



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:51 PM UTC

PDB ID : 1JHW / pdb_00001jhw
Title : Ca²⁺-binding Mimicry in the Crystal Structure of the Eu³⁺-Bound Mutant Human Macrophage Capping Protein Cap G
Authors : Vorobiev, S.M.; Southwick, F.S.; Almo, S.C.
Deposited on : 2001-06-28
Resolution : 2.80 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
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

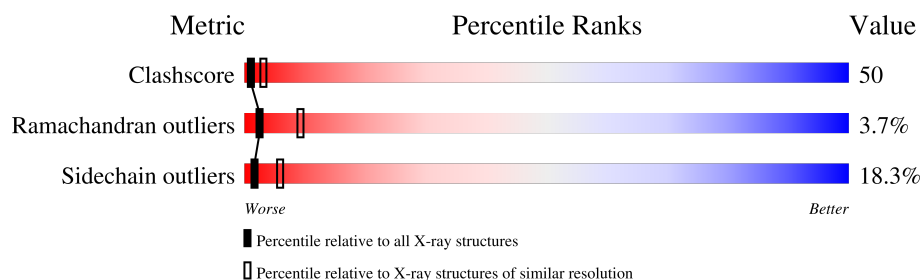
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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	347	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2529 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 MACROPHAGE CAPPING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2436	1551	421	455	9			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	GLN	-	SEE REMARK 999	UNP P40121
A	84	LEU	-	SEE REMARK 999	UNP P40121
A	85	ASP	-	SEE REMARK 999	UNP P40121
A	86	ASP	-	SEE REMARK 999	UNP P40121
A	87	TYR	-	SEE REMARK 999	UNP P40121
A	88	LEU	-	SEE REMARK 999	UNP P40121
A	89	GLY	-	SEE REMARK 999	UNP P40121
A	90	GLY	-	SEE REMARK 999	UNP P40121
A	124	GLY	-	SEE REMARK 999	UNP P40121
A	125	PHE	-	SEE REMARK 999	UNP P40121
A	126	LYS	-	SEE REMARK 999	UNP P40121
A	127	HIS	-	SEE REMARK 999	UNP P40121
A	128	VAL	-	SEE REMARK 999	UNP P40121
A	129	VAL	-	SEE REMARK 999	UNP P40121
A	130	PRO	-	SEE REMARK 999	UNP P40121
A	131	ASN	-	SEE REMARK 999	UNP P40121
A	132	GLU	-	SEE REMARK 999	UNP P40121
A	133	VAL	-	SEE REMARK 999	UNP P40121
A	134	VAL	-	SEE REMARK 999	UNP P40121
A	135	VAL	-	SEE REMARK 999	UNP P40121
A	136	GLN	-	SEE REMARK 999	UNP P40121
A	137	ARG	-	SEE REMARK 999	UNP P40121

- Molecule 2 is EUROPIUM (III) ION (CCD ID: EU3) (formula: Eu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Eu	0	0
			2	2		

- Molecule 3 is water.

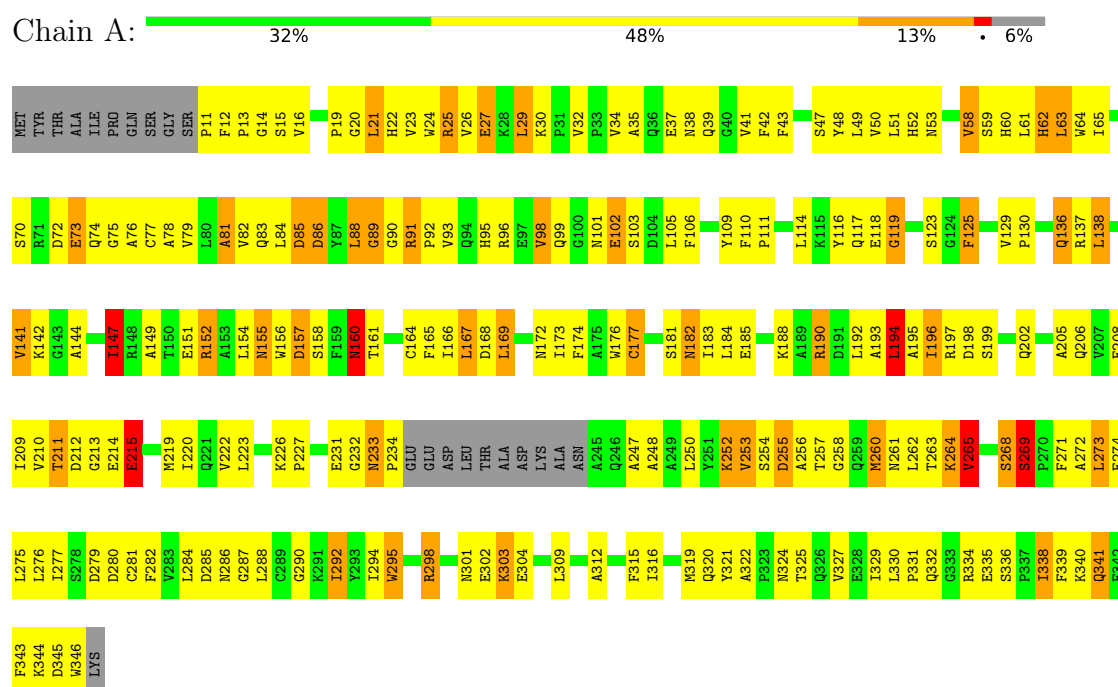
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	91	Total	O	0	0
			91	91		

3 Residue-property plots [i](#)

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

Note EDS was not executed.

• Molecule 1: MACROPHAGE CAPPING PROTEIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	205.60 Å 205.60 Å 56.42 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.73 – 2.80	Depositor
% Data completeness (in resolution range)	92.8 (24.73-2.80)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.248 , 0.296	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2529	wwPDB-VP
Average B, all atoms (Å ²)	76.0	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: EU3

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	1.09	2/2491 (0.1%)	1.35	35/3390 (1.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	MET	SD-CE	-5.93	1.64	1.79
1	A	27	GLU	CA-C	-5.10	1.46	1.52

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	341	GLN	N-CA-C	-9.35	99.22	110.44
1	A	81	ALA	N-CA-C	-8.22	102.01	110.97
1	A	43	PHE	N-CA-C	-8.19	97.90	110.10
1	A	233	ASN	N-CA-C	8.02	122.43	110.32
1	A	88	LEU	N-CA-C	-7.33	103.76	114.39
1	A	188	LYS	N-CA-C	-6.66	103.95	111.07
1	A	268	SER	N-CA-C	-6.54	100.28	110.42
1	A	182	ASN	N-CA-C	6.53	118.44	110.41
1	A	255	ASP	N-CA-C	-6.36	104.67	112.88
1	A	160	ASN	N-CA-C	-6.35	99.75	109.41
1	A	183	ILE	N-CA-C	-6.34	102.94	111.44
1	A	177	CYS	N-CA-C	6.26	118.62	108.41
1	A	290	GLY	N-CA-C	6.26	128.01	113.18
1	A	276	LEU	N-CA-C	6.24	118.77	109.59
1	A	232	GLY	N-CA-C	6.14	127.74	113.18
1	A	147	ILE	N-CA-C	6.12	117.59	108.23
1	A	15	SER	N-CA-C	-6.08	105.16	113.30
1	A	136	GLN	N-CA-C	-6.02	99.39	108.96
1	A	86	ASP	N-CA-C	5.82	117.70	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	SER	CA-C-N	-5.82	112.57	119.84
1	A	269	SER	C-N-CA	-5.82	112.57	119.84
1	A	303	LYS	N-CA-C	-5.78	104.34	111.33
1	A	110	PHE	CA-C-N	5.69	126.95	119.84
1	A	110	PHE	C-N-CA	5.69	126.95	119.84
1	A	215	GLU	N-CA-C	5.62	116.49	109.57
1	A	194	LEU	N-CA-C	-5.51	105.43	111.82
1	A	25	ARG	N-CA-C	-5.48	100.24	108.96
1	A	29	LEU	N-CA-C	-5.43	107.03	113.97
1	A	269	SER	N-CA-C	5.33	121.59	109.81
1	A	85	ASP	N-CA-C	-5.32	104.89	111.33
1	A	312	ALA	N-CA-C	-5.22	105.59	111.28
1	A	265	VAL	N-CA-C	5.22	117.58	111.05
1	A	11	PRO	N-CA-CB	5.13	108.64	103.00
1	A	262	LEU	N-CA-C	-5.09	100.60	108.90
1	A	14	GLY	N-CA-C	-5.03	108.12	115.72

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	2436	0	2296	238	0
2	A	2	0	0	0	0
3	A	91	0	0	4	0
All	All	2529	0	2296	238	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 50.

All (238) 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:253:VAL:HG12	1:A:260:MET:CE	1.85	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ARG:HG2	1:A:152:ARG:HH11	1.22	1.00
1:A:155:ASN:HD22	1:A:157:ASP:H	1.11	0.96
1:A:253:VAL:HG12	1:A:260:MET:HE2	1.46	0.96
1:A:12:PHE:CE1	1:A:84:LEU:HB2	2.04	0.92
1:A:89:GLY:O	1:A:91:ARG:N	2.03	0.92
1:A:152:ARG:HG2	1:A:152:ARG:NH1	1.76	0.92
1:A:53:ASN:HB3	1:A:59:SER:OG	1.73	0.87
1:A:58:VAL:HG12	1:A:59:SER:H	1.37	0.87
1:A:16:VAL:HG11	1:A:84:LEU:HD11	1.57	0.86
1:A:273:LEU:O	1:A:273:LEU:HD12	1.74	0.86
1:A:34:VAL:HG12	1:A:38:ASN:HB2	1.58	0.85
1:A:277:ILE:HG22	1:A:279:ASP:H	1.40	0.83
1:A:316:ILE:HA	1:A:321:TYR:HD1	1.45	0.82
1:A:154:LEU:HD12	1:A:263:THR:HG23	1.61	0.82
1:A:138:LEU:HD12	1:A:167:LEU:HD22	1.61	0.81
1:A:106:PHE:O	1:A:109:TYR:HD1	1.64	0.80
1:A:155:ASN:ND2	1:A:157:ASP:H	1.80	0.79
1:A:38:ASN:O	1:A:41:VAL:HG12	1.84	0.78
1:A:138:LEU:HB2	1:A:154:LEU:CD2	2.14	0.77
1:A:152:ARG:HH11	1:A:152:ARG:CG	1.96	0.77
1:A:190:ARG:O	1:A:194:LEU:HB2	1.84	0.77
1:A:65:ILE:HG13	1:A:65:ILE:O	1.86	0.76
1:A:138:LEU:HB2	1:A:154:LEU:HD23	1.68	0.76
1:A:298:ARG:H	1:A:332:GLN:NE2	1.85	0.73
1:A:114:LEU:HD13	1:A:116:TYR:HE2	1.53	0.73
1:A:137:ARG:HD3	1:A:151:GLU:OE1	1.87	0.73
1:A:327:VAL:O	1:A:327:VAL:HG13	1.87	0.73
1:A:138:LEU:CD1	1:A:167:LEU:HD22	2.18	0.73
1:A:309:LEU:HD21	1:A:329:ILE:HD11	1.68	0.73
1:A:172:ASN:ND2	1:A:206:GLN:HB2	2.04	0.72
1:A:166:ILE:HD13	1:A:193:ALA:HB2	1.72	0.71
1:A:63:LEU:CD1	1:A:77:CYS:SG	2.79	0.71
1:A:65:ILE:HD12	1:A:74:GLN:NE2	2.06	0.71
1:A:89:GLY:C	1:A:91:ARG:H	1.96	0.71
1:A:330:LEU:HD22	1:A:336:SER:H	1.56	0.71
1:A:64:TRP:CZ2	1:A:99:GLN:HB2	2.26	0.70
1:A:50:VAL:HG11	1:A:106:PHE:HE1	1.56	0.70
1:A:253:VAL:HG12	1:A:260:MET:HE3	1.72	0.70
1:A:316:ILE:HA	1:A:321:TYR:CD1	2.26	0.69
1:A:70:SER:HB3	1:A:73:GLU:CB	2.22	0.69
1:A:12:PHE:HE1	1:A:84:LEU:HB2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLN:HA	1:A:102:GLU:OE2	1.93	0.69
1:A:253:VAL:CG1	1:A:260:MET:HE2	2.22	0.69
1:A:298:ARG:HG3	1:A:332:GLN:NE2	2.08	0.68
1:A:59:SER:O	1:A:93:VAL:HG23	1.93	0.68
1:A:35:ALA:HB3	1:A:38:ASN:ND2	2.08	0.67
1:A:88:LEU:HD12	1:A:92:PRO:HG3	1.76	0.67
1:A:331:PRO:HG2	1:A:334:ARG:HB2	1.77	0.67
1:A:34:VAL:CG1	1:A:38:ASN:HB2	2.25	0.66
1:A:277:ILE:CG2	1:A:279:ASP:H	2.09	0.65
1:A:106:PHE:HA	1:A:109:TYR:CE1	2.31	0.65
1:A:277:ILE:HG22	1:A:279:ASP:N	2.12	0.65
1:A:86:ASP:C	1:A:89:GLY:H	2.04	0.65
1:A:88:LEU:HD12	1:A:92:PRO:CG	2.27	0.65
1:A:149:ALA:HB2	1:A:192:LEU:HD21	1.78	0.64
1:A:144:ALA:HB1	3:A:518:HOH:O	1.97	0.64
1:A:63:LEU:HD12	1:A:77:CYS:SG	2.37	0.63
1:A:25:ARG:HG3	1:A:48:TYR:CZ	2.33	0.63
1:A:64:TRP:HZ2	1:A:99:GLN:HB2	1.64	0.63
1:A:53:ASN:CB	1:A:59:SER:OG	2.46	0.62
1:A:41:VAL:HG21	1:A:117:GLN:HE21	1.64	0.62
1:A:160:ASN:ND2	1:A:231:GLU:O	2.32	0.62
1:A:272:ALA:O	1:A:275:LEU:HB2	2.00	0.62
1:A:86:ASP:C	1:A:88:LEU:H	2.07	0.61
1:A:138:LEU:CB	1:A:154:LEU:HD23	2.30	0.60
1:A:155:ASN:ND2	1:A:157:ASP:HB2	2.17	0.60
1:A:209:ILE:HD12	1:A:209:ILE:N	2.16	0.60
1:A:65:ILE:HD11	1:A:98:VAL:CG1	2.32	0.60
1:A:155:ASN:HD22	1:A:157:ASP:N	1.93	0.60
1:A:22:HIS:O	1:A:50:VAL:HA	2.02	0.60
1:A:103:SER:C	1:A:105:LEU:H	2.08	0.60
1:A:190:ARG:HH11	1:A:190:ARG:CG	2.16	0.59
1:A:88:LEU:O	1:A:91:ARG:HD3	2.03	0.59
1:A:209:ILE:HD12	1:A:209:ILE:H	1.68	0.59
1:A:212:ASP:OD1	1:A:226:LYS:NZ	2.30	0.58
1:A:78:ALA:O	1:A:81:ALA:HB3	2.03	0.58
1:A:106:PHE:HA	1:A:109:TYR:HE1	1.68	0.58
1:A:58:VAL:HG12	1:A:59:SER:N	2.15	0.58
1:A:103:SER:C	1:A:105:LEU:N	2.58	0.58
1:A:190:ARG:HH11	1:A:190:ARG:HG3	1.69	0.58
1:A:172:ASN:HD21	1:A:206:GLN:HB2	1.69	0.57
1:A:138:LEU:HB2	1:A:154:LEU:HD21	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:LEU:HD11	1:A:109:TYR:HB3	1.87	0.56
1:A:330:LEU:HD22	1:A:335:GLU:HA	1.87	0.56
1:A:292:ILE:O	1:A:327:VAL:HA	2.05	0.56
1:A:82:VAL:O	1:A:83:GLN:C	2.47	0.56
1:A:86:ASP:HA	1:A:89:GLY:HA2	1.87	0.56
1:A:103:SER:OG	1:A:106:PHE:N	2.28	0.56
1:A:125:PHE:C	1:A:125:PHE:CD2	2.84	0.56
1:A:38:ASN:O	1:A:41:VAL:CG1	2.54	0.56
1:A:88:LEU:O	1:A:91:ARG:HB2	2.06	0.56
1:A:316:ILE:CD1	1:A:325:THR:HB	2.36	0.55
1:A:168:ASP:C	1:A:169:LEU:HD23	2.31	0.55
1:A:273:LEU:HD12	1:A:273:LEU:C	2.31	0.55
1:A:89:GLY:O	1:A:91:ARG:HB2	2.06	0.55
1:A:91:ARG:HB3	1:A:92:PRO:HD3	1.88	0.54
1:A:50:VAL:HG11	1:A:106:PHE:CE1	2.39	0.54
1:A:213:GLY:N	1:A:215:GLU:OE2	2.41	0.54
1:A:336:SER:OG	1:A:338:ILE:HG22	2.08	0.54
1:A:147:ILE:CG2	1:A:192:LEU:HD22	2.37	0.54
1:A:211:THR:O	1:A:212:ASP:C	2.51	0.54
1:A:339:PHE:HE2	1:A:346:TRP:CZ3	2.25	0.54
1:A:16:VAL:HG13	1:A:24:TRP:HH2	1.73	0.53
1:A:344:LYS:O	1:A:345:ASP:C	2.51	0.53
1:A:22:HIS:HB2	1:A:24:TRP:CH2	2.43	0.53
1:A:25:ARG:HB2	1:A:48:TYR:CE2	2.44	0.53
1:A:65:ILE:HD11	1:A:98:VAL:HG12	1.90	0.52
1:A:264:LYS:NZ	3:A:555:HOH:O	2.42	0.52
1:A:23:VAL:HG23	1:A:23:VAL:O	2.08	0.52
1:A:24:TRP:HA	1:A:32:VAL:O	2.10	0.52
1:A:86:ASP:C	1:A:88:LEU:N	2.66	0.52
1:A:103:SER:O	1:A:106:PHE:N	2.42	0.52
1:A:298:ARG:HG2	1:A:298:ARG:HH11	1.74	0.52
1:A:51:LEU:HD13	1:A:61:LEU:HB2	1.91	0.52
1:A:137:ARG:HD3	1:A:151:GLU:CD	2.34	0.52
1:A:23:VAL:HG12	1:A:50:VAL:HG23	1.92	0.52
1:A:330:LEU:HD21	1:A:336:SER:HB3	1.90	0.52
1:A:330:LEU:CD2	1:A:336:SER:H	2.21	0.52
1:A:103:SER:O	1:A:105:LEU:N	2.42	0.52
1:A:341:GLN:O	1:A:341:GLN:HG3	2.09	0.52
1:A:72:ASP:O	1:A:75:GLY:N	2.43	0.51
1:A:72:ASP:O	1:A:74:GLN:N	2.43	0.51
1:A:339:PHE:CE2	1:A:346:TRP:CZ3	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:ASP:C	1:A:74:GLN:N	2.63	0.51
1:A:147:ILE:HD13	1:A:147:ILE:N	2.24	0.51
1:A:19:PRO:HA	1:A:53:ASN:OD1	2.11	0.51
1:A:190:ARG:CG	1:A:190:ARG:NH1	2.73	0.51
1:A:330:LEU:HD22	1:A:336:SER:N	2.25	0.50
1:A:91:ARG:CB	1:A:92:PRO:HD3	2.41	0.50
1:A:255:ASP:O	1:A:256:ALA:C	2.54	0.50
1:A:61:LEU:HD22	1:A:84:LEU:HD23	1.93	0.50
1:A:23:VAL:HA	1:A:49:LEU:O	2.12	0.50
1:A:106:PHE:O	1:A:109:TYR:CD1	2.55	0.50
1:A:269:SER:O	1:A:271:PHE:N	2.45	0.50
1:A:75:GLY:O	1:A:76:ALA:C	2.55	0.50
1:A:169:LEU:HD23	1:A:169:LEU:N	2.26	0.50
1:A:316:ILE:HD11	1:A:325:THR:HB	1.93	0.49
1:A:25:ARG:HA	1:A:48:TYR:CD2	2.47	0.49
1:A:105:LEU:O	1:A:109:TYR:CE1	2.66	0.49
1:A:118:GLU:O	1:A:119:GLY:C	2.56	0.49
1:A:85:ASP:O	1:A:89:GLY:N	2.46	0.49
1:A:164:CYS:C	1:A:165:PHE:CD1	2.90	0.48
1:A:298:ARG:H	1:A:332:GLN:HE21	1.56	0.48
1:A:62:HIS:HE1	1:A:105:LEU:HD23	1.78	0.48
1:A:295:TRP:CZ2	1:A:332:GLN:HG3	2.49	0.48
1:A:301:ASN:HD21	1:A:303:LYS:HB2	1.77	0.48
1:A:42:PHE:HB3	1:A:64:TRP:CZ3	2.48	0.48
1:A:88:LEU:CD1	1:A:92:PRO:HG3	2.43	0.48
1:A:38:ASN:O	1:A:39:GLN:C	2.55	0.48
1:A:154:LEU:HD12	1:A:263:THR:CG2	2.39	0.48
1:A:202:GLN:O	1:A:202:GLN:HG2	2.14	0.48
1:A:96:ARG:HD2	3:A:536:HOH:O	2.14	0.47
1:A:256:ALA:C	1:A:258:GLY:H	2.22	0.47
1:A:252:LYS:HB2	1:A:282:PHE:CE2	2.49	0.47
1:A:338:ILE:CG2	1:A:339:PHE:N	2.77	0.47
1:A:302:GLU:O	1:A:302:GLU:HG3	2.15	0.47
1:A:149:ALA:HB2	1:A:192:LEU:CD2	2.42	0.47
1:A:338:ILE:HG23	1:A:339:PHE:N	2.28	0.47
1:A:195:ALA:O	1:A:196:ILE:C	2.59	0.46
1:A:141:VAL:O	1:A:142:LYS:CG	2.64	0.46
1:A:195:ALA:O	1:A:197:ARG:N	2.48	0.46
1:A:250:LEU:HG	1:A:265:VAL:HG22	1.96	0.46
1:A:294:ILE:CD1	1:A:309:LEU:HA	2.45	0.46
1:A:335:GLU:CD	1:A:346:TRP:CZ2	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:VAL:O	1:A:82:VAL:HB	2.15	0.46
1:A:195:ALA:O	1:A:198:ASP:N	2.49	0.46
1:A:247:ALA:O	1:A:248:ALA:C	2.58	0.46
1:A:281:CYS:C	1:A:282:PHE:CD1	2.94	0.46
1:A:129:VAL:O	1:A:130:PRO:C	2.58	0.45
1:A:155:ASN:O	1:A:158:SER:HB2	2.16	0.45
1:A:254:SER:HB2	1:A:280:ASP:CG	2.41	0.45
1:A:316:ILE:HG23	1:A:321:TYR:HB2	1.97	0.45
1:A:335:GLU:HB2	1:A:340:LYS:CE	2.47	0.45
1:A:88:LEU:HD12	1:A:92:PRO:HG2	1.97	0.45
1:A:340:LYS:HB3	1:A:346:TRP:HB3	1.98	0.45
1:A:16:VAL:HG13	1:A:24:TRP:CH2	2.51	0.45
1:A:42:PHE:N	1:A:42:PHE:CD2	2.85	0.45
1:A:72:ASP:C	1:A:74:GLN:H	2.25	0.45
1:A:26:VAL:HG21	1:A:77:CYS:SG	2.57	0.45
1:A:86:ASP:O	1:A:89:GLY:N	2.50	0.45
1:A:316:ILE:HA	1:A:321:TYR:HB2	1.98	0.45
1:A:147:ILE:N	1:A:147:ILE:CD1	2.78	0.44
1:A:136:GLN:CG	1:A:261:ASN:HD22	2.30	0.44
1:A:12:PHE:CE1	1:A:84:LEU:HD13	2.53	0.44
1:A:252:LYS:HG3	1:A:282:PHE:CZ	2.52	0.44
1:A:321:TYR:O	1:A:322:ALA:C	2.60	0.44
1:A:156:TRP:CH2	1:A:219:MET:HE2	2.52	0.44
1:A:58:VAL:CG1	1:A:59:SER:H	2.19	0.44
1:A:277:ILE:HG21	1:A:280:ASP:OD2	2.18	0.44
1:A:294:ILE:HD12	1:A:309:LEU:HD23	1.99	0.44
1:A:233:ASN:HA	1:A:234:PRO:HD3	1.65	0.44
1:A:250:LEU:HG	1:A:265:VAL:CG2	2.48	0.44
1:A:294:ILE:HD11	1:A:309:LEU:HA	2.00	0.43
1:A:298:ARG:H	1:A:332:GLN:HE22	1.64	0.43
1:A:22:HIS:O	1:A:51:LEU:N	2.38	0.43
1:A:65:ILE:O	1:A:65:ILE:CG1	2.62	0.43
1:A:327:VAL:O	1:A:327:VAL:CG1	2.60	0.43
1:A:274:GLU:CD	1:A:274:GLU:H	2.25	0.43
1:A:316:ILE:HD11	1:A:325:THR:CG2	2.48	0.43
1:A:23:VAL:HG12	1:A:50:VAL:CG2	2.48	0.43
1:A:154:LEU:HD23	1:A:154:LEU:HA	1.74	0.43
1:A:254:SER:OG	1:A:280:ASP:OD1	2.29	0.43
1:A:287:GLY:O	1:A:288:LEU:C	2.61	0.43
1:A:34:VAL:O	1:A:35:ALA:C	2.62	0.43
1:A:166:ILE:HA	1:A:174:PHE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:ILE:HD11	1:A:98:VAL:HG13	2.01	0.42
1:A:280:ASP:HA	1:A:304:GLU:OE1	2.18	0.42
1:A:268:SER:O	1:A:271:PHE:CE2	2.73	0.42
1:A:99:GLN:HG3	1:A:116:TYR:CE1	2.54	0.42
1:A:156:TRP:CZ2	1:A:223:LEU:HD13	2.53	0.42
1:A:160:ASN:OD1	1:A:160:ASN:C	2.62	0.42
1:A:176:TRP:NE1	1:A:215:GLU:OE1	2.51	0.42
1:A:177:CYS:N	1:A:210:VAL:O	2.51	0.42
1:A:114:LEU:HD13	1:A:116:TYR:CE2	2.43	0.42
1:A:288:LEU:HD12	1:A:288:LEU:HA	1.77	0.42
1:A:315:PHE:HA	1:A:319:MET:HE2	2.02	0.42
1:A:72:ASP:O	1:A:73:GLU:C	2.63	0.41
1:A:123:SER:C	1:A:125:PHE:N	2.78	0.41
1:A:12:PHE:HB3	1:A:13:PRO:HD2	2.03	0.41
1:A:156:TRP:C	1:A:158:SER:H	2.29	0.41
1:A:60:HIS:HD2	1:A:95:HIS:CE1	2.39	0.41
1:A:182:ASN:HB3	1:A:184:LEU:H	1.86	0.41
1:A:286:ASN:O	1:A:286:ASN:CG	2.63	0.41
1:A:167:LEU:HD11	1:A:219:MET:HE3	2.02	0.41
1:A:181:SER:HB2	1:A:185:GLU:OE2	2.20	0.41
1:A:298:ARG:N	1:A:332:GLN:HE21	2.18	0.41
1:A:316:ILE:HD13	1:A:325:THR:HB	2.02	0.41
1:A:123:SER:C	1:A:125:PHE:H	2.28	0.41
1:A:156:TRP:C	1:A:158:SER:N	2.77	0.41
1:A:192:LEU:O	1:A:195:ALA:HB3	2.21	0.41
1:A:89:GLY:C	1:A:91:ARG:N	2.69	0.41
1:A:169:LEU:HD13	1:A:222:VAL:HG21	2.02	0.41
1:A:25:ARG:NH2	3:A:552:HOH:O	2.53	0.41
1:A:285:ASP:HA	1:A:292:ILE:HG12	2.02	0.40
1:A:25:ARG:HG3	1:A:48:TYR:CE1	2.56	0.40
1:A:20:GLY:O	1:A:52:HIS:HA	2.22	0.40
1:A:277:ILE:C	1:A:279:ASP:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	322/347 (93%)	256 (80%)	54 (17%)	12 (4%)	2 9

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	90	GLY
1	A	111	PRO
1	A	89	GLY
1	A	196	ILE
1	A	343	PHE
1	A	58	VAL
1	A	73	GLU
1	A	205	ALA
1	A	257	THR
1	A	227	PRO
1	A	119	GLY

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	241/288 (84%)	197 (82%)	44 (18%)	2 6

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	29	LEU
1	A	30	LYS
1	A	37	GLU
1	A	47	SER

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Mol	Chain	Res	Type
1	A	62	HIS
1	A	63	LEU
1	A	91	ARG
1	A	98	VAL
1	A	101	ASN
1	A	102	GLU
1	A	125	PHE
1	A	138	LEU
1	A	141	VAL
1	A	147	ILE
1	A	152	ARG
1	A	155	ASN
1	A	157	ASP
1	A	160	ASN
1	A	161	THR
1	A	167	LEU
1	A	169	LEU
1	A	173	ILE
1	A	190	ARG
1	A	194	LEU
1	A	199	SER
1	A	208	GLU
1	A	211	THR
1	A	214	GLU
1	A	215	GLU
1	A	220	ILE
1	A	252	LYS
1	A	253	VAL
1	A	264	LYS
1	A	265	VAL
1	A	269	SER
1	A	273	LEU
1	A	284	LEU
1	A	292	ILE
1	A	295	TRP
1	A	298	ARG
1	A	320	GLN
1	A	324	ASN
1	A	338	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	60	HIS
1	A	101	ASN
1	A	117	GLN
1	A	155	ASN
1	A	172	ASN
1	A	182	ASN
1	A	261	ASN
1	A	286	ASN
1	A	301	ASN
1	A	332	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

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.