12
All	All	0.47	2/10403 (0.0%)	0.70	14/13977 (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	B	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	580	ASN	C-N	-16.58	0.95	1.34
1	B	279	GLY	C-N	-14.11	1.01	1.34

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	223	TYR	CB-CA-C	-19.83	70.74	110.40
1	B	581	LYS	O-C-N	-18.33	93.38	122.70
1	B	260	ASN	N-CA-C	15.72	153.45	111.00
1	B	260	ASN	CB-CA-C	-14.85	80.71	110.40
1	B	261	SER	N-CA-CB	11.32	127.48	110.50
1	A	224	LEU	N-CA-CB	11.22	132.83	110.40
1	B	638	ASP	N-CA-C	-10.88	81.62	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	581	LYS	CA-C-N	8.77	136.50	117.20
1	B	639	LYS	N-CA-CB	8.28	125.50	110.60
1	B	581	LYS	C-N-CA	8.17	142.13	121.70
1	B	580	ASN	C-N-CA	8.11	141.97	121.70
1	B	279	GLY	C-N-CA	8.09	141.93	121.70
1	A	224	LEU	N-CA-C	-7.55	90.62	111.00
1	B	279	GLY	O-C-N	-6.68	112.02	122.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	218	LYS	Peptide
1	B	580	ASN	Mainchain
1	B	581	LYS	Mainchain
1	B	583	HIS	Peptide

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	5105	0	5102	300	0
1	B	5105	0	5100	435	1
2	C	34	0	29	18	0
2	D	34	0	30	8	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	C	20	0	19	33	0
5	D	20	0	20	25	0
6	A	116	0	0	22	1
6	B	97	0	0	19	0
6	C	1	0	0	0	0
6	D	2	0	0	0	0
All	All	10542	0	10300	743	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 36.

All (743) 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:B:165:THR:HG23	5:D:101:AMV:C12	1.14	1.62
1:A:165:THR:HG23	5:C:101:AMV:C12	1.35	1.56
1:B:165:THR:CG2	5:D:101:AMV:H122	1.03	1.47
1:A:240:SER:HA	5:C:101:AMV:N2	1.32	1.44
1:B:504:SER:CB	1:B:507:ASN:HA	1.48	1.43
1:A:165:THR:CG2	5:C:101:AMV:H123	1.50	1.41
1:B:504:SER:HB2	1:B:507:ASN:CA	1.52	1.38
1:A:240:SER:CA	5:C:101:AMV:HA	1.40	1.35
1:B:583:HIS:HB2	1:B:587:ILE:CG1	1.53	1.35
1:B:378:GLU:HG2	1:B:382:LYS:NZ	1.41	1.33
1:A:216:THR:HB	2:C:3:FGA:O	1.18	1.30
1:A:239:GLU:HB3	5:C:101:AMV:C12	1.64	1.27
1:B:261:SER:H	1:B:264:LEU:CB	1.51	1.22
1:B:459:ILE:HG23	1:B:597:LYS:NZ	1.52	1.21
1:A:165:THR:CG2	5:C:101:AMV:C12	2.11	1.21
1:A:239:GLU:O	5:C:101:AMV:C7	1.92	1.17
1:A:505:ASN:HD22	1:A:523:GLU:HG3	1.08	1.17
1:B:378:GLU:OE2	1:B:382:LYS:HE2	1.45	1.14
1:B:261:SER:HA	1:B:264:LEU:HB3	1.25	1.14
1:B:579:VAL:CG1	1:B:587:ILE:HG22	1.76	1.14
1:A:277:VAL:HG11	5:C:101:AMV:H112	1.29	1.14
1:B:165:THR:HG22	5:D:101:AMV:H122	1.30	1.12
1:B:378:GLU:CG	1:B:382:LYS:NZ	2.13	1.10
1:B:579:VAL:HA	1:B:587:ILE:HG21	1.17	1.09
1:A:304:ASP:C	1:A:305:ASN:HB2	1.72	1.09
1:B:261:SER:H	1:B:264:LEU:HB2	0.95	1.08
1:B:583:HIS:HB2	1:B:587:ILE:HG12	1.19	1.08
1:B:165:THR:CG2	5:D:101:AMV:C12	1.88	1.07
1:B:268:GLU:HG3	1:B:269:TYR:CE1	1.89	1.07
1:B:636:VAL:HA	1:B:639:LYS:HE3	1.19	1.07
1:A:165:THR:HG23	5:C:101:AMV:H122	1.29	1.07
1:B:268:GLU:HG3	1:B:269:TYR:CD1	1.90	1.07
1:B:239:GLU:HB3	5:D:101:AMV:H123	1.29	1.07
1:B:207:GLN:H	1:B:210:THR:HG21	1.17	1.06
1:B:583:HIS:HB2	1:B:587:ILE:HG13	1.30	1.06
2:C:3:FGA:OE1	2:C:4:LYS:HB3	1.24	1.06
1:A:239:GLU:CB	5:C:101:AMV:H121	1.86	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:579:VAL:HG13	1:B:587:ILE:CG2	1.84	1.06
1:A:239:GLU:O	5:C:101:AMV:O7	1.71	1.05
1:A:519:TYR:CE2	1:A:521:GLN:HG3	1.91	1.04
1:B:456:LYS:O	1:B:460:GLU:HG3	1.56	1.03
1:B:219:LYS:HB2	1:B:220:MET:HA	1.08	1.03
1:B:373:TYR:HA	2:D:3:FGA:O	1.58	1.03
1:B:259:ILE:HD13	1:B:264:LEU:HD13	1.40	1.02
1:B:91:ASN:O	1:B:92:LYS:HG3	1.60	1.01
1:B:261:SER:N	1:B:264:LEU:HB2	1.75	1.01
1:B:207:GLN:H	1:B:210:THR:CG2	1.72	1.01
1:A:239:GLU:HB3	5:C:101:AMV:H121	1.01	1.01
1:A:277:VAL:HG11	5:C:101:AMV:C11	1.91	1.01
1:B:87:LYS:HG2	1:B:93:LYS:HE2	1.41	1.00
1:B:165:THR:HG23	5:D:101:AMV:O1	1.59	1.00
1:B:305:ASN:OD1	1:B:306:SER:N	1.94	1.00
1:B:219:LYS:HB2	1:B:220:MET:CA	1.91	1.00
1:B:219:LYS:CB	1:B:220:MET:HA	1.89	1.00
1:B:470:VAL:O	1:B:474:LEU:HD13	1.63	0.99
1:A:216:THR:CB	2:C:3:FGA:O	2.11	0.98
1:B:261:SER:O	1:B:265:LYS:HE3	1.62	0.98
1:B:576:GLN:HB2	1:B:595:ILE:HG22	1.45	0.98
1:B:583:HIS:CB	1:B:587:ILE:HG12	1.94	0.97
1:B:261:SER:N	1:B:264:LEU:CB	2.27	0.97
1:B:87:LYS:CG	1:B:93:LYS:HE2	1.95	0.96
1:A:165:THR:HG21	5:C:101:AMV:H123	1.48	0.96
1:B:322:LYS:HA	1:B:322:LYS:HE2	1.47	0.94
1:B:348:THR:HG22	1:B:532:LEU:HD22	1.48	0.94
1:B:378:GLU:HG2	1:B:382:LYS:HZ3	0.82	0.94
1:B:579:VAL:HA	1:B:587:ILE:CG2	1.97	0.94
1:A:165:THR:HG23	5:C:101:AMV:H123	0.98	0.94
1:B:277:VAL:HG11	5:D:101:AMV:H113	1.47	0.94
1:B:523:GLU:OE2	1:B:604:LYS:HE2	1.68	0.93
1:B:577:GLN:O	1:B:581:LYS:HB2	1.66	0.93
1:B:268:GLU:CG	1:B:269:TYR:CE1	2.52	0.93
1:A:569:ASN:C	6:A:801:HOH:O	2.06	0.93
1:B:459:ILE:HG23	1:B:597:LYS:HZ3	1.10	0.93
1:A:435:ASP:OD1	1:A:437:SER:N	2.02	0.92
1:B:636:VAL:HA	1:B:639:LYS:CE	1.98	0.92
1:B:264:LEU:HD21	1:B:274:ASP:HB3	1.52	0.91
1:B:165:THR:HG21	5:D:101:AMV:H122	1.50	0.91
1:B:30:ILE:HD11	1:B:93:LYS:HD2	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:3:FGA:OE1	2:C:4:LYS:CB	2.13	0.90
1:B:259:ILE:HD11	1:B:264:LEU:HA	1.55	0.89
1:B:241:ARG:HD3	5:D:101:AMV:H6C2	1.52	0.89
1:B:87:LYS:HG2	1:B:93:LYS:CE	2.02	0.88
1:B:460:GLU:OE1	1:B:581:LYS:HE2	1.73	0.88
1:A:331:LYS:NZ	1:A:668:GLU:OXT	2.07	0.88
1:A:505:ASN:ND2	1:A:523:GLU:HG3	1.88	0.88
1:B:274:ASP:O	1:B:276:ALA:N	2.07	0.88
1:B:378:GLU:CG	1:B:382:LYS:HZ1	1.85	0.88
1:B:562:ILE:HG13	1:B:563:ILE:HG22	1.55	0.88
1:B:459:ILE:HG23	1:B:597:LYS:HZ1	1.39	0.87
1:A:223:TYR:O	1:A:223:TYR:CD2	2.28	0.87
1:B:268:GLU:CD	1:B:269:TYR:HE1	1.77	0.87
1:B:579:VAL:CA	1:B:587:ILE:HG21	2.04	0.87
1:B:617:PHE:HB2	1:B:645:ASN:HB3	1.57	0.87
1:A:60:VAL:HG22	1:A:64:GLU:OE1	1.73	0.86
1:B:640:GLY:O	1:B:641:MET:O	1.91	0.86
1:B:537:ALA:HB3	1:B:562:ILE:HD11	1.56	0.86
1:A:112:VAL:HG13	1:A:134:PRO:HB3	1.57	0.85
1:A:532:LEU:HD23	1:A:532:LEU:O	1.76	0.85
1:B:261:SER:CA	1:B:264:LEU:HB3	2.07	0.84
1:B:577:GLN:O	1:B:581:LYS:CG	2.25	0.84
1:A:532:LEU:HD23	1:A:532:LEU:C	1.98	0.84
1:B:264:LEU:HD12	1:B:264:LEU:O	1.78	0.84
1:A:182:ASP:O	1:A:186:ILE:HG12	1.76	0.84
1:B:577:GLN:HB3	1:B:581:LYS:HD3	1.59	0.83
1:B:583:HIS:CB	1:B:587:ILE:CG1	2.48	0.83
1:B:268:GLU:CG	1:B:269:TYR:HE1	1.91	0.83
1:A:84:LYS:CG	1:A:96:ASP:HB2	2.08	0.82
1:B:577:GLN:O	1:B:581:LYS:CB	2.27	0.82
1:B:537:ALA:CB	1:B:562:ILE:HD11	2.10	0.82
1:B:577:GLN:HB3	1:B:581:LYS:CD	2.09	0.82
1:A:298:ARG:HG3	1:A:298:ARG:HH11	1.43	0.81
1:B:579:VAL:HG13	1:B:587:ILE:HG22	0.88	0.81
1:B:93:LYS:HE3	1:B:123:TRP:CZ2	2.14	0.81
1:B:43:LYS:HZ3	1:B:63:THR:HG21	1.46	0.81
1:B:261:SER:HB2	1:B:265:LYS:HE2	1.61	0.81
1:A:223:TYR:CD2	1:A:224:LEU:HG	2.16	0.81
1:B:240:SER:HA	5:D:101:AMV:H2	1.63	0.81
1:B:207:GLN:N	1:B:210:THR:CG2	2.44	0.80
1:B:580:ASN:HA	1:B:584:LYS:HB2	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:576:GLN:HB2	1:B:595:ILE:CG2	2.12	0.80
1:B:640:GLY:O	1:B:641:MET:C	2.19	0.80
1:A:186:ILE:HD11	1:A:231:PHE:CG	2.17	0.80
1:A:216:THR:HB	2:C:3:FGA:C	2.11	0.79
1:B:179:SER:OG	1:B:181:LYS:HG2	1.81	0.79
1:A:240:SER:HA	5:C:101:AMV:C2	2.11	0.79
1:A:613:GLN:HG2	1:A:641:MET:HE3	1.63	0.79
1:B:373:TYR:CA	2:D:3:FGA:O	2.31	0.79
1:B:239:GLU:CB	5:D:101:AMV:H123	2.11	0.78
1:A:70:TYR:HB3	1:A:75:VAL:CG2	2.14	0.78
1:A:263:GLU:OE1	1:A:280:LYS:NZ	2.16	0.78
1:B:665:ASP:HB3	1:B:668:GLU:HB3	1.65	0.78
1:B:274:ASP:C	1:B:276:ALA:H	1.86	0.78
1:B:38:GLU:OE2	1:B:83:ARG:NH2	2.17	0.78
1:B:87:LYS:CG	1:B:93:LYS:CE	2.62	0.78
1:B:273:LYS:HE2	1:B:273:LYS:H	1.47	0.78
1:B:191:SER:HB3	1:B:376:SER:HB3	1.67	0.77
1:B:596:GLY:HA2	6:B:862:HOH:O	1.84	0.77
1:A:223:TYR:O	1:A:224:LEU:HG	1.84	0.77
1:B:256:VAL:CG1	1:B:277:VAL:HG12	2.14	0.77
1:B:59:GLU:O	1:B:63:THR:HB	1.83	0.77
1:B:269:TYR:HB3	1:B:272:TYR:CE1	2.19	0.76
1:B:587:ILE:HD12	1:B:617:PHE:CZ	2.20	0.76
1:A:392:LEU:HD12	6:A:821:HOH:O	1.85	0.76
1:A:568:ILE:O	6:A:801:HOH:O	2.03	0.76
1:A:510:ASN:OD1	1:A:511:GLU:N	2.18	0.76
1:A:245:LEU:HD11	1:A:330:ALA:HB1	1.66	0.76
1:A:570:LEU:N	6:A:801:HOH:O	2.17	0.76
1:B:435:ASP:OD1	1:B:437:SER:HB3	1.86	0.76
1:B:519:TYR:CE2	1:B:521:GLN:HG3	2.21	0.76
1:B:378:GLU:CG	1:B:382:LYS:HZ3	1.76	0.75
1:A:223:TYR:HD2	1:A:224:LEU:HG	1.49	0.75
1:B:348:THR:HG22	1:B:532:LEU:CD2	2.16	0.75
1:B:256:VAL:HG12	1:B:277:VAL:HG12	1.68	0.75
1:A:84:LYS:HG2	1:A:96:ASP:HB2	1.68	0.75
1:A:239:GLU:HB3	5:C:101:AMV:O1	1.87	0.75
1:A:189:GLU:HG3	1:A:227:PHE:CE1	2.22	0.75
1:B:277:VAL:HG11	5:D:101:AMV:C11	2.16	0.74
1:B:222:GLU:OE1	1:B:223:TYR:N	2.20	0.74
1:B:273:LYS:H	1:B:273:LYS:CE	2.00	0.74
1:B:353:GLN:O	1:B:545:ASN:ND2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:LYS:HE3	1:B:597:LYS:NZ	2.03	0.74
1:A:350:ILE:CG2	1:A:532:LEU:HD21	2.17	0.74
1:B:165:THR:HG23	5:D:101:AMV:C1	2.17	0.74
1:A:98:GLN:OE1	1:A:111:ASN:ND2	2.21	0.74
1:B:378:GLU:CD	1:B:382:LYS:HE2	2.07	0.74
1:A:264:LEU:O	1:A:265:LYS:HG2	1.88	0.74
1:B:44:GLN:HA	1:B:44:GLN:OE1	1.86	0.73
1:A:415:ASN:HA	6:A:811:HOH:O	1.87	0.73
1:B:523:GLU:CD	1:B:604:LYS:HE2	2.08	0.73
1:A:432:TRP:CH2	1:A:469:ARG:HD3	2.24	0.72
1:B:151:ARG:NH2	1:B:284:GLU:OE1	2.23	0.72
1:B:643:SER:O	1:B:646:ALA:HB3	1.88	0.72
1:B:261:SER:HA	1:B:264:LEU:CB	2.13	0.72
1:A:304:ASP:C	1:A:305:ASN:CB	2.54	0.72
1:A:73:LEU:HD23	1:A:144:ILE:HD11	1.71	0.72
1:B:374:GLY:HA3	2:D:4:LYS:HG3	1.69	0.72
1:A:414:LEU:HD13	1:A:567:ASN:HB3	1.71	0.71
1:A:197:ILE:O	1:A:201:MET:HG2	1.91	0.71
1:B:43:LYS:NZ	1:B:63:THR:HG21	2.06	0.71
1:B:193:SER:HB3	1:B:196:TYR:H	1.55	0.71
1:B:348:THR:HB	6:B:854:HOH:O	1.91	0.71
1:A:613:GLN:HG2	1:A:641:MET:CE	2.20	0.71
1:A:56:ASP:OD1	6:A:802:HOH:O	2.07	0.71
1:A:187:ALA:HB1	1:A:192:ILE:O	1.91	0.71
1:B:436:LYS:O	1:B:438:TRP:N	2.24	0.70
1:B:207:GLN:N	1:B:210:THR:HG21	1.98	0.70
1:B:474:LEU:HD11	6:B:847:HOH:O	1.92	0.70
1:B:460:GLU:HA	1:B:578:VAL:HG22	1.74	0.70
1:A:88:VAL:HB	1:A:92:LYS:HB3	1.74	0.70
1:B:259:ILE:CD1	1:B:264:LEU:HD13	2.21	0.70
1:B:634:LYS:HG2	1:B:635:ASP:OD1	1.92	0.70
1:B:456:LYS:O	1:B:460:GLU:CG	2.35	0.69
1:B:145:GLU:OE1	1:B:145:GLU:HA	1.91	0.69
1:A:573:ASP:O	1:A:577:GLN:NE2	2.25	0.69
1:B:508:LEU:HD21	1:B:524:ILE:HD11	1.75	0.69
1:B:261:SER:CB	1:B:265:LYS:HE2	2.22	0.69
1:B:613:GLN:NE2	1:B:637:GLN:HB3	2.08	0.69
1:A:480:GLU:HB2	1:A:508:LEU:HD23	1.74	0.68
1:B:165:THR:HG22	5:D:101:AMV:C12	1.96	0.68
1:A:557:VAL:HG11	1:A:560:LYS:HD3	1.75	0.68
1:B:406:LYS:HE3	1:B:597:LYS:HZ2	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:633:VAL:HG12	1:B:636:VAL:HG22	1.76	0.68
1:A:260:ASN:OD1	1:A:263:GLU:HB2	1.94	0.68
1:B:460:GLU:HA	1:B:578:VAL:CG2	2.22	0.68
1:B:274:ASP:OD1	1:B:274:ASP:N	2.26	0.68
1:A:504:SER:HB2	1:A:508:LEU:HD13	1.76	0.67
1:A:34:ILE:HG22	1:A:83:ARG:HH21	1.59	0.67
1:A:99:TYR:HD2	1:A:112:VAL:HG11	1.59	0.67
1:A:387:LYS:NZ	6:A:805:HOH:O	2.28	0.67
1:B:597:LYS:HG3	6:B:833:HOH:O	1.93	0.67
1:B:612:ARG:NH1	1:B:635:ASP:CG	2.48	0.67
1:A:223:TYR:CE2	1:A:224:LEU:CD2	2.77	0.67
1:A:505:ASN:HD22	1:A:523:GLU:CG	1.99	0.67
1:A:286:LEU:HD23	1:A:287:TYR:CE2	2.30	0.67
1:B:241:ARG:HA	5:D:101:AMV:C6	2.24	0.67
1:A:411:MET:HE1	1:A:562:ILE:HD12	1.76	0.67
1:B:87:LYS:HG2	1:B:93:LYS:NZ	2.10	0.67
1:B:261:SER:N	1:B:264:LEU:HB3	1.99	0.67
1:B:397:ILE:HA	1:B:499:TYR:HD2	1.60	0.67
1:B:88:VAL:O	1:B:89:SER:HB3	1.95	0.66
1:A:70:TYR:HB3	1:A:75:VAL:HG21	1.76	0.66
1:B:268:GLU:CD	1:B:269:TYR:CE1	2.65	0.66
1:A:112:VAL:CG1	1:A:134:PRO:HB3	2.25	0.66
1:B:268:GLU:HG3	1:B:269:TYR:HD1	1.52	0.66
2:C:3:FGA:OXT	2:C:3:FGA:HG2	1.95	0.66
1:A:374:GLY:HA3	2:C:4:LYS:CG	2.26	0.66
1:A:108:ILE:HD13	1:A:313:LEU:HD13	1.77	0.66
1:A:70:TYR:HB3	1:A:75:VAL:HG22	1.77	0.66
1:A:597:LYS:NZ	1:A:598:SER:O	2.29	0.66
1:A:84:LYS:HG3	1:A:86:LYS:NZ	2.11	0.66
1:B:241:ARG:HA	5:D:101:AMV:H6C1	1.78	0.65
1:A:118:LYS:HE3	1:A:121:GLY:HA2	1.79	0.65
1:B:507:ASN:OD1	6:B:801:HOH:O	2.14	0.65
1:A:224:LEU:O	1:A:228:ALA:N	2.28	0.65
1:B:251:HIS:H	1:B:251:HIS:CD2	2.15	0.65
1:B:579:VAL:HG21	1:B:594:LEU:O	1.97	0.65
1:B:262:GLU:O	1:B:262:GLU:HG3	1.95	0.65
1:A:491:ASP:HA	1:A:500:ASN:ND2	2.12	0.65
1:B:259:ILE:CD1	1:B:264:LEU:HA	2.26	0.65
1:B:460:GLU:O	1:B:578:VAL:HG22	1.97	0.65
5:C:101:AMV:C7	5:C:101:AMV:H9	2.27	0.65
1:A:41:ASN:O	1:A:45:VAL:HG23	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:LYS:CE	6:A:844:HOH:O	2.44	0.64
1:B:207:GLN:O	1:B:210:THR:HG22	1.97	0.64
1:B:87:LYS:N	1:B:87:LYS:HD2	2.12	0.64
1:B:575:MET:HA	1:B:597:LYS:HE3	1.79	0.64
1:B:644:TYR:CE1	1:B:647:LYS:HE2	2.33	0.64
1:B:123:TRP:O	6:B:802:HOH:O	2.15	0.64
1:B:612:ARG:HA	1:B:637:GLN:NE2	2.13	0.64
1:B:263:GLU:OE2	1:B:280:LYS:NZ	2.29	0.64
1:A:389:GLU:HA	6:A:866:HOH:O	1.97	0.64
1:A:543:ASN:OD1	1:A:560:LYS:HA	1.98	0.64
1:B:261:SER:HB2	1:B:265:LYS:CE	2.28	0.64
1:B:636:VAL:CA	1:B:639:LYS:HE3	2.12	0.64
1:B:587:ILE:CD1	1:B:617:PHE:CE2	2.80	0.64
1:B:222:GLU:OE1	1:B:222:GLU:C	2.35	0.64
1:B:595:ILE:HG13	1:B:595:ILE:O	1.97	0.63
1:B:259:ILE:HA	1:B:263:GLU:OE2	1.98	0.63
1:B:265:LYS:HD3	1:B:265:LYS:N	2.13	0.63
1:B:322:LYS:HE2	1:B:322:LYS:CA	2.27	0.63
1:A:414:LEU:HB3	1:A:567:ASN:HD22	1.63	0.63
1:B:239:GLU:HB3	5:D:101:AMV:C12	2.18	0.63
1:B:579:VAL:O	1:B:584:LYS:HA	1.98	0.63
1:A:305:ASN:OD1	1:B:68:LYS:CB	2.46	0.63
1:B:577:GLN:C	1:B:581:LYS:HD3	2.19	0.63
1:A:274:ASP:N	1:A:274:ASP:OD1	2.31	0.63
1:B:269:TYR:HB3	1:B:272:TYR:HE1	1.62	0.63
1:A:270:LYS:HD2	1:A:271:GLY:N	2.15	0.62
1:B:504:SER:HB2	1:B:507:ASN:HA	0.69	0.62
1:A:505:ASN:HB3	1:A:513:LEU:HD21	1.82	0.62
1:B:542:GLY:O	1:B:562:ILE:HG12	2.00	0.62
1:A:222:GLU:O	1:A:223:TYR:C	2.38	0.62
1:A:557:VAL:HG11	1:A:560:LYS:CD	2.30	0.62
1:A:263:GLU:O	1:A:266:GLN:HB2	1.99	0.62
1:B:631:ILE:O	1:B:645:ASN:ND2	2.32	0.62
1:A:28:LYS:O	1:A:32:ASN:ND2	2.33	0.62
1:A:269:TYR:CZ	1:A:278:ILE:HD12	2.35	0.61
1:A:414:LEU:HB3	1:A:567:ASN:ND2	2.15	0.61
1:B:222:GLU:OE1	1:B:223:TYR:CG	2.52	0.61
1:A:491:ASP:CG	1:A:500:ASN:HD21	2.03	0.61
1:B:219:LYS:CB	1:B:220:MET:CA	2.60	0.61
1:B:165:THR:CG2	5:D:101:AMV:H121	2.20	0.61
1:A:277:VAL:CG1	5:C:101:AMV:H112	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:ARG:HG3	1:A:298:ARG:NH1	2.16	0.61
1:A:239:GLU:O	5:C:101:AMV:N2	2.33	0.60
1:A:421:ASP:OD1	1:A:421:ASP:N	2.29	0.60
1:B:579:VAL:CA	1:B:587:ILE:CG2	2.72	0.60
1:B:635:ASP:HA	1:B:637:GLN:HE22	1.66	0.60
1:B:91:ASN:OD1	1:B:118:LYS:HE2	2.01	0.60
1:B:577:GLN:O	1:B:581:LYS:HG3	2.00	0.60
1:A:506:LYS:C	1:A:508:LEU:H	2.03	0.60
1:B:90:LYS:O	6:B:803:HOH:O	2.16	0.60
1:B:378:GLU:HG3	1:B:382:LYS:HZ1	1.67	0.60
1:A:86:LYS:HD3	1:A:86:LYS:N	2.17	0.60
1:A:374:GLY:HA3	2:C:4:LYS:HG2	1.83	0.60
1:A:298:ARG:NH1	1:A:315:GLU:HG3	2.17	0.60
1:B:224:LEU:C	1:B:224:LEU:HD23	2.22	0.60
1:B:436:LYS:C	1:B:438:TRP:H	2.03	0.60
1:A:304:ASP:O	1:A:305:ASN:HB2	2.02	0.60
1:A:350:ILE:HG22	1:A:532:LEU:HD21	1.83	0.60
1:B:408:LEU:O	1:B:412:ILE:HG13	2.01	0.60
1:B:459:ILE:CG2	1:B:597:LYS:HZ3	2.00	0.60
1:B:230:LYS:HD3	1:B:231:PHE:CE1	2.37	0.59
1:B:577:GLN:O	1:B:581:LYS:HD3	2.03	0.59
1:B:664:TYR:CE2	1:B:666:ILE:HG22	2.37	0.59
1:A:84:LYS:HG3	1:A:86:LYS:HZ2	1.68	0.59
1:A:93:LYS:HG3	1:A:123:TRP:CH2	2.38	0.59
1:B:647:LYS:HD2	1:B:651:LYS:HZ1	1.67	0.59
1:A:595:ILE:HD11	1:A:620:TYR:CZ	2.37	0.59
1:A:57:ASN:ND2	1:A:127:TRP:CE3	2.71	0.59
1:A:223:TYR:CE2	1:A:224:LEU:HD21	2.37	0.59
1:B:598:SER:OG	1:B:642:ALA:O	2.20	0.59
1:B:43:LYS:CE	1:B:63:THR:HG21	2.32	0.59
1:A:173:ILE:HG23	1:A:178:VAL:HB	1.85	0.58
1:A:411:MET:HE3	1:A:562:ILE:HG13	1.84	0.58
1:A:614:ILE:CD1	1:A:634:LYS:HG3	2.33	0.58
1:B:448:VAL:HG12	1:B:448:VAL:O	2.02	0.58
1:A:240:SER:HA	5:C:101:AMV:HA	0.52	0.58
1:A:34:ILE:HG22	1:A:83:ARG:NH2	2.17	0.58
1:A:254:GLY:HA3	1:A:281:LYS:O	2.03	0.58
2:D:4:LYS:NZ	2:D:5:DAL:O	2.36	0.58
1:B:265:LYS:O	1:B:266:GLN:HG3	2.02	0.58
1:B:207:GLN:N	1:B:210:THR:HG22	2.18	0.58
1:A:374:GLY:CA	2:C:4:LYS:HG3	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:ARG:NH2	1:A:448:VAL:HG13	2.19	0.57
1:A:350:ILE:HG21	1:A:532:LEU:HD21	1.86	0.57
1:A:190:LEU:HB3	1:A:215:LYS:HG3	1.85	0.57
1:B:577:GLN:O	1:B:581:LYS:CD	2.52	0.57
1:B:269:TYR:CA	1:B:272:TYR:HE1	2.17	0.57
1:B:378:GLU:OE2	1:B:382:LYS:CE	2.38	0.57
1:B:99:TYR:HB2	1:B:112:VAL:HG22	1.86	0.57
1:A:99:TYR:CD2	1:A:134:PRO:HD3	2.40	0.57
1:A:479:PHE:HD2	1:A:508:LEU:HD21	1.69	0.56
1:A:505:ASN:HB2	1:A:523:GLU:HB2	1.87	0.56
1:B:79:ASN:HB3	1:B:81:GLN:OE1	2.05	0.56
1:B:171:ILE:HG12	1:B:235:THR:HG22	1.87	0.56
1:A:318:LYS:HE3	1:A:320:ASP:OD2	2.04	0.56
1:B:261:SER:C	1:B:265:LYS:HE3	2.23	0.56
1:B:540:ASN:HB3	1:B:543:ASN:O	2.05	0.56
1:B:268:GLU:CG	1:B:269:TYR:CD1	2.77	0.56
1:B:287:TYR:CZ	1:B:550:LEU:HD11	2.40	0.56
1:B:298:ARG:HG2	1:B:300:THR:HG23	1.87	0.56
1:B:617:PHE:CE2	1:B:646:ALA:HA	2.41	0.56
1:A:223:TYR:HE2	1:A:224:LEU:HD21	1.71	0.56
1:A:300:THR:HG22	1:A:312:THR:HA	1.87	0.56
1:A:532:LEU:C	1:A:532:LEU:CD2	2.73	0.56
1:B:50:SER:O	1:B:54:LYS:HG3	2.05	0.56
1:B:583:HIS:NE2	1:B:598:SER:O	2.39	0.56
1:B:272:TYR:N	1:B:272:TYR:CD1	2.73	0.56
1:B:577:GLN:HB3	1:B:581:LYS:HD2	1.86	0.56
1:B:269:TYR:CD1	1:B:269:TYR:N	2.73	0.56
1:B:637:GLN:CD	1:B:637:GLN:H	2.09	0.56
1:A:353:GLN:OE1	1:A:353:GLN:N	2.32	0.55
1:B:46:TYR:O	1:B:54:LYS:HD3	2.06	0.55
1:A:189:GLU:HG3	1:A:227:PHE:CD1	2.42	0.55
1:B:275:ASP:N	1:B:275:ASP:OD1	2.40	0.55
1:B:40:LYS:HB3	6:B:828:HOH:O	2.05	0.55
1:A:397:ILE:HA	1:A:499:TYR:CD2	2.42	0.55
1:B:436:LYS:C	1:B:438:TRP:N	2.58	0.55
1:B:264:LEU:HD12	1:B:264:LEU:C	2.27	0.55
1:B:378:GLU:CD	1:B:382:LYS:CE	2.75	0.55
1:B:507:ASN:ND2	6:B:817:HOH:O	2.39	0.55
1:B:44:GLN:O	1:B:48:ASP:HB2	2.08	0.54
1:B:348:THR:CG2	1:B:532:LEU:CD2	2.86	0.54
1:B:504:SER:HB3	1:B:507:ASN:HA	1.74	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:519:TYR:HE2	1:B:521:GLN:HG3	1.71	0.54
1:A:262:GLU:O	1:A:262:GLU:OE1	2.25	0.54
6:A:814:HOH:O	5:C:101:AMV:H6C1	2.06	0.54
1:A:189:GLU:OE1	1:A:223:TYR:OH	2.12	0.54
1:A:327:THR:HB	1:A:356:GLU:HB3	1.89	0.54
1:B:80:ILE:HA	1:B:98:GLN:O	2.08	0.54
1:B:240:SER:CA	5:D:101:AMV:H2	2.36	0.54
1:B:387:LYS:HD2	1:B:387:LYS:O	2.08	0.54
1:B:477:LYS:NZ	6:B:811:HOH:O	2.33	0.54
1:B:576:GLN:CB	1:B:595:ILE:CG2	2.86	0.54
1:A:62:MET:O	1:A:66:PRO:HG2	2.07	0.54
1:B:166:GLY:HA3	1:B:242:ASN:HB2	1.89	0.54
1:B:647:LYS:NZ	1:B:651:LYS:NZ	2.56	0.54
1:A:270:LYS:CD	1:A:271:GLY:N	2.70	0.54
1:B:156:ASP:HB2	1:B:328:ILE:O	2.08	0.54
1:A:454:ASP:HB2	6:A:833:HOH:O	2.08	0.54
1:B:256:VAL:HG11	1:B:277:VAL:HG12	1.88	0.54
1:B:577:GLN:OE1	1:B:577:GLN:HA	2.06	0.54
1:B:580:ASN:ND2	1:B:588:TYR:HD1	2.06	0.54
1:A:143:HIS:ND1	1:A:302:VAL:HG21	2.23	0.53
1:A:264:LEU:O	1:A:265:LYS:CG	2.56	0.53
1:B:129:HIS:HB3	1:B:136:MET:HG2	1.89	0.53
1:B:27:ASP:OD1	1:B:93:LYS:NZ	2.41	0.53
1:B:91:ASN:O	1:B:92:LYS:CG	2.45	0.53
1:B:217:VAL:HB	1:B:219:LYS:HG2	1.89	0.53
1:A:240:SER:HA	5:C:101:AMV:C7	2.32	0.53
1:B:351:HIS:HD2	1:B:626:ASN:O	1.92	0.53
1:B:378:GLU:HG2	1:B:382:LYS:CE	2.35	0.53
1:A:263:GLU:CD	1:A:280:LYS:HZ2	2.12	0.53
1:A:411:MET:CE	1:A:562:ILE:HG13	2.38	0.53
1:B:474:LEU:CD1	1:B:474:LEU:N	2.71	0.53
1:A:65:ARG:HB3	1:A:66:PRO:HD3	1.89	0.53
1:A:580:ASN:O	1:A:584:LYS:HB3	2.09	0.53
1:A:595:ILE:HD11	1:A:620:TYR:OH	2.08	0.53
1:B:30:ILE:HD11	1:B:93:LYS:CD	2.32	0.53
1:B:523:GLU:OE1	1:B:604:LYS:HE2	2.09	0.53
1:A:247:LYS:HD3	6:A:813:HOH:O	2.09	0.53
1:B:269:TYR:CB	1:B:272:TYR:HE1	2.22	0.53
1:B:33:THR:O	1:B:36:ALA:HB3	2.09	0.53
1:A:57:ASN:ND2	1:A:127:TRP:HE3	2.07	0.52
1:B:436:LYS:HD3	1:B:436:LYS:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:562:ILE:HG13	1:B:563:ILE:N	2.23	0.52
1:B:259:ILE:HG22	1:B:276:ALA:O	2.10	0.52
1:A:327:THR:OG1	1:A:549:LEU:HA	2.09	0.52
1:B:393:ASN:CG	1:B:396:GLN:HB2	2.29	0.52
1:B:532:LEU:HD13	1:B:630:ALA:HB2	1.90	0.52
1:A:506:LYS:O	1:A:506:LYS:HG2	2.09	0.52
1:B:265:LYS:HD3	1:B:265:LYS:H	1.74	0.52
1:B:363:THR:HA	1:B:364:PRO:C	2.30	0.52
1:B:523:GLU:OE2	1:B:604:LYS:CE	2.52	0.52
1:B:647:LYS:O	1:B:651:LYS:HB2	2.10	0.52
1:A:614:ILE:HD13	1:A:634:LYS:HG3	1.91	0.52
1:A:223:TYR:O	1:A:223:TYR:HD2	1.90	0.52
1:A:305:ASN:OD1	1:B:68:LYS:HB3	2.10	0.52
1:A:411:MET:CE	1:A:562:ILE:CD1	2.87	0.52
1:A:158:ASN:O	1:A:159:ASN:HB2	2.09	0.52
1:A:162:LEU:O	1:A:244:PRO:HD2	2.09	0.52
1:A:571:LEU:N	6:A:801:HOH:O	2.43	0.52
1:B:504:SER:HB2	1:B:507:ASN:CB	2.33	0.52
1:A:506:LYS:C	1:A:508:LEU:N	2.64	0.51
1:B:611:GLY:HA2	1:B:612:ARG:HB2	1.92	0.51
1:B:569:ASN:HA	1:B:572:THR:OG1	2.11	0.51
1:B:579:VAL:HG21	1:B:595:ILE:HA	1.92	0.51
1:A:411:MET:CE	1:A:562:ILE:HD12	2.40	0.51
1:A:413:GLY:O	1:A:417:LYS:N	2.42	0.51
1:B:87:LYS:CB	1:B:93:LYS:HE2	2.41	0.51
1:B:487:GLY:O	1:B:530:GLN:NE2	2.43	0.51
1:B:565:LYS:HZ3	1:B:565:LYS:HB3	1.74	0.51
1:A:390:PRO:HD2	6:A:866:HOH:O	2.11	0.51
1:A:189:GLU:CB	1:A:227:PHE:CE1	2.94	0.51
1:A:411:MET:HE3	1:A:562:ILE:CD1	2.41	0.51
1:B:302:VAL:HG11	1:B:307:ASN:ND2	2.26	0.51
1:B:414:LEU:HB3	1:B:567:ASN:ND2	2.26	0.51
1:B:502:GLN:C	1:B:503:ILE:HD13	2.30	0.51
1:A:108:ILE:CD1	1:A:313:LEU:HD13	2.41	0.51
1:A:358:LEU:HD12	1:A:627:MET:HG3	1.91	0.51
1:B:471:ALA:HB1	1:B:514:LEU:HD22	1.92	0.51
1:B:491:ASP:OD1	1:B:500:ASN:ND2	2.43	0.51
1:A:584:LYS:O	1:A:588:TYR:HB3	2.11	0.51
1:B:269:TYR:CA	1:B:272:TYR:CE1	2.93	0.51
1:B:536:SER:HA	1:B:628:MET:CE	2.41	0.51
1:A:62:MET:HG2	1:A:127:TRP:CE2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:ILE:HD12	1:A:535:TYR:CE2	2.46	0.50
1:A:516:ASP:HA	1:A:519:TYR:CE1	2.46	0.50
1:A:571:LEU:O	1:A:575:MET:HG3	2.11	0.50
1:B:333:GLN:NE2	1:B:361:VAL:HG22	2.26	0.50
1:B:521:GLN:HE21	1:B:521:GLN:HA	1.77	0.50
1:A:505:ASN:HB2	1:A:523:GLU:CB	2.41	0.50
1:B:436:LYS:N	1:B:436:LYS:CD	2.73	0.50
1:B:647:LYS:NZ	1:B:651:LYS:HZ2	2.08	0.50
1:A:580:ASN:O	1:A:584:LYS:HD2	2.11	0.50
1:B:537:ALA:CB	1:B:562:ILE:CD1	2.87	0.50
1:B:579:VAL:CG1	1:B:587:ILE:CG2	2.65	0.50
1:B:474:LEU:CD1	6:B:847:HOH:O	2.55	0.50
1:B:579:VAL:CG2	1:B:596:GLY:H	2.24	0.50
1:B:580:ASN:ND2	1:B:588:TYR:CD1	2.79	0.50
1:B:474:LEU:N	1:B:474:LEU:HD12	2.26	0.50
1:A:75:VAL:HG12	1:A:103:THR:HG22	1.92	0.50
1:A:574:GLY:O	1:A:577:GLN:HB2	2.12	0.50
1:B:577:GLN:CB	1:B:581:LYS:HD3	2.38	0.50
1:A:223:TYR:CE2	1:A:224:LEU:HD23	2.46	0.50
1:A:373:TYR:CD1	2:C:3:FGA:O	2.65	0.50
1:B:583:HIS:CB	1:B:587:ILE:HG13	2.22	0.50
1:B:617:PHE:HD1	1:B:618:ILE:N	2.09	0.50
1:A:99:TYR:CE2	1:A:134:PRO:HD3	2.46	0.50
1:A:603:LEU:HD23	1:A:612:ARG:HD3	1.94	0.50
1:B:269:TYR:CB	1:B:272:TYR:CE1	2.93	0.50
1:B:88:VAL:O	1:B:92:LYS:HB2	2.11	0.49
1:B:587:ILE:HD11	1:B:646:ALA:HB2	1.93	0.49
1:B:436:LYS:CD	1:B:436:LYS:H	2.25	0.49
1:A:114:PHE:HD1	6:A:849:HOH:O	1.95	0.49
1:B:433:GLN:HB3	1:B:442:ASN:OD1	2.12	0.49
1:B:595:ILE:HD11	1:B:620:TYR:OH	2.11	0.49
1:B:436:LYS:O	1:B:439:GLY:N	2.42	0.49
1:B:75:VAL:HG12	1:B:103:THR:HG22	1.93	0.49
1:B:273:LYS:NZ	1:B:273:LYS:N	2.60	0.49
1:A:84:LYS:CD	1:A:96:ASP:HB2	2.42	0.49
1:B:636:VAL:HG12	1:B:636:VAL:O	2.13	0.49
1:A:668:GLU:O	1:A:668:GLU:HG2	2.13	0.49
1:B:575:MET:HB3	6:B:862:HOH:O	2.11	0.49
1:B:662:LYS:NZ	6:B:818:HOH:O	2.46	0.49
2:D:3:FGA:C	2:D:3:FGA:OE1	2.61	0.49
1:A:223:TYR:CD2	1:A:224:LEU:CG	2.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:ASP:O	1:B:275:ASP:C	2.49	0.49
1:B:277:VAL:CG1	5:D:101:AMV:H113	2.32	0.49
1:A:554:LYS:NZ	1:B:665:ASP:OD2	2.44	0.49
1:A:586:ASP:OD2	1:A:643:SER:HB2	2.13	0.49
1:B:424:SER:OG	1:B:452:ASN:HB3	2.12	0.49
1:B:644:TYR:CE1	1:B:647:LYS:CE	2.95	0.49
1:A:42:PHE:HB3	1:A:63:THR:HG22	1.94	0.48
1:A:519:TYR:HE2	1:A:521:GLN:HG3	1.66	0.48
1:B:617:PHE:CB	1:B:645:ASN:HB3	2.37	0.48
1:B:527:ASN:OD1	1:B:529:VAL:HB	2.12	0.48
1:A:506:LYS:O	1:A:508:LEU:N	2.46	0.48
1:A:507:ASN:O	1:A:508:LEU:HB3	2.12	0.48
1:B:165:THR:HA	5:D:101:AMV:O6	2.13	0.48
1:B:585:GLU:HG2	1:B:586:ASP:H	1.78	0.48
1:B:633:VAL:CG1	1:B:636:VAL:HG22	2.43	0.48
1:B:456:LYS:HD3	1:B:573:ASP:HB3	1.95	0.48
1:B:504:SER:CB	1:B:507:ASN:CA	2.40	0.48
1:A:240:SER:C	5:C:101:AMV:H2	2.34	0.48
1:A:304:ASP:C	1:A:305:ASN:N	2.67	0.48
1:A:305:ASN:OD1	1:B:68:LYS:HB2	2.12	0.48
1:A:491:ASP:HA	1:A:500:ASN:CG	2.33	0.48
1:A:241:ARG:N	5:C:101:AMV:H2	2.28	0.48
1:A:403:SER:HB3	6:A:890:HOH:O	2.12	0.48
1:B:573:ASP:O	1:B:577:GLN:HG2	2.13	0.48
1:B:612:ARG:HA	1:B:637:GLN:CD	2.34	0.48
1:A:65:ARG:N	1:A:66:PRO:CD	2.77	0.48
1:A:514:LEU:O	1:A:514:LEU:HD23	2.12	0.48
1:B:125:LEU:HD22	1:B:127:TRP:HA	1.96	0.48
1:B:207:GLN:C	1:B:210:THR:HG22	2.34	0.48
1:B:91:ASN:HA	6:B:803:HOH:O	2.14	0.48
1:B:419:LEU:HD23	1:B:420:ASP:N	2.30	0.47
1:A:504:SER:CB	1:A:508:LEU:HD13	2.42	0.47
1:B:245:LEU:HD22	1:B:334:LYS:HD3	1.97	0.47
1:B:507:ASN:HB3	1:B:508:LEU:H	1.44	0.47
1:A:403:SER:OG	1:A:599:GLY:HA3	2.13	0.47
1:B:222:GLU:HA	1:B:225:SER:OG	2.14	0.47
1:B:259:ILE:CG2	1:B:274:ASP:O	2.62	0.47
1:B:587:ILE:HD12	1:B:617:PHE:CE2	2.45	0.47
1:A:70:TYR:CB	1:A:75:VAL:HG21	2.44	0.47
1:A:156:ASP:OD1	1:A:156:ASP:C	2.52	0.47
1:B:273:LYS:CE	1:B:273:LYS:N	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:LYS:HD2	1:A:96:ASP:HB2	1.97	0.47
1:A:189:GLU:CG	1:A:227:PHE:CE1	2.95	0.47
1:A:326:LEU:HD22	1:A:549:LEU:HD13	1.96	0.47
1:B:251:HIS:CD2	1:B:251:HIS:N	2.82	0.47
1:B:496:TYR:CG	1:B:497:PRO:HD2	2.50	0.47
1:B:241:ARG:HD3	5:D:101:AMV:C6	2.34	0.47
1:A:496:TYR:CD1	1:A:497:PRO:HD2	2.50	0.47
1:B:519:TYR:CE2	1:B:521:GLN:CG	2.96	0.47
1:B:579:VAL:CB	1:B:587:ILE:HG22	2.40	0.47
1:B:597:LYS:HG2	6:B:862:HOH:O	2.14	0.47
1:B:612:ARG:NH1	1:B:635:ASP:OD2	2.48	0.47
1:A:346:SER:HB3	1:A:394:LYS:HB3	1.96	0.46
1:B:87:LYS:N	1:B:87:LYS:CD	2.73	0.46
1:B:579:VAL:CB	1:B:587:ILE:CG2	2.92	0.46
1:A:70:TYR:CG	1:A:75:VAL:HG21	2.50	0.46
1:A:151:ARG:N	5:C:101:AMV:O6	2.33	0.46
1:A:263:GLU:CD	1:A:280:LYS:NZ	2.68	0.46
1:A:441:TYR:OH	1:A:516:ASP:OD1	2.31	0.46
1:B:419:LEU:HD23	1:B:420:ASP:H	1.80	0.46
1:B:259:ILE:HG13	1:B:263:GLU:HG3	1.97	0.46
1:B:269:TYR:HA	1:B:272:TYR:CE1	2.50	0.46
1:A:292:GLN:OE1	1:A:292:GLN:HA	2.15	0.46
1:A:504:SER:CB	1:A:508:LEU:HB2	2.46	0.46
1:A:133:ILE:HB	1:A:136:MET:HE2	1.97	0.46
1:B:540:ASN:O	1:B:541:ASN:HB2	2.16	0.46
1:B:633:VAL:HG12	1:B:634:LYS:N	2.31	0.46
1:A:643:SER:HB3	6:A:817:HOH:O	2.15	0.46
1:B:264:LEU:HD21	1:B:274:ASP:CB	2.36	0.46
1:A:215:LYS:HE2	1:A:373:TYR:O	2.16	0.46
1:A:505:ASN:HB2	1:A:523:GLU:HG3	1.98	0.46
1:B:241:ARG:CA	5:D:101:AMV:H6C1	2.45	0.46
1:B:563:ILE:HG12	1:B:568:ILE:HG13	1.98	0.46
2:C:4:LYS:HA	2:C:5:DAL:HA	1.61	0.46
1:B:470:VAL:HG13	6:B:847:HOH:O	2.16	0.45
1:B:617:PHE:HE2	1:B:646:ALA:HA	1.81	0.45
1:A:604:LYS:HA	1:A:604:LYS:HD3	1.60	0.45
1:B:302:VAL:HG12	1:B:303:ASP:N	2.30	0.45
1:B:421:ASP:OD1	1:B:422:LYS:HG2	2.17	0.45
1:B:527:ASN:ND2	1:B:528:PRO:HD2	2.31	0.45
1:A:330:ALA:O	1:A:334:LYS:HB2	2.17	0.45
1:A:372:MET:HB3	2:C:2:ALA:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:373:TYR:HD1	2:D:3:FGA:H	1.64	0.45
1:A:82:ASP:OD1	1:A:82:ASP:N	2.47	0.45
1:A:568:ILE:C	6:A:801:HOH:O	2.53	0.45
1:B:99:TYR:HB2	1:B:112:VAL:CG2	2.46	0.45
1:B:344:TYR:CD1	1:B:344:TYR:C	2.90	0.45
1:B:460:GLU:CA	1:B:578:VAL:HG22	2.44	0.45
1:B:87:LYS:HG3	1:B:93:LYS:CE	2.45	0.45
1:B:118:LYS:HG3	1:B:122:MET:O	2.16	0.45
1:B:255:TYR:HB3	1:B:368:VAL:HB	1.99	0.45
1:A:333:GLN:NE2	1:A:360:LEU:O	2.43	0.45
1:B:145:GLU:OE1	1:B:145:GLU:CA	2.57	0.45
1:B:41:ASN:N	1:B:41:ASN:ND2	2.64	0.45
1:B:373:TYR:CB	2:D:3:FGA:O	2.64	0.45
1:B:665:ASP:CB	1:B:668:GLU:HB3	2.42	0.45
1:A:52:ILE:HA	1:A:55:SER:HB3	1.99	0.45
1:A:129:HIS:CE1	1:A:138:LYS:HG3	2.52	0.45
1:A:223:TYR:CD2	1:A:224:LEU:CD2	3.00	0.45
1:A:504:SER:OG	1:A:505:ASN:N	2.50	0.45
1:B:166:GLY:O	5:D:101:AMV:H121	2.16	0.45
1:B:384:THR:HG22	1:B:391:LEU:CD2	2.47	0.45
1:A:264:LEU:O	1:A:265:LYS:CB	2.64	0.45
1:B:87:LYS:HG2	1:B:93:LYS:HZ1	1.82	0.45
1:B:118:LYS:HA	1:B:122:MET:O	2.17	0.45
1:A:144:ILE:C	1:A:145:GLU:HG2	2.37	0.44
1:A:584:LYS:HE3	6:A:844:HOH:O	2.15	0.44
1:B:158:ASN:O	1:B:159:ASN:HB2	2.17	0.44
1:A:87:LYS:O	1:A:87:LYS:HG3	2.17	0.44
1:A:219:LYS:HB3	1:A:219:LYS:HE3	1.91	0.44
1:A:635:ASP:HA	1:A:637:GLN:OE1	2.16	0.44
1:A:33:THR:HG22	1:A:34:ILE:N	2.32	0.44
1:B:41:ASN:O	1:B:42:PHE:CG	2.70	0.44
1:B:349:ALA:HB3	1:B:359:ALA:HB3	1.98	0.44
1:A:99:TYR:HB3	1:A:134:PRO:HG3	1.99	0.44
1:A:239:GLU:CB	5:C:101:AMV:C12	2.59	0.44
1:A:283:LEU:HD12	1:A:326:LEU:HD11	2.00	0.44
1:A:583:HIS:CD2	1:A:598:SER:OG	2.70	0.44
1:B:584:LYS:HG3	1:B:585:GLU:N	2.31	0.44
1:A:99:TYR:CD2	1:A:112:VAL:HG11	2.48	0.44
1:A:245:LEU:HD22	1:A:334:LYS:HE2	2.00	0.44
1:B:41:ASN:O	1:B:42:PHE:CD2	2.70	0.44
1:A:343:ASP:HB3	1:A:633:VAL:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:ASN:HD22	1:A:519:TYR:HD2	1.65	0.44
1:B:33:THR:OG1	1:B:48:ASP:OD2	2.23	0.44
1:B:100:LYS:HA	1:B:108:ILE:O	2.18	0.44
1:B:89:SER:OG	1:B:90:LYS:N	2.51	0.44
1:B:268:GLU:OE2	1:B:269:TYR:HE1	1.98	0.44
1:B:276:ALA:HA	6:B:844:HOH:O	2.18	0.44
1:A:109:ASP:HB2	6:A:836:HOH:O	2.17	0.44
1:A:304:ASP:C	1:A:305:ASN:CA	2.86	0.44
1:A:398:THR:HA	1:A:527:ASN:HA	2.00	0.44
1:B:504:SER:OG	1:B:507:ASN:OD1	2.34	0.44
1:A:46:TYR:O	1:A:54:LYS:HD3	2.18	0.44
1:A:240:SER:CA	5:C:101:AMV:C2	2.89	0.44
1:A:658:GLU:OE1	1:A:662:LYS:HD3	2.18	0.43
1:B:459:ILE:CG2	1:B:597:LYS:HZ1	2.21	0.43
1:B:571:LEU:O	1:B:575:MET:HG3	2.17	0.43
1:A:407:ILE:O	1:A:411:MET:HG3	2.18	0.43
1:B:596:GLY:CA	6:B:862:HOH:O	2.54	0.43
1:A:514:LEU:C	1:A:514:LEU:CD2	2.86	0.43
2:D:2:ALA:O	2:D:3:FGA:HB3	2.18	0.43
1:A:374:GLY:CA	2:C:4:LYS:CG	2.94	0.43
1:B:612:ARG:H	1:B:637:GLN:CD	2.21	0.43
2:C:4:LYS:HD2	2:C:5:DAL:HA	1.99	0.43
1:A:264:LEU:HD12	1:A:265:LYS:H	1.84	0.43
1:B:162:LEU:O	1:B:244:PRO:HD2	2.17	0.43
1:B:224:LEU:HG	1:B:224:LEU:O	2.17	0.43
1:A:569:ASN:CA	6:A:801:HOH:O	2.62	0.43
1:B:53:SER:CB	1:B:127:TRP:H	2.31	0.43
1:B:88:VAL:O	1:B:88:VAL:HG23	2.18	0.43
1:B:378:GLU:CG	1:B:382:LYS:CE	2.93	0.43
1:B:261:SER:CB	1:B:265:LYS:CE	2.94	0.43
1:B:638:ASP:O	1:B:639:LYS:HG3	2.18	0.43
1:A:189:GLU:HB2	1:A:227:PHE:CE1	2.54	0.42
1:B:27:ASP:C	1:B:29:GLU:N	2.71	0.42
1:A:298:ARG:HH12	1:A:315:GLU:HG3	1.82	0.42
1:B:118:LYS:NZ	6:B:803:HOH:O	2.52	0.42
1:B:259:ILE:HG12	1:B:260:ASN:N	2.34	0.42
1:B:506:LYS:O	1:B:507:ASN:HB2	2.19	0.42
1:A:53:SER:CB	1:A:127:TRP:H	2.32	0.42
1:B:65:ARG:N	1:B:66:PRO:CD	2.81	0.42
1:B:249:THR:HB	1:B:253:LEU:HD12	2.01	0.42
1:B:331:LYS:HE2	1:B:668:GLU:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:PHE:CD1	1:B:395:PHE:C	2.92	0.42
1:B:498:PHE:CE1	1:B:529:VAL:HG21	2.54	0.42
1:B:180:LYS:HG3	1:B:183:TYR:CE2	2.55	0.42
1:B:459:ILE:CG2	1:B:597:LYS:NZ	2.47	0.42
1:B:504:SER:OG	1:B:507:ASN:CG	2.58	0.42
1:B:526:ILE:HG22	1:B:527:ASN:N	2.35	0.42
1:A:153:LYS:HA	1:A:163:ALA:O	2.19	0.42
1:A:350:ILE:HG21	1:A:532:LEU:CD2	2.49	0.42
1:A:374:GLY:HA2	2:C:4:LYS:HG3	2.02	0.42
1:A:445:ARG:HD3	1:A:465:ILE:HD12	2.00	0.42
1:B:149:SER:N	1:B:295:ASP:OD1	2.50	0.42
1:B:175:PRO:HG3	1:B:201:MET:CE	2.50	0.42
1:B:388:LYS:O	1:B:394:LYS:NZ	2.41	0.42
1:B:539:GLU:OE1	1:B:539:GLU:HA	2.19	0.42
1:A:344:TYR:CE1	1:A:394:LYS:HE2	2.54	0.42
1:B:95:VAL:O	1:B:113:GLN:HA	2.20	0.42
1:B:579:VAL:O	1:B:584:LYS:CA	2.67	0.42
1:B:222:GLU:O	1:B:225:SER:OG	2.30	0.42
1:B:617:PHE:CD2	1:B:646:ALA:HA	2.55	0.42
5:C:101:AMV:H111	5:C:101:AMV:H3	1.81	0.42
1:A:219:LYS:HG2	1:A:221:ASP:H	1.85	0.42
1:A:373:TYR:HE1	2:C:2:ALA:HA	1.85	0.42
1:A:510:ASN:OD1	1:A:510:ASN:C	2.58	0.42
1:B:398:THR:HG21	1:B:500:ASN:O	2.20	0.42
1:B:408:LEU:HD22	1:B:534:ILE:HG21	2.02	0.42
1:A:372:MET:HB3	2:C:2:ALA:HB2	2.02	0.41
1:A:498:PHE:CE1	1:A:529:VAL:HG21	2.55	0.41
1:B:367:ASP:OD1	1:B:369:TYR:CD2	2.73	0.41
1:A:137:GLN:N	1:A:140:GLN:OE1	2.48	0.41
1:B:348:THR:CG2	1:B:532:LEU:HD22	2.33	0.41
1:B:384:THR:HG22	1:B:391:LEU:HD22	2.01	0.41
1:A:90:LYS:HE3	1:A:90:LYS:HB2	1.67	0.41
1:A:238:THR:OG1	1:A:239:GLU:N	2.54	0.41
1:B:119:GLU:OE2	1:B:124:LYS:HG3	2.21	0.41
1:A:240:SER:N	5:C:101:AMV:HA	2.08	0.41
1:A:363:THR:HA	1:A:364:PRO:C	2.41	0.41
1:A:411:MET:HE3	1:A:562:ILE:CG1	2.48	0.41
1:B:93:LYS:HG3	1:B:123:TRP:CZ3	2.55	0.41
1:B:180:LYS:HE3	1:B:180:LYS:HB2	1.68	0.41
1:B:284:GLU:O	1:B:288:ASP:HB2	2.20	0.41
1:B:397:ILE:HA	1:B:499:TYR:CD2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:LYS:CE	1:B:597:LYS:HD3	2.50	0.41
1:B:587:ILE:HD12	1:B:617:PHE:HZ	1.77	0.41
1:B:647:LYS:HZ2	1:B:651:LYS:NZ	2.17	0.41
1:B:663:LYS:HA	1:B:663:LYS:HD3	1.95	0.41
1:B:184:LYS:HB3	1:B:194:GLU:OE1	2.20	0.41
1:B:405:GLN:OE1	1:B:483:MET:CE	2.69	0.41
1:A:519:TYR:CE2	1:A:521:GLN:CG	2.83	0.41
1:B:180:LYS:HA	1:B:183:TYR:CE1	2.55	0.41
1:B:269:TYR:HA	1:B:272:TYR:OH	2.19	0.41
1:B:468:ALA:O	1:B:472:LEU:HG	2.21	0.41
1:B:584:LYS:O	1:B:588:TYR:HB3	2.21	0.41
1:A:218:LYS:O	1:A:218:LYS:HG3	2.20	0.41
1:A:255:TYR:CZ	1:A:371:PHE:HB3	2.55	0.41
1:A:302:VAL:CG1	1:A:307:ASN:HA	2.51	0.41
1:B:224:LEU:C	1:B:224:LEU:CD2	2.87	0.41
1:A:29:GLU:HA	1:A:32:ASN:HD22	1.85	0.41
1:A:50:SER:O	1:A:54:LYS:HG3	2.20	0.41
1:B:207:GLN:CA	1:B:210:THR:HG22	2.50	0.41
1:A:223:TYR:CD2	1:A:223:TYR:C	2.76	0.41
1:A:240:SER:HA	5:C:101:AMV:H2	1.99	0.41
5:C:101:AMV:N2	5:C:101:AMV:H9	2.35	0.41
1:A:60:VAL:O	1:A:64:GLU:HB2	2.21	0.41
1:A:85:ILE:C	1:A:86:LYS:HD3	2.40	0.41
1:A:181:LYS:H	1:A:181:LYS:HG3	1.63	0.41
1:A:216:THR:O	1:A:373:TYR:HB3	2.21	0.41
1:A:350:ILE:O	1:A:352:PRO:HD3	2.20	0.41
1:A:368:VAL:O	1:A:372:MET:HG3	2.21	0.41
1:A:372:MET:O	2:C:2:ALA:HB1	2.20	0.41
1:B:612:ARG:NH1	1:B:635:ASP:OD1	2.53	0.41
1:B:617:PHE:C	1:B:617:PHE:CD1	2.94	0.41
1:A:220:MET:O	1:A:221:ASP:C	2.59	0.40
1:A:510:ASN:O	1:A:514:LEU:HB2	2.21	0.40
1:A:186:ILE:HD11	1:A:231:PHE:CD1	2.56	0.40
1:A:224:LEU:CA	1:A:227:PHE:HB3	2.50	0.40
1:A:503:ILE:HD12	1:A:524:ILE:HG23	2.02	0.40
1:A:616:TRP:HZ3	1:A:630:ALA:HB1	1.86	0.40
1:B:560:LYS:HD3	1:B:560:LYS:HA	1.90	0.40
1:A:239:GLU:CG	5:C:101:AMV:H121	2.47	0.40
1:A:513:LEU:HD12	1:A:513:LEU:HA	1.85	0.40
1:A:597:LYS:NZ	6:A:809:HOH:O	2.33	0.40
1:B:112:VAL:HG13	1:B:134:PRO:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:501:ALA:HA	1:B:525:LEU:O	2.22	0.40
1:B:504:SER:CB	1:B:507:ASN:CG	2.89	0.40
1:B:644:TYR:CD1	1:B:647:LYS:HE2	2.55	0.40
1:A:65:ARG:N	1:A:66:PRO:HD2	2.36	0.40
1:A:259:ILE:HD13	1:A:264:LEU:HD22	2.04	0.40
1:A:544:ILE:HD11	1:A:562:ILE:HD13	2.03	0.40
1:B:87:LYS:HB3	1:B:93:LYS:HE2	2.02	0.40
1:B:165:THR:CA	5:D:101:AMV:O6	2.69	0.40
1:B:302:VAL:CG1	1:B:303:ASP:N	2.85	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:LYS:NZ	6:A:802:HOH:O[2_554]	2.12	0.08

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	630/642 (98%)	605 (96%)	22 (4%)	3 (0%)	29	40
1	B	632/642 (98%)	602 (95%)	20 (3%)	10 (2%)	9	12
All	All	1262/1284 (98%)	1207 (96%)	42 (3%)	13 (1%)	15	22

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	261	SER
1	B	266	GLN
1	B	641	MET
1	A	223	TYR

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Mol	Chain	Res	Type
1	A	224	LEU
1	B	42	PHE
1	B	275	ASP
1	B	437	SER
1	B	581	LYS
1	B	219	LYS
1	B	639	LYS
1	A	222	GLU
1	B	579	VAL

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	567/572 (99%)	519 (92%)	48 (8%)	10	13
1	B	567/572 (99%)	500 (88%)	67 (12%)	5	5
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	0	1 (100%)	0	0
All	All	1136/1146 (99%)	1020 (90%)	116 (10%)	7	8

All (116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ILE
1	A	33	THR
1	A	64	GLU
1	A	72	SER
1	A	77	ASP
1	A	82	ASP
1	A	90	LYS
1	A	99	TYR
1	A	112	VAL
1	A	119	GLU
1	A	120	ASP
1	A	141	SER

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Mol	Chain	Res	Type
1	A	148	LYS
1	A	156	ASP
1	A	176	LYS
1	A	180	LYS
1	A	181	LYS
1	A	188	LYS
1	A	208	ASP
1	A	252	LEU
1	A	264	LEU
1	A	270	LYS
1	A	274	ASP
1	A	292	GLN
1	A	341	LYS
1	A	367	ASP
1	A	368	VAL
1	A	378	GLU
1	A	391	LEU
1	A	394	LYS
1	A	421	ASP
1	A	436	LYS
1	A	474	LEU
1	A	490	GLU
1	A	509	ASP
1	A	512	ILE
1	A	514	LEU
1	A	554	LYS
1	A	556	LYS
1	A	573	ASP
1	A	581	LYS
1	A	584	LYS
1	A	585	GLU
1	A	604	LYS
1	A	613	GLN
1	A	617	PHE
1	A	655	GLU
1	A	668	GLU
1	B	31	ASN
1	B	38	GLU
1	B	41	ASN
1	B	44	GLN
1	B	48	ASP
1	B	50	SER

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Mol	Chain	Res	Type
1	B	76	LYS
1	B	81	GLN
1	B	82	ASP
1	B	87	LYS
1	B	99	TYR
1	B	100	LYS
1	B	112	VAL
1	B	119	GLU
1	B	125	LEU
1	B	141	SER
1	B	176	LYS
1	B	184	LYS
1	B	193	SER
1	B	208	ASP
1	B	215	LYS
1	B	220	MET
1	B	222	GLU
1	B	224	LEU
1	B	251	HIS
1	B	264	LEU
1	B	265	LYS
1	B	269	TYR
1	B	270	LYS
1	B	272	TYR
1	B	273	LYS
1	B	274	ASP
1	B	286	LEU
1	B	307	ASN
1	B	308	THR
1	B	344	TYR
1	B	348	THR
1	B	378	GLU
1	B	382	LYS
1	B	385	GLU
1	B	391	LEU
1	B	419	LEU
1	B	436	LYS
1	B	448	VAL
1	B	456	LYS
1	B	484	LYS
1	B	503	ILE
1	B	506	LYS

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Mol	Chain	Res	Type
1	B	514	LEU
1	B	521	GLN
1	B	543	ASN
1	B	549	LEU
1	B	560	LYS
1	B	565	LYS
1	B	570	LEU
1	B	573	ASP
1	B	576	GLN
1	B	580	ASN
1	B	584	LYS
1	B	617	PHE
1	B	622	LYS
1	B	635	ASP
1	B	639	LYS
1	B	641	MET
1	B	643	SER
1	B	662	LYS
1	B	668	GLU
2	D	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	98	GLN
1	A	111	ASN
1	A	567	ASN
1	B	41	ASN
1	B	98	GLN
1	B	251	HIS
1	B	613	GLN
1	B	632	ASN
1	B	645	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues are 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	$\# Z > 2$
2	FGA	D	3	2	7,8,9	1.73	1 (14%)	7,9,11	1.94	2 (28%)
2	FGA	C	3	2	7,8,9	1.74	1 (14%)	7,9,11	1.22	0

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
2	FGA	D	3	2	-	0/7/8/9	-
2	FGA	C	3	2	-	1/7/8/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	FGA	OE1-CD	3.56	1.40	1.19
2	D	3	FGA	OE1-CD	3.41	1.39	1.19

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	FGA	CB-CG-CD	3.44	122.07	112.29
2	D	3	FGA	OE1-CD-CG	-2.43	110.92	126.89

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	3	FGA	CA-CB-CG-CD

There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	FGA	6	0
2	C	3	FGA	7	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	AMV	D	101	2	19,20,21	1.90	6 (31%)	22,27,29	2.27	4 (18%)
5	AMV	C	101	2	19,20,21	2.65	8 (42%)	22,27,29	4.46	10 (45%)

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
5	AMV	D	101	2	-	5/12/34/36	0/1/1/1
5	AMV	C	101	2	-	8/12/34/36	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	101	AMV	C1-C2	-5.32	1.44	1.53
5	C	101	AMV	C11-C9	5.25	1.62	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	101	AMV	C6-C5	-4.73	1.36	1.51
5	D	101	AMV	O1-C1	-3.81	1.33	1.40
5	C	101	AMV	C2-N2	3.77	1.51	1.45
5	C	101	AMV	C7-N2	3.60	1.46	1.34
5	D	101	AMV	O5-C1	3.46	1.50	1.41
5	D	101	AMV	C7-N2	3.38	1.46	1.34
5	C	101	AMV	C3-C2	-3.10	1.47	1.53
5	D	101	AMV	C11-C9	2.93	1.57	1.51
5	C	101	AMV	O3-C3	-2.79	1.36	1.43
5	D	101	AMV	C2-N2	2.52	1.49	1.45
5	D	101	AMV	O3-C9	2.36	1.48	1.45
5	C	101	AMV	O11-C10	2.14	1.28	1.19

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	101	AMV	C2-N2-C7	11.46	151.06	123.18
5	C	101	AMV	C12-O1-C1	10.83	129.99	113.27
5	C	101	AMV	O1-C1-C2	7.82	120.13	108.14
5	D	101	AMV	C1-C2-N2	-6.19	100.34	111.00
5	C	101	AMV	O5-C5-C4	-5.26	100.14	109.69
5	C	101	AMV	O3-C3-C4	5.23	121.18	107.28
5	D	101	AMV	C1-C2-C3	4.65	118.41	109.88
5	C	101	AMV	O5-C5-C6	4.64	117.96	106.44
5	D	101	AMV	C3-C4-C5	4.54	119.33	109.66
5	C	101	AMV	O5-C1-C2	-3.55	103.65	110.58
5	C	101	AMV	O4-C4-C3	-3.19	101.49	109.94
5	C	101	AMV	C1-C2-C3	2.80	115.01	109.88
5	C	101	AMV	C8-C7-N2	2.42	120.19	116.10
5	D	101	AMV	O1-C1-C2	2.41	111.83	108.14

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	101	AMV	C2-C1-O1-C12
5	C	101	AMV	O5-C1-O1-C12
5	D	101	AMV	C2-C1-O1-C12
5	D	101	AMV	C1-C2-N2-C7
5	D	101	AMV	O5-C1-O1-C12
5	C	101	AMV	O5-C5-C6-O6
5	C	101	AMV	C8-C7-N2-C2

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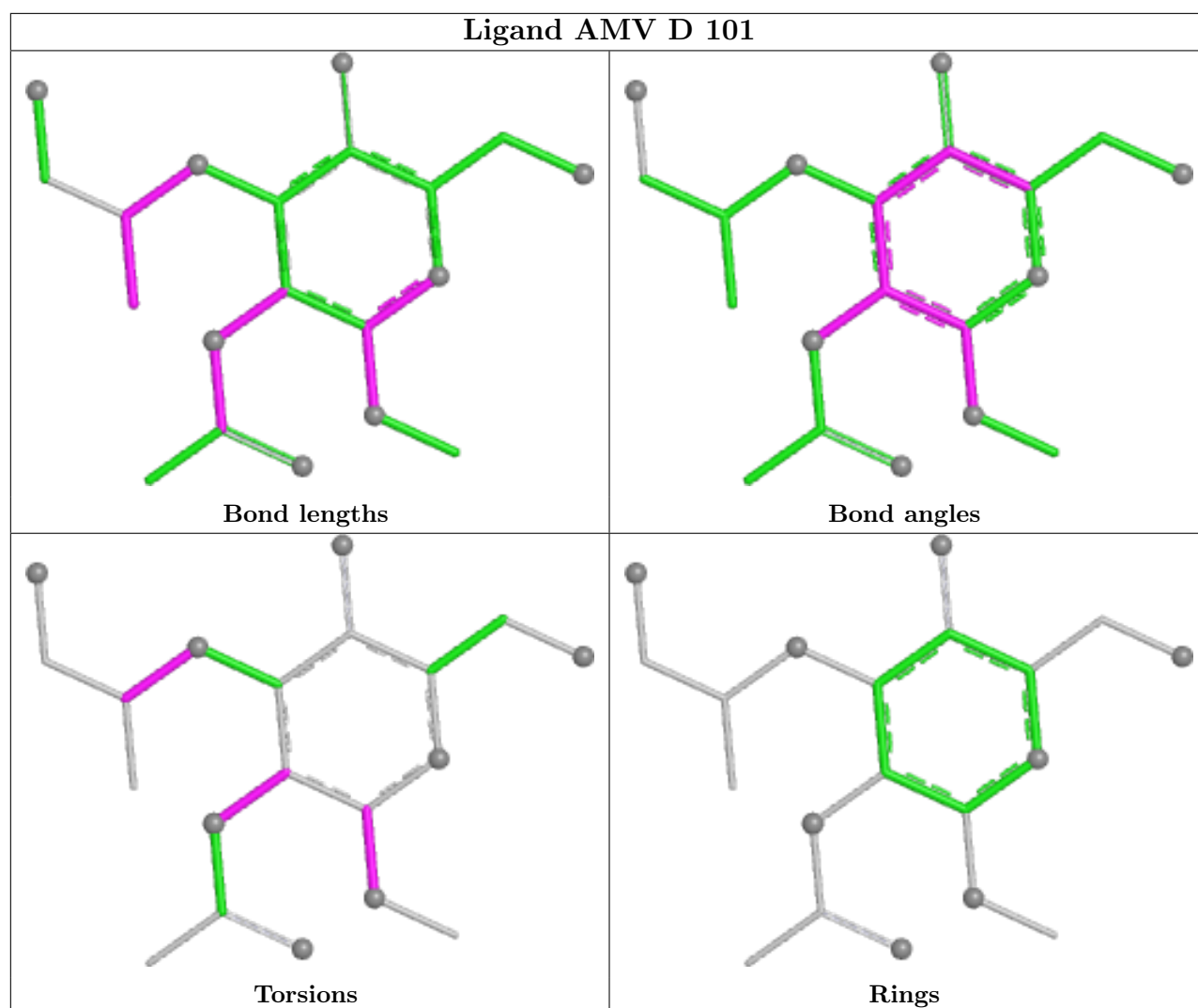
Mol	Chain	Res	Type	Atoms
5	C	101	AMV	O7-C7-N2-C2
5	C	101	AMV	C4-C5-C6-O6
5	C	101	AMV	C3-C2-N2-C7
5	D	101	AMV	C3-C2-N2-C7
5	C	101	AMV	C11-C9-O3-C3
5	D	101	AMV	C11-C9-O3-C3

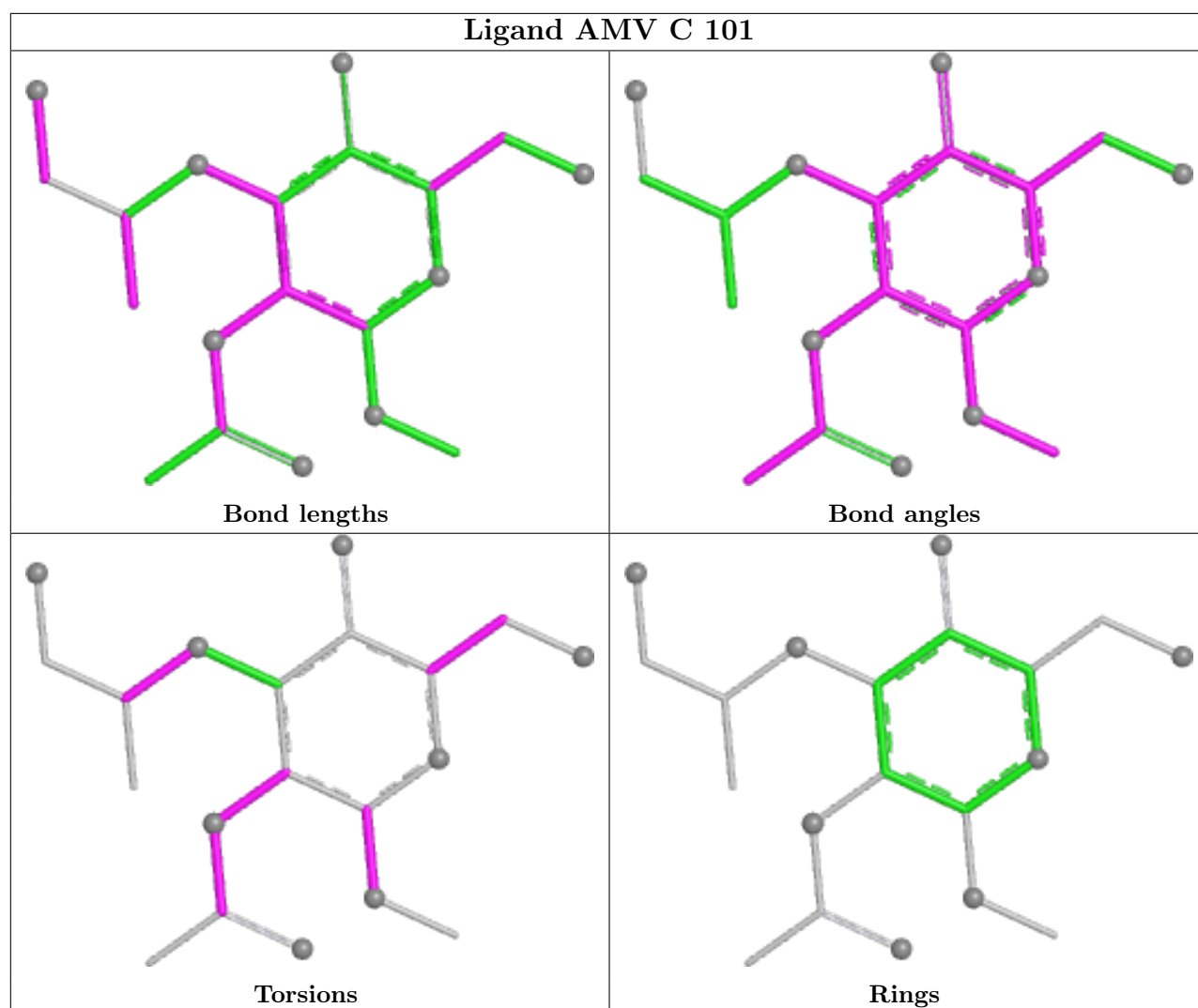
There are no ring outliers.

2 monomers are involved in 58 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	101	AMV	25	0
5	C	101	AMV	33	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	B	2
1	A	1
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	304:ASP	C	305:ASN	N	2.67
1	C	3:FGA	CD	4:LYS	N	1.65
1	B	279:GLY	C	280:LYS	N	1.01
1	B	580:ASN	C	581:LYS	N	0.95

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	636/642 (99%)	0.08	11 (1%) 70 76	16, 39, 74, 129	0
1	B	636/642 (99%)	0.41	47 (7%) 14 18	19, 43, 99, 147	0
2	C	2/5 (40%)	5.14	2 (100%) 0 0	111, 111, 111, 122	0
2	D	2/5 (40%)	6.94	2 (100%) 0 0	125, 125, 125, 130	0
All	All	1276/1294 (98%)	0.26	62 (4%) 29 35	16, 40, 90, 147	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	2	ALA	9.3
1	B	643	SER	9.0
2	C	2	ALA	7.8
1	B	580	ASN	7.2
1	B	586	ASP	6.7
1	B	582	THR	6.1
1	B	642	ALA	5.7
1	A	504	SER	5.4
1	B	505	ASN	5.4
1	B	585	GLU	5.2
1	B	305	ASN	5.1
1	B	584	LYS	4.9
1	B	587	ILE	4.8
2	D	4	LYS	4.6
1	B	506	LYS	4.0
1	B	269	TYR	4.0
1	B	581	LYS	3.9
1	B	639	LYS	3.9
1	B	578	VAL	3.9
1	B	223	TYR	3.8
1	B	644	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	583	HIS	3.6
1	B	579	VAL	3.6
1	B	636	VAL	3.5
1	B	222	GLU	3.5
1	B	267	LYS	3.3
1	B	264	LEU	3.2
1	A	507	ASN	3.2
1	B	577	GLN	3.1
1	A	506	LYS	3.1
1	A	221	ASP	3.1
1	B	266	GLN	3.0
1	B	41	ASN	3.0
1	A	505	ASN	2.9
1	B	661	ASN	2.9
1	B	121	GLY	2.8
1	B	265	LYS	2.8
1	B	88	VAL	2.7
1	B	274	ASP	2.7
1	B	381	ASN	2.6
1	B	272	TYR	2.6
1	A	266	GLN	2.6
1	B	446	TYR	2.6
1	A	476	SER	2.5
1	B	441	TYR	2.5
1	A	223	TYR	2.5
1	B	588	TYR	2.5
1	B	76	LYS	2.5
1	B	276	ALA	2.5
2	C	4	LYS	2.4
1	A	222	GLU	2.4
1	B	86	LYS	2.4
1	B	220	MET	2.4
1	B	512	ILE	2.4
1	A	269	TYR	2.4
1	B	273	LYS	2.3
1	B	120	ASP	2.2
1	B	659	ASN	2.2
1	B	90	LYS	2.2
1	B	637	GLN	2.1
1	B	591	TYR	2.1
1	A	487	GLY	2.1

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	DAL	D	6	6/6	0.05	0.97	132,135,136,136	0
2	FGA	D	3	9/10	0.40	0.81	130,134,136,137	0
2	DAL	C	6	6/6	0.44	0.34	85,93,96,97	0
2	FGA	C	3	9/10	0.49	0.51	118,125,127,128	0
2	DAL	D	5	5/6	0.50	0.61	128,129,133,133	0
2	DAL	C	5	5/6	0.78	0.34	97,98,98,100	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

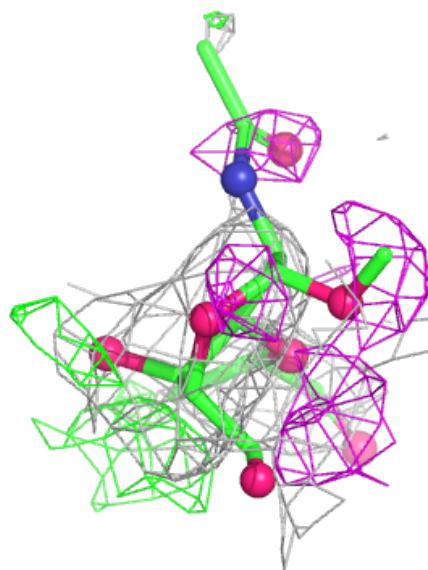
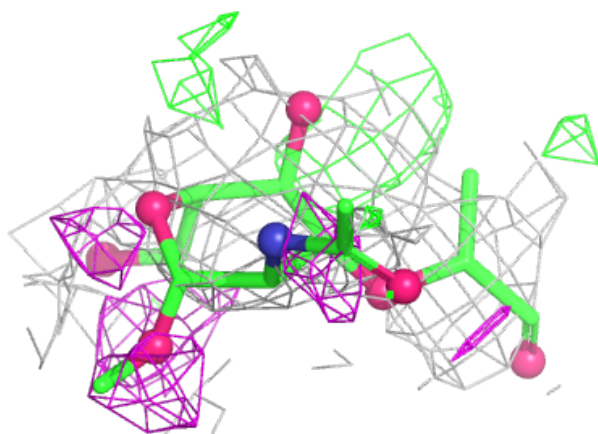
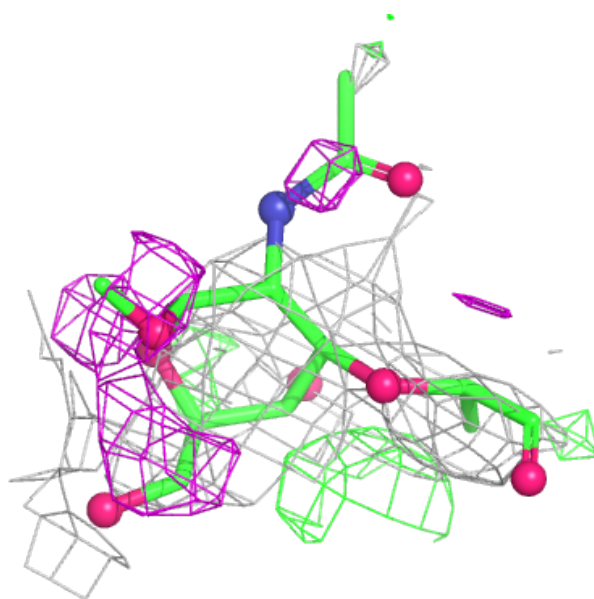
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

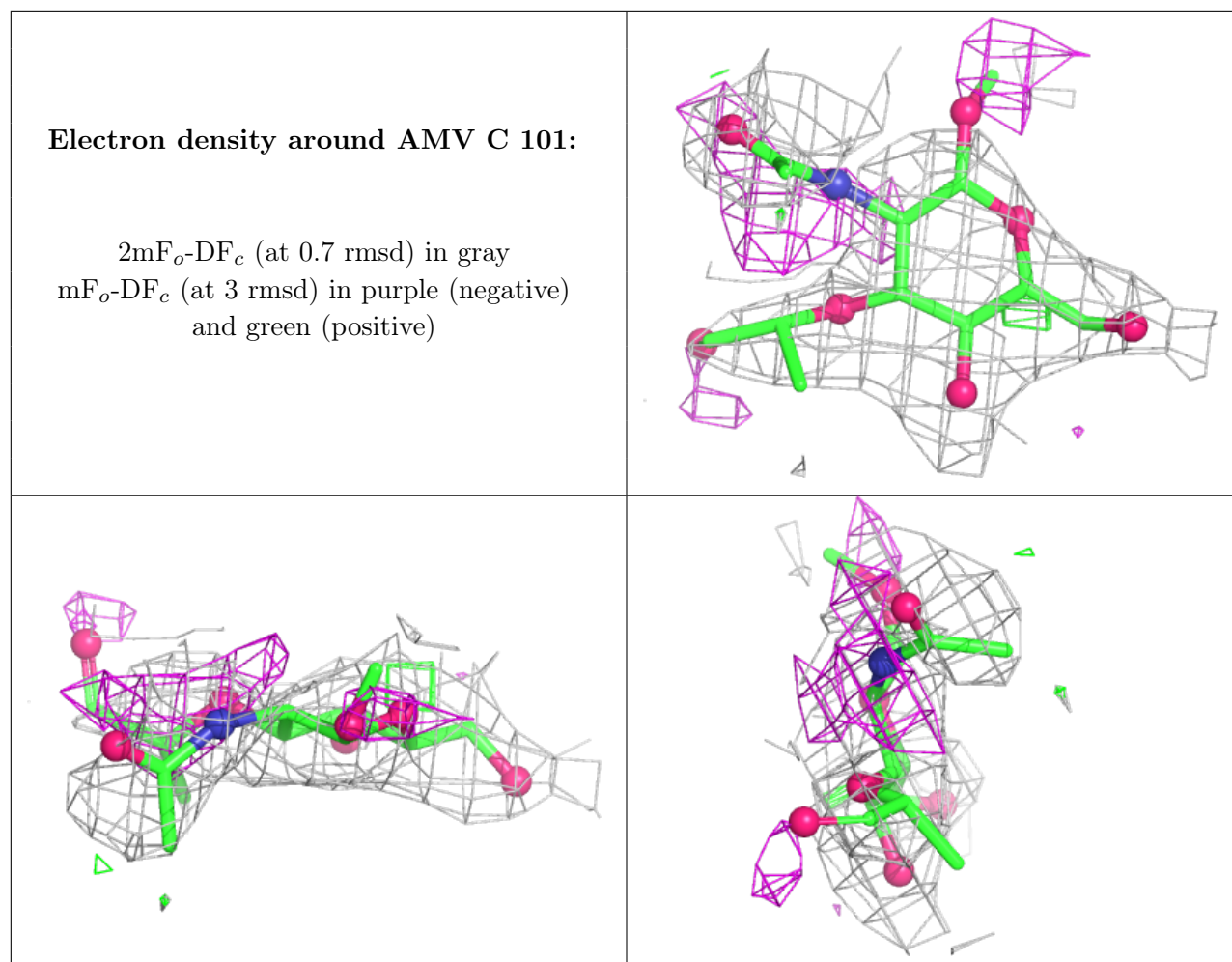
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	AMV	D	101	20/21	0.60	0.60	85,103,118,120	0
5	AMV	C	101	20/21	0.73	0.43	65,79,111,115	0
4	CL	A	702	1/1	0.97	0.12	31,31,31,31	0
3	CD	A	701	1/1	0.98	0.09	37,37,37,37	0
4	CL	B	703	1/1	0.98	0.07	21,21,21,21	0
3	CD	B	701	1/1	0.98	0.14	30,30,30,30	0
3	CD	B	702	1/1	0.98	0.12	30,30,30,30	0
4	CL	B	704	1/1	0.99	0.17	23,23,23,23	0
4	CL	A	704	1/1	0.99	0.12	34,34,34,34	0
3	CD	A	703	1/1	0.99	0.13	30,30,30,30	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.

Electron density around AMV D 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers ⓘ

There are no such residues in this entry.