



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:34 PM UTC

PDB ID : 1B0R / pdb_00001b0r
Title : CRYSTAL STRUCTURE OF HLA-A*0201 COMPLEXED WITH A PEPTIDE WITH THE CARBOXYL-TERMINAL GROUP SUBSTITUTED BY A METHYL GROUP
Authors : Bouvier, M.; Guo, H.; Smith, K.J.; Wiley, D.C.
Deposited on : 1998-11-12
Resolution : 2.90 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

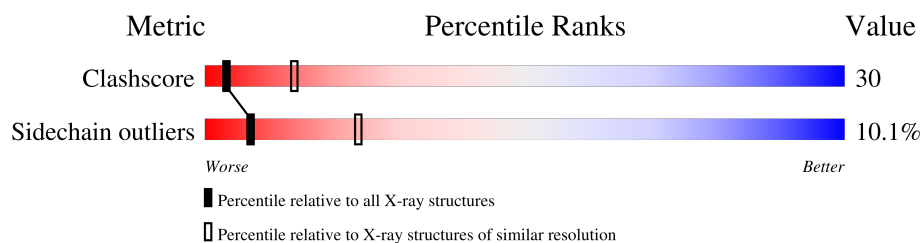
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	190562	2690 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	275	
2	B	100	
3	C	9	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CDE	C	709	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3090 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 PROTEIN (HLA-A*0201).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2202	1379	402	412	9			

- Molecule 2 is a protein called PROTEIN (HLA-A*0201).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	400	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called PROTEIN (INFLUENZA MATRIX PEPTIDE).

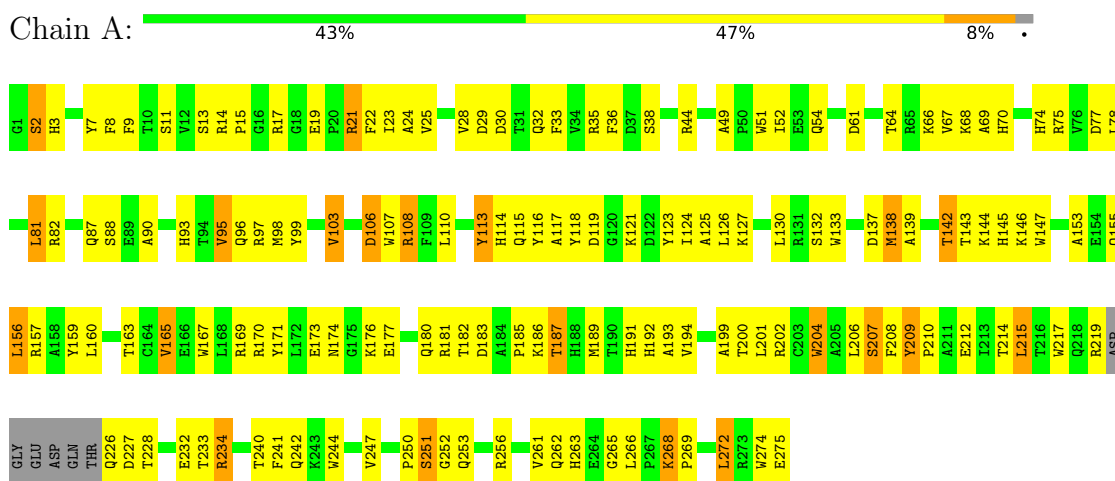
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	7	Total	C	N	O	0	0	0
			51	37	7	7			

3 Residue-property plots

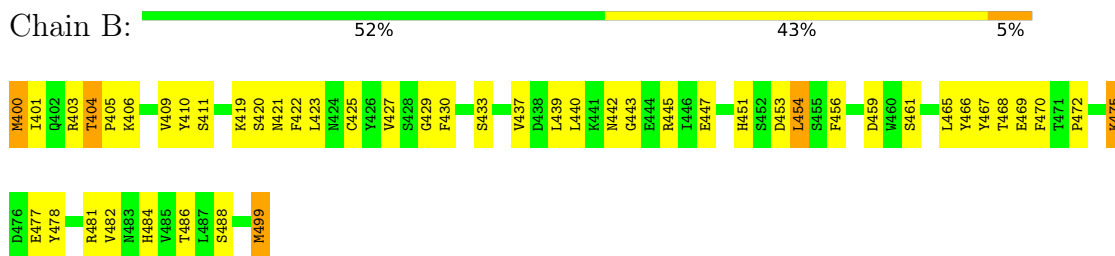
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

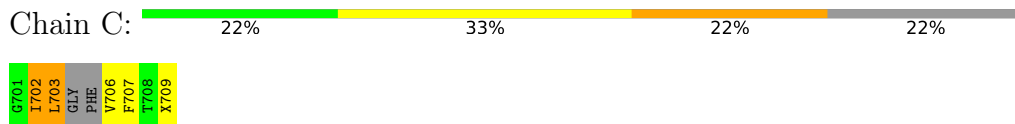
- Molecule 1: PROTEIN (HLA-A*0201)



- Molecule 2: PROTEIN (HLA-A*0201)



- Molecule 3: PROTEIN (INFLUENZA MATRIX PEPTIDE)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.60 Å 74.40 Å 121.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.90	Depositor
% Data completeness (in resolution range)	90.5 (6.00-2.90)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.253 , 0.314	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3090	wwPDB-VP
Average B, all atoms (Å ²)	15.0	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: CDE

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	0.65	0/2266	1.14	12/3073 (0.4%)
2	B	0.69	0/860	1.09	3/1162 (0.3%)
3	C	1.03	0/44	1.01	0/57
All	All	0.67	0/3170	1.12	15/4292 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	ASP	N-CA-C	-11.80	93.01	110.48
1	A	138	MET	N-CA-C	-7.80	102.39	112.23
1	A	251	SER	N-CA-C	7.03	121.13	109.46
1	A	61	ASP	N-CA-C	-6.70	103.97	111.28
1	A	69	ALA	N-CA-C	-6.65	104.11	111.36
1	A	29	ASP	CB-CA-C	-6.58	108.99	116.63
2	B	406	LYS	N-CA-C	-6.50	98.60	109.07
1	A	187	THR	N-CA-C	6.29	119.83	110.52
1	A	142	THR	N-CA-C	-6.20	104.22	110.97
1	A	204	TRP	N-CA-C	5.94	119.15	109.59
1	A	207	SER	N-CA-C	5.82	119.58	111.90
1	A	194	VAL	N-CA-C	-5.78	106.08	111.45
2	B	421	ASN	N-CA-C	-5.44	101.03	108.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	433	SER	N-CA-C	5.44	117.29	111.36
1	A	252	GLY	N-CA-C	-5.13	107.00	114.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	209	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2202	0	2063	153	0
2	B	837	0	800	44	0
3	C	51	0	59	13	0
All	All	3090	0	2922	182	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 30.

All (182) 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:187:THR:HG21	1:A:261:VAL:HG21	1.34	1.06
1:A:19:GLU:HB3	1:A:75:ARG:HH21	1.15	1.04
1:A:19:GLU:HB3	1:A:75:ARG:NH2	1.75	1.00
1:A:127:LYS:HD2	1:A:132:SER:HB2	1.46	0.95
1:A:108:ARG:HH11	1:A:108:ARG:HG2	1.33	0.94
1:A:21:ARG:HG2	1:A:21:ARG:HH11	1.38	0.88
1:A:193:ALA:HA	1:A:199:ALA:HA	1.58	0.85
1:A:49:ALA:O	1:A:52:ILE:HG22	1.77	0.83
1:A:119:ASP:HB3	2:B:400:MET:HB3	1.60	0.82
1:A:97:ARG:NH1	3:C:706:VAL:HB	1.95	0.81
1:A:22:PHE:H	1:A:38:SER:HB2	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:440:LEU:HD21	2:B:481:ARG:NH1	2.00	0.77
1:A:119:ASP:HB3	2:B:400:MET:CB	2.17	0.74
1:A:11:SER:HA	1:A:21:ARG:O	1.89	0.72
2:B:422:PHE:CE2	2:B:469:GLU:HG3	2.24	0.72
1:A:19:GLU:CB	1:A:75:ARG:NH2	2.53	0.72
1:A:98:MET:HE3	1:A:115:GLN:HE21	1.58	0.69
1:A:108:ARG:HG2	1:A:108:ARG:NH1	2.00	0.67
1:A:121:LYS:HE2	2:B:401:ILE:CD1	2.23	0.67
1:A:107:TRP:HZ2	1:A:180:GLN:OE1	1.78	0.66
1:A:214:THR:HB	1:A:262:GLN:HB2	1.76	0.66
1:A:155:GLN:HE22	3:C:707:PHE:HZ	1.44	0.66
1:A:44:ARG:HA	1:A:64:THR:HG23	1.79	0.65
1:A:114:HIS:O	1:A:115:GLN:HG2	1.97	0.63
2:B:405:PRO:HB2	2:B:427:VAL:HG12	1.80	0.63
1:A:127:LYS:HD2	1:A:132:SER:CB	2.24	0.62
1:A:11:SER:HB3	1:A:95:VAL:CG1	2.30	0.62
1:A:19:GLU:CB	1:A:75:ARG:HH21	2.03	0.61
1:A:81:LEU:HD23	1:A:118:TYR:CD1	2.34	0.61
1:A:209:TYR:CD1	1:A:241:PHE:HE1	2.19	0.60
1:A:121:LYS:HE2	2:B:401:ILE:HG13	1.83	0.60
1:A:130:LEU:HB2	1:A:157:ARG:HD2	1.84	0.60
1:A:108:ARG:HH11	1:A:108:ARG:CG	2.12	0.60
1:A:143:THR:HG21	3:C:709:CDE:HG23	1.83	0.59
1:A:64:THR:O	1:A:67:VAL:HG12	2.02	0.59
1:A:121:LYS:HE2	2:B:401:ILE:HD11	1.83	0.59
1:A:2:SER:O	1:A:3:HIS:CD2	2.55	0.59
2:B:440:LEU:HD21	2:B:481:ARG:HH12	1.66	0.59
1:A:64:THR:O	1:A:68:LYS:HG2	2.01	0.58
2:B:425:CYS:HB2	2:B:439:LEU:HD21	1.85	0.58
1:A:210:PRO:O	1:A:263:HIS:HE1	1.87	0.58
2:B:405:PRO:HB2	2:B:427:VAL:CG1	2.34	0.58
1:A:44:ARG:HA	1:A:64:THR:CG2	2.34	0.58
1:A:98:MET:HE3	1:A:115:GLN:NE2	2.19	0.57
2:B:475:LYS:HD3	2:B:475:LYS:H	1.70	0.56
1:A:13:SER:O	1:A:15:PRO:HD3	2.05	0.56
1:A:155:GLN:NE2	3:C:707:PHE:CZ	2.70	0.56
1:A:187:THR:HB	1:A:272:LEU:HD21	1.87	0.55
1:A:93:HIS:HD2	1:A:119:ASP:OD2	1.89	0.55
1:A:176:LYS:NZ	1:A:181:ARG:HH22	2.05	0.55
1:A:98:MET:O	1:A:114:HIS:O	2.25	0.55
1:A:121:LYS:HE2	2:B:401:ILE:CG1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:ARG:HG3	1:A:87:GLN:HB2	1.88	0.55
1:A:95:VAL:HG23	1:A:116:TYR:CZ	2.42	0.54
1:A:115:GLN:HA	1:A:125:ALA:HA	1.89	0.54
1:A:176:LYS:HZ2	1:A:181:ARG:NH2	2.04	0.54
2:B:442:ASN:HA	2:B:477:GLU:HG3	1.89	0.54
1:A:67:VAL:O	1:A:70:HIS:HB2	2.09	0.53
1:A:25:VAL:HB	1:A:32:GLN:NE2	2.24	0.53
1:A:167:TRP:CZ3	1:A:170:ARG:NE	2.77	0.53
2:B:419:LYS:O	2:B:472:PRO:HD2	2.09	0.53
1:A:54:GLN:HE22	1:A:174:ASN:HB3	1.74	0.52
2:B:405:PRO:CA	2:B:430:PHE:HB3	2.39	0.52
1:A:208:PHE:CE1	1:A:241:PHE:HB2	2.45	0.52
1:A:28:VAL:HG23	1:A:33:PHE:CE1	2.44	0.52
2:B:422:PHE:CZ	2:B:469:GLU:HG3	2.44	0.52
1:A:187:THR:HA	1:A:204:TRP:O	2.10	0.52
1:A:66:LYS:HE2	3:C:702:ILE:HG13	1.91	0.52
1:A:74:HIS:HE1	1:A:97:ARG:NH1	2.08	0.52
1:A:147:TRP:CZ2	3:C:709:CDE:HG22	2.45	0.52
1:A:234:ARG:HG3	2:B:410:TYR:CZ	2.44	0.52
1:A:30:ASP:HB3	1:A:241:PHE:CZ	2.45	0.52
1:A:8:PHE:HB3	2:B:456:PHE:CE2	2.46	0.51
2:B:423:LEU:HB3	2:B:468:THR:HG22	1.91	0.51
1:A:11:SER:HB3	1:A:95:VAL:HG13	1.91	0.51
1:A:97:ARG:HH12	3:C:706:VAL:HB	1.71	0.51
1:A:121:LYS:HG2	2:B:401:ILE:HD12	1.93	0.51
1:A:119:ASP:CB	2:B:400:MET:HB3	2.35	0.51
1:A:177:GLU:O	1:A:181:ARG:HG3	2.11	0.50
1:A:78:LEU:HD21	1:A:95:VAL:HG12	1.92	0.50
1:A:202:ARG:NH1	2:B:499:MET:HG3	2.26	0.50
1:A:142:THR:HG22	1:A:146:LYS:HE3	1.94	0.50
1:A:176:LYS:NZ	1:A:181:ARG:NH2	2.60	0.50
1:A:23:ILE:HD12	2:B:454:LEU:HD12	1.95	0.49
1:A:107:TRP:HB3	1:A:169:ARG:HG2	1.93	0.49
1:A:170:ARG:HA	1:A:173:GLU:OE2	2.12	0.49
1:A:234:ARG:HG3	2:B:410:TYR:CE2	2.47	0.49
1:A:77:ASP:HB3	1:A:116:TYR:OH	2.12	0.49
1:A:97:ARG:NH1	3:C:706:VAL:CB	2.71	0.49
1:A:117:ALA:HB1	1:A:121:LYS:O	2.12	0.49
1:A:209:TYR:HD1	1:A:241:PHE:HE1	1.59	0.49
1:A:191:HIS:HB2	1:A:274:TRP:CZ2	2.48	0.48
2:B:405:PRO:HA	2:B:430:PHE:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:ARG:CZ	1:A:23:ILE:HD11	2.43	0.48
1:A:30:ASP:HB3	1:A:241:PHE:HZ	1.78	0.48
1:A:139:ALA:O	1:A:142:THR:HB	2.12	0.48
1:A:219:ARG:HA	1:A:256:ARG:O	2.13	0.48
1:A:185:PRO:HD2	1:A:266:LEU:HG	1.96	0.48
2:B:451:HIS:HA	2:B:465:LEU:O	2.14	0.48
1:A:66:LYS:O	1:A:70:HIS:ND1	2.40	0.48
1:A:99:TYR:HA	1:A:113:TYR:O	2.14	0.48
2:B:440:LEU:HD22	2:B:443:GLY:O	2.13	0.47
1:A:28:VAL:HG23	1:A:33:PHE:CD1	2.49	0.47
1:A:204:TRP:CH2	1:A:244:TRP:CD1	3.03	0.47
1:A:24:ALA:O	1:A:35:ARG:HA	2.14	0.47
1:A:98:MET:SD	1:A:98:MET:C	2.98	0.47
1:A:119:ASP:HB3	2:B:400:MET:HB2	1.96	0.47
1:A:182:THR:HG22	1:A:183:ASP:N	2.29	0.47
2:B:437:VAL:HG22	2:B:482:VAL:HG22	1.97	0.47
2:B:445:ARG:HH21	2:B:447:GLU:HG2	1.80	0.47
2:B:484:HIS:O	2:B:486:THR:N	2.48	0.47
1:A:186:LYS:HD2	1:A:207:SER:OG	2.14	0.47
1:A:95:VAL:HG21	1:A:116:TYR:OH	2.15	0.46
1:A:192:HIS:O	1:A:200:THR:N	2.47	0.46
1:A:9:PHE:O	1:A:96:GLN:HA	2.15	0.46
1:A:156:LEU:O	1:A:159:TYR:N	2.47	0.46
1:A:124:ILE:HD11	1:A:144:LYS:HB2	1.98	0.46
1:A:204:TRP:CE3	1:A:206:LEU:HD21	2.51	0.46
2:B:484:HIS:C	2:B:486:THR:H	2.24	0.46
1:A:74:HIS:CE1	1:A:97:ARG:NH1	2.83	0.46
1:A:133:TRP:NE1	1:A:153:ALA:HB2	2.31	0.46
2:B:423:LEU:HB3	2:B:468:THR:CG2	2.46	0.45
1:A:142:THR:CG2	1:A:146:LYS:HE3	2.46	0.45
1:A:19:GLU:CG	1:A:75:ARG:NH2	2.79	0.45
1:A:19:GLU:HG2	1:A:75:ARG:NH2	2.32	0.45
1:A:30:ASP:HB2	1:A:209:TYR:HE1	1.82	0.45
1:A:11:SER:O	1:A:95:VAL:HG12	2.17	0.45
1:A:35:ARG:HD3	2:B:453:ASP:OD2	2.17	0.45
1:A:167:TRP:CE3	1:A:171:TYR:CE1	3.04	0.45
1:A:268:LYS:NZ	1:A:269:PRO:HD2	2.32	0.45
3:C:702:ILE:HB	3:C:703:LEU:H	1.68	0.45
1:A:22:PHE:N	1:A:38:SER:HB2	2.24	0.44
1:A:209:TYR:HD1	1:A:241:PHE:CE1	2.34	0.44
1:A:52:ILE:HD12	1:A:52:ILE:HA	1.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:GLN:OE1	1:A:256:ARG:NH1	2.51	0.44
1:A:2:SER:HB2	1:A:103:VAL:O	2.18	0.44
1:A:250:PRO:HB2	1:A:253:GLN:HG3	1.99	0.43
2:B:403:ARG:NH2	2:B:459:ASP:O	2.51	0.43
1:A:95:VAL:CG2	1:A:116:TYR:CZ	3.01	0.43
1:A:130:LEU:HD13	1:A:160:LEU:HD12	2.01	0.43
1:A:202:ARG:HH12	2:B:499:MET:HG3	1.82	0.43
1:A:232:GLU:O	1:A:233:THR:C	2.61	0.43
1:A:206:LEU:HD23	1:A:242:GLN:HB3	2.01	0.43
1:A:114:HIS:O	1:A:115:GLN:CG	2.64	0.43
1:A:123:TYR:CE2	3:C:709:CDE:HG12	2.54	0.43
1:A:251:SER:O	1:A:253:GLN:HG2	2.19	0.43
2:B:470:PHE:HD2	2:B:478:TYR:CE2	2.37	0.43
1:A:21:ARG:NH1	1:A:21:ARG:CG	2.82	0.42
1:A:21:ARG:NH1	1:A:23:ILE:HD11	2.34	0.42
1:A:217:TRP:HD1	1:A:228:THR:HG23	1.84	0.42
1:A:8:PHE:CD1	1:A:8:PHE:N	2.87	0.42
2:B:422:PHE:HA	2:B:468:THR:O	2.19	0.42
1:A:176:LYS:HA	1:A:180:GLN:HG3	2.00	0.42
2:B:439:LEU:HD11	2:B:466:TYR:O	2.20	0.42
1:A:207:SER:HA	1:A:240:THR:HB	2.00	0.42
1:A:263:HIS:CD2	1:A:265:GLY:H	2.38	0.42
1:A:268:LYS:CE	1:A:269:PRO:HD2	2.50	0.41
2:B:410:TYR:CD1	2:B:410:TYR:N	2.87	0.41
1:A:54:GLN:NE2	1:A:174:ASN:HB3	2.36	0.41
2:B:423:LEU:O	2:B:467:TYR:HA	2.20	0.41
1:A:21:ARG:HG2	1:A:21:ARG:NH1	2.16	0.41
1:A:88:SER:OG	1:A:90:ALA:HB3	2.20	0.41
1:A:33:PHE:HB3	1:A:51:TRP:CZ2	2.55	0.41
1:A:165:VAL:O	1:A:169:ARG:HG3	2.20	0.41
1:A:185:PRO:HD3	1:A:263:HIS:CD2	2.56	0.41
1:A:2:SER:HB2	1:A:3:HIS:H	1.77	0.41
1:A:226:GLN:O	1:A:227:ASP:HB2	2.20	0.41
1:A:170:ARG:HG3	1:A:174:ASN:ND2	2.36	0.41
1:A:189:MET:SD	1:A:201:LEU:HG	2.60	0.41
1:A:253:GLN:O	1:A:256:ARG:HG3	2.21	0.41
2:B:429:GLY:HA2	2:B:461:SER:HB2	2.02	0.41
1:A:145:HIS:O	1:A:146:LYS:C	2.63	0.41
1:A:227:ASP:O	1:A:247:VAL:HG23	2.21	0.41
2:B:404:THR:HG23	2:B:486:THR:HB	2.03	0.41
1:A:116:TYR:CE1	3:C:709:CDE:HG11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:TYR:CE2	3:C:702:ILE:HG23	2.56	0.40
1:A:70:HIS:HE1	3:C:703:LEU:O	2.04	0.40
1:A:215:LEU:HD12	1:A:215:LEU:HA	1.82	0.40
1:A:107:TRP:CZ2	1:A:180:GLN:OE1	2.65	0.40
1:A:126:LEU:HD13	1:A:133:TRP:CH2	2.56	0.40
1:A:23:ILE:HA	1:A:36:PHE:O	2.21	0.40
1:A:187:THR:HG22	1:A:204:TRP:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	226/231 (98%)	204 (90%)	22 (10%)	8	25
2	B	95/95 (100%)	86 (90%)	9 (10%)	8	26
3	C	5/6 (83%)	3 (60%)	2 (40%)	0	0
All	All	326/332 (98%)	293 (90%)	33 (10%)	7	24

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	14	ARG
1	A	17	ARG
1	A	21	ARG
1	A	81	LEU

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Mol	Chain	Res	Type
1	A	95	VAL
1	A	103	VAL
1	A	106	ASP
1	A	108	ARG
1	A	110	LEU
1	A	113	TYR
1	A	137	ASP
1	A	138	MET
1	A	156	LEU
1	A	163	THR
1	A	165	VAL
1	A	212	GLU
1	A	215	LEU
1	A	234	ARG
1	A	268	LYS
1	A	272	LEU
1	A	275	GLU
2	B	400	MET
2	B	404	THR
2	B	409	VAL
2	B	411	SER
2	B	420	SER
2	B	454	LEU
2	B	475	LYS
2	B	488	SER
2	B	499	MET
3	C	702	ILE
3	C	703	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	93	HIS
1	A	114	HIS
1	A	115	GLN
1	A	155	GLN
1	A	174	ASN
1	A	218	GLN
1	A	263	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	CDE	C	709	3	5,5,5	0.81	0	4,6,6	0.57	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
3	CDE	C	709	3	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	709	CDE	N-CA-CB-CG1
3	C	709	CDE	N-CA-CB-CG2
3	C	709	CDE	C-CA-CB-CG1
3	C	709	CDE	C-CA-CB-CG2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	709	CDE	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.