



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:17 AM UTC

PDB ID : 1MD7 / pdb_00001md7
Title : Monomeric structure of the zymogen of complement protease C1r
Authors : Budayova-Spano, M.; Grabarse, W.; Thielens, N.M.; Hillen, H.; Lacroix, M.; Schmidt, M.; Fontecilla-Camps, J.; Arlaud, G.J.; Gaboriaud, C.
Deposited on : 2002-08-07
Resolution : 3.20 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

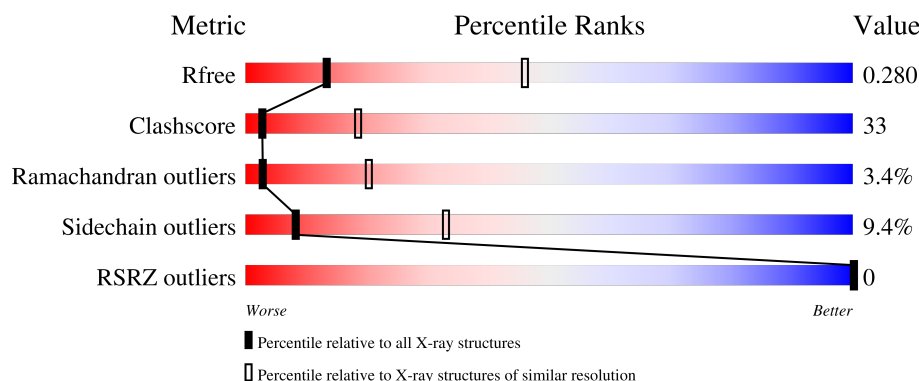
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

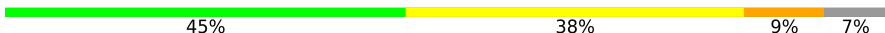
The reported resolution of this entry is 3.20 Å.

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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	328	

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	NAG	A	1001	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2531 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 C1R COMPLEMENT SERINE PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	304	2400	1522	418	443	17	27	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	637	ALA	SER	engineered mutation	UNP P00736

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	14	8	1	5	0	0

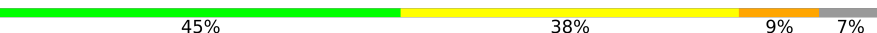
- Molecule 3 is water.

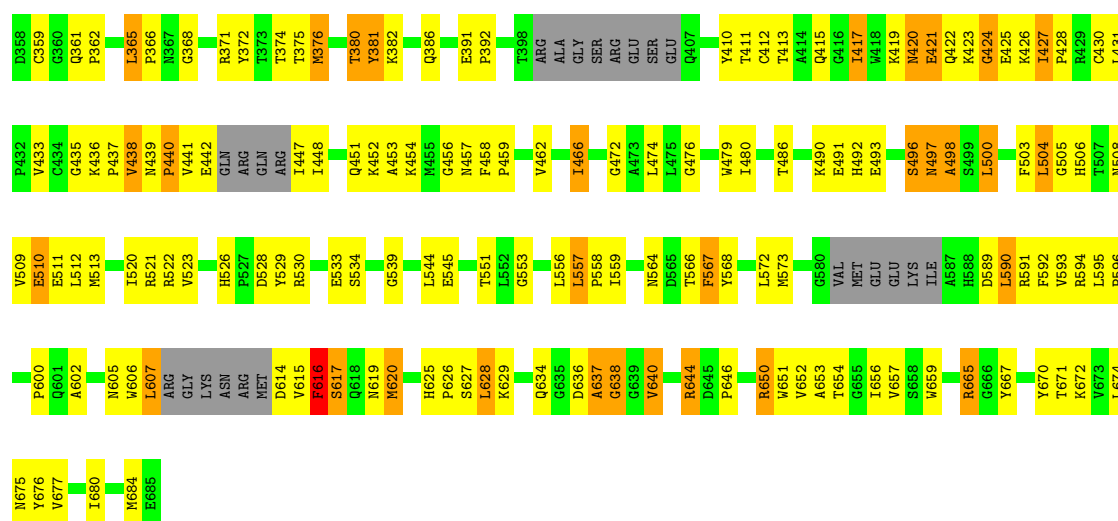
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total 117	O 117	0	0

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: C1R COMPLEMENT SERINE PROTEASE

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	167.06Å 167.06Å 43.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	11.94 – 3.20 11.94 – 3.20	Depositor EDS
% Data completeness (in resolution range)	93.9 (11.94-3.20) 93.9 (11.94-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 3.17Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.217 , 0.285 0.217 , 0.280	Depositor DCC
R_{free} test set	584 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	49.0	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.059 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2531	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.50	0/2463	1.06	16/3339 (0.5%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	ASN	N-CA-C	-11.00	96.02	110.43
1	A	557	LEU	CA-C-N	6.52	126.89	119.92
1	A	557	LEU	C-N-CA	6.52	126.89	119.92
1	A	376	MET	N-CA-C	6.39	119.92	109.76
1	A	451	GLN	N-CA-C	5.95	118.50	109.63
1	A	616	PHE	N-CA-C	-5.88	106.16	113.15
1	A	638	GLY	N-CA-C	-5.68	107.11	115.30
1	A	496	SER	N-CA-C	5.61	117.06	108.42
1	A	458	PHE	CA-C-N	5.57	125.27	119.64
1	A	458	PHE	C-N-CA	5.57	125.27	119.64
1	A	438	VAL	N-CA-C	-5.47	107.04	111.91
1	A	628	LEU	N-CA-C	5.34	118.59	111.75
1	A	427	ILE	N-CA-C	5.31	113.96	109.02
1	A	650	ARG	N-CA-C	-5.28	104.45	108.78
1	A	650	ARG	CB-CA-C	-5.25	109.50	117.07
1	A	659	TRP	N-CA-C	5.09	119.21	113.15

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	2400	0	2285	154	0
2	A	14	0	13	0	0
3	A	117	0	0	9	0
All	All	2531	0	2298	154	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 33.

All (154) 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:665:ARG:HD2	1:A:665:ARG:H	1.26	1.00
1:A:447:ILE:HG12	1:A:448:ILE:H	1.23	0.99
1:A:454:LYS:H	1:A:457:ASN:HD22	1.22	0.84
1:A:665:ARG:H	1:A:665:ARG:CD	1.93	0.81
1:A:454:LYS:H	1:A:457:ASN:ND2	1.78	0.80
1:A:605:ASN:HD22	1:A:665:ARG:HH12	1.30	0.79
1:A:620:MET:HE2	1:A:671:THR:HA	1.68	0.74
1:A:526:HIS:CD2	1:A:528:ASP:H	2.06	0.73
1:A:665:ARG:HD2	1:A:665:ARG:N	2.03	0.73
1:A:437:PRO:HG2	1:A:440:PRO:HG3	1.70	0.72
1:A:619:ASN:C	1:A:620:MET:HG2	2.12	0.72
1:A:447:ILE:HG12	1:A:448:ILE:N	2.03	0.72
1:A:607:LEU:N	1:A:607:LEU:HD12	2.07	0.69
1:A:595:LEU:HD23	1:A:595:LEU:H	1.58	0.69
1:A:466:ILE:HG12	1:A:500:LEU:HD23	1.76	0.68
1:A:626:PRO:HD3	1:A:667:TYR:OH	1.93	0.68
1:A:480:ILE:HG13	1:A:544:LEU:HB2	1.76	0.68
1:A:674:LEU:HA	1:A:677:VAL:HG23	1.74	0.68
1:A:605:ASN:HD22	1:A:665:ARG:NH1	1.91	0.67
1:A:526:HIS:HD2	1:A:528:ASP:HB2	1.60	0.66
1:A:374:THR:O	1:A:375:THR:C	2.36	0.65
1:A:572:LEU:HD12	1:A:573:MET:N	2.11	0.65
1:A:391:GLU:HG3	1:A:392:PRO:HA	1.77	0.65
1:A:625:HIS:ND1	1:A:626:PRO:HD2	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:674:LEU:HD12	1:A:674:LEU:O	1.97	0.65
1:A:534:SER:HA	3:A:2044:HOH:O	1.96	0.65
1:A:646:PRO:HA	3:A:2105:HOH:O	1.97	0.65
1:A:680:ILE:HG22	1:A:684:MET:HE2	1.79	0.65
1:A:526:HIS:CD2	1:A:528:ASP:HB2	2.33	0.64
1:A:526:HIS:HD2	1:A:528:ASP:H	1.44	0.64
1:A:665:ARG:HH11	1:A:665:ARG:HG2	1.61	0.64
1:A:605:ASN:HB2	1:A:665:ARG:HH22	1.62	0.64
1:A:462:VAL:HG22	1:A:504:LEU:HG	1.80	0.64
1:A:626:PRO:HA	1:A:665:ARG:O	2.01	0.61
1:A:410:TYR:HA	1:A:419:LYS:O	1.99	0.61
1:A:420:ASN:O	1:A:422:GLN:N	2.31	0.61
1:A:427:ILE:HD11	3:A:2010:HOH:O	2.00	0.61
1:A:616:PHE:C	1:A:616:PHE:CD2	2.79	0.60
1:A:365:LEU:HD13	1:A:428:PRO:HG2	1.84	0.60
1:A:564:ASN:OD1	1:A:566:THR:HG23	2.01	0.60
1:A:636:ASP:O	1:A:637:ALA:HB2	2.02	0.60
1:A:615:VAL:HG23	3:A:2016:HOH:O	2.01	0.60
1:A:420:ASN:C	1:A:420:ASN:HD22	2.10	0.59
1:A:413:THR:HG23	1:A:417:ILE:O	2.03	0.58
1:A:553:GLY:O	1:A:557:LEU:HD11	2.04	0.58
1:A:437:PRO:HB3	1:A:459:PRO:HG3	1.86	0.57
1:A:417:ILE:HD13	1:A:417:ILE:N	2.19	0.57
1:A:614:ASP:C	1:A:616:PHE:H	2.10	0.57
1:A:602:ALA:HB1	1:A:667:TYR:CD2	2.40	0.56
1:A:573:MET:HE3	1:A:594:ARG:NH1	2.21	0.56
1:A:572:LEU:HD12	1:A:573:MET:H	1.71	0.55
1:A:672:LYS:HE3	1:A:675:ASN:OD1	2.07	0.55
1:A:371:ARG:HD2	3:A:2015:HOH:O	2.05	0.55
1:A:441:VAL:HG13	1:A:457:ASN:OD1	2.06	0.55
1:A:480:ILE:HD12	1:A:480:ILE:C	2.32	0.55
1:A:424:GLY:O	1:A:425:GLU:HB3	2.07	0.54
1:A:365:LEU:HD23	1:A:368:GLY:HA3	1.88	0.54
1:A:480:ILE:HD11	1:A:544:LEU:HD12	1.89	0.54
1:A:480:ILE:HD11	1:A:544:LEU:CD1	2.38	0.53
1:A:417:ILE:HD13	1:A:417:ILE:H	1.73	0.53
1:A:567:PHE:O	1:A:572:LEU:HD23	2.09	0.53
1:A:529:TYR:HB2	1:A:539:GLY:O	2.08	0.53
1:A:496:SER:C	1:A:497:ASN:O	2.43	0.53
1:A:509:VAL:O	1:A:513:MET:HG2	2.09	0.52
1:A:438:VAL:HG13	1:A:439:ASN:ND2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:TYR:CE2	1:A:654:THR:HB	2.44	0.52
1:A:665:ARG:NH1	1:A:665:ARG:HG2	2.25	0.52
1:A:607:LEU:N	1:A:607:LEU:CD1	2.73	0.51
1:A:491:GLU:O	1:A:492:HIS:HB2	2.11	0.51
1:A:391:GLU:CG	1:A:392:PRO:HA	2.41	0.51
1:A:521:ARG:HD3	1:A:545:GLU:OE2	2.10	0.51
1:A:508:ASN:O	1:A:512:LEU:HG	2.11	0.50
1:A:448:ILE:HG12	1:A:573:MET:HE1	1.95	0.49
1:A:427:ILE:HG23	1:A:428:PRO:HD2	1.95	0.49
1:A:452:LYS:O	1:A:592:PHE:HE2	1.96	0.49
1:A:410:TYR:OH	1:A:428:PRO:HD3	2.13	0.49
1:A:670:TYR:CD1	1:A:670:TYR:N	2.80	0.48
1:A:476:GLY:O	1:A:558:PRO:HG3	2.13	0.48
1:A:530:ARG:HH11	1:A:530:ARG:HG3	1.78	0.48
1:A:559:ILE:HD13	1:A:653:ALA:HB2	1.94	0.48
1:A:497:ASN:O	1:A:498:ALA:HB2	2.12	0.48
1:A:420:ASN:C	1:A:420:ASN:ND2	2.69	0.48
1:A:462:VAL:HB	1:A:472:GLY:O	2.13	0.48
1:A:420:ASN:HD22	1:A:421:GLU:N	2.10	0.48
1:A:591:ARG:HG2	1:A:591:ARG:HH11	1.79	0.48
1:A:616:PHE:CD2	1:A:616:PHE:O	2.67	0.47
1:A:380:THR:O	1:A:381:TYR:C	2.57	0.47
1:A:420:ASN:C	1:A:422:GLN:H	2.19	0.47
1:A:439:ASN:N	1:A:440:PRO:HD3	2.29	0.47
1:A:620:MET:HE3	1:A:671:THR:HG23	1.96	0.47
1:A:510:GLU:H	1:A:510:GLU:CD	2.22	0.47
1:A:628:LEU:O	1:A:629:LYS:HB2	2.14	0.47
1:A:376:MET:HB3	1:A:376:MET:HE2	1.82	0.47
1:A:440:PRO:HA	3:A:2117:HOH:O	2.15	0.47
1:A:453:ALA:HB3	1:A:590:LEU:HD23	1.95	0.47
1:A:625:HIS:CG	1:A:626:PRO:HD2	2.50	0.47
1:A:423:LYS:O	1:A:424:GLY:O	2.33	0.46
1:A:615:VAL:C	1:A:617:SER:H	2.22	0.46
1:A:433:VAL:O	1:A:433:VAL:HG23	2.16	0.46
1:A:490:LYS:O	1:A:493:GLU:CB	2.63	0.46
1:A:600:PRO:HG2	3:A:2068:HOH:O	2.16	0.46
1:A:365:LEU:CD1	1:A:428:PRO:HG2	2.45	0.46
1:A:556:LEU:C	1:A:557:LEU:HD12	2.41	0.46
1:A:479:TRP:HH2	1:A:522:ARG:HH21	1.64	0.46
1:A:417:ILE:HD11	1:A:419:LYS:NZ	2.31	0.45
1:A:490:LYS:O	1:A:493:GLU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:644:ARG:HD2	3:A:2105:HOH:O	2.15	0.45
1:A:650:ARG:O	1:A:651:TRP:CD1	2.70	0.45
1:A:430:CYS:O	1:A:431:LEU:HD23	2.16	0.45
1:A:361:GLN:O	1:A:362:PRO:C	2.59	0.45
1:A:551:THR:HG22	1:A:551:THR:O	2.17	0.45
1:A:573:MET:SD	1:A:596:PRO:HB3	2.57	0.45
1:A:506:HIS:HD2	1:A:508:ASN:H	1.65	0.45
1:A:381:TYR:O	1:A:382:LYS:HB2	2.16	0.44
1:A:616:PHE:O	1:A:616:PHE:CG	2.70	0.44
1:A:505:GLY:O	1:A:506:HIS:HB2	2.16	0.44
1:A:453:ALA:CB	1:A:590:LEU:HD23	2.48	0.44
1:A:503:PHE:C	1:A:504:LEU:HD12	2.43	0.44
1:A:506:HIS:CD2	1:A:508:ASN:H	2.36	0.43
1:A:593:VAL:HG23	1:A:634:GLN:HG2	2.00	0.43
1:A:503:PHE:CD1	1:A:503:PHE:N	2.86	0.43
1:A:436:LYS:HB2	1:A:436:LYS:HE3	1.77	0.43
1:A:638:GLY:HA2	1:A:656:ILE:HG22	2.01	0.43
1:A:372:TYR:HB2	1:A:376:MET:HE2	2.00	0.43
1:A:506:HIS:CD2	1:A:511:GLU:CB	3.02	0.43
1:A:506:HIS:NE2	1:A:511:GLU:HG3	2.34	0.43
1:A:625:HIS:CD2	1:A:627:SER:OG	2.72	0.43
1:A:441:VAL:O	1:A:442:GLU:C	2.62	0.42
1:A:381:TYR:CD1	1:A:382:LYS:N	2.88	0.42
1:A:656:ILE:O	1:A:657:VAL:C	2.60	0.42
1:A:523:VAL:HG13	1:A:544:LEU:CD2	2.49	0.42
1:A:520:ILE:HD12	1:A:520:ILE:N	2.35	0.42
1:A:456:GLY:O	1:A:459:PRO:HD3	2.19	0.42
1:A:365:LEU:HA	1:A:366:PRO:HD2	1.91	0.42
1:A:438:VAL:O	1:A:439:ASN:CG	2.63	0.42
1:A:448:ILE:CG1	1:A:573:MET:HE1	2.50	0.42
1:A:676:TYR:O	1:A:680:ILE:HG12	2.19	0.42
1:A:480:ILE:HD12	1:A:480:ILE:O	2.21	0.41
1:A:640:VAL:CG2	1:A:653:ALA:HB1	2.50	0.41
1:A:366:PRO:HG2	3:A:2039:HOH:O	2.19	0.41
1:A:595:LEU:HD23	1:A:595:LEU:N	2.31	0.41
1:A:634:GLN:HA	1:A:634:GLN:OE1	2.19	0.41
1:A:447:ILE:C	1:A:448:ILE:HG13	2.45	0.41
1:A:684:MET:HE3	1:A:684:MET:HB2	1.94	0.41
1:A:620:MET:HE2	1:A:671:THR:CA	2.45	0.41
1:A:365:LEU:HD23	1:A:368:GLY:CA	2.50	0.41
1:A:479:TRP:CZ3	1:A:545:GLU:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:ILE:HD12	1:A:486:THR:CG2	2.51	0.41
1:A:415:GLN:HB2	1:A:417:ILE:CD1	2.51	0.40
1:A:614:ASP:C	1:A:616:PHE:N	2.78	0.40
1:A:625:HIS:C	1:A:627:SER:H	2.29	0.40
1:A:374:THR:HG22	1:A:375:THR:N	2.36	0.40
1:A:365:LEU:HD23	1:A:368:GLY:C	2.47	0.40
1:A:441:VAL:CG1	1:A:457:ASN:OD1	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	294/328 (90%)	240 (82%)	44 (15%)	10 (3%)	3	20

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	421	GLU
1	A	424	GLY
1	A	637	ALA
1	A	359	CYS
1	A	381	TYR
1	A	412	CYS
1	A	435	GLY
1	A	498	ALA
1	A	466	ILE
1	A	440	PRO

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	255/276 (92%)	231 (91%)	24 (9%)	8 33

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	365	LEU
1	A	380	THR
1	A	386	GLN
1	A	411	THR
1	A	417	ILE
1	A	420	ASN
1	A	426	LYS
1	A	474	LEU
1	A	500	LEU
1	A	504	LEU
1	A	510	GLU
1	A	533	GLU
1	A	567	PHE
1	A	589	ASP
1	A	590	LEU
1	A	606	TRP
1	A	607	LEU
1	A	616	PHE
1	A	617	SER
1	A	620	MET
1	A	640	VAL
1	A	644	ARG
1	A	652	VAL
1	A	665	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	ASN

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Mol	Chain	Res	Type
1	A	379	ASN
1	A	397	GLN
1	A	420	ASN
1	A	439	ASN
1	A	451	GLN
1	A	457	ASN
1	A	461	GLN
1	A	495	GLN
1	A	506	HIS
1	A	526	HIS
1	A	531	GLN
1	A	548	ASN
1	A	599	ASN
1	A	601	GLN
1	A	605	ASN
1	A	625	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1001	1	14,14,15	0.69	0	17,19,21	0.93	1 (5%)

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	NAG	A	1001	1	1/1/5/7	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	NAG	C2-N2-C7	-3.08	118.77	122.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1001	NAG	C1

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	NAG	C8-C7-N2-C2
2	A	1001	NAG	O7-C7-N2-C2
2	A	1001	NAG	O5-C5-C6-O6
2	A	1001	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	304/328 (92%)	-1.74	0 100 100	10, 23, 67, 95	7 (2%)

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	NAG	A	1001	14/15	0.99	0.04	78,87,91,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.