



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:13 AM UTC

PDB ID : 3DRK / pdb_00003drk
Title : Crystal structure of Lactococcal OppA co-crystallized with Neuropeptide S in an open conformation
Authors : Berntsson, R.P.-A.; Doeven, M.K.; Duurkens, R.H.; Sengupta, D.; Marrink, S.-J.; Thunnissen, A.-M.; Poolman, B.; Slotboom, D.-J.
Deposited on : 2008-07-11
Resolution : 1.80 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)	:	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

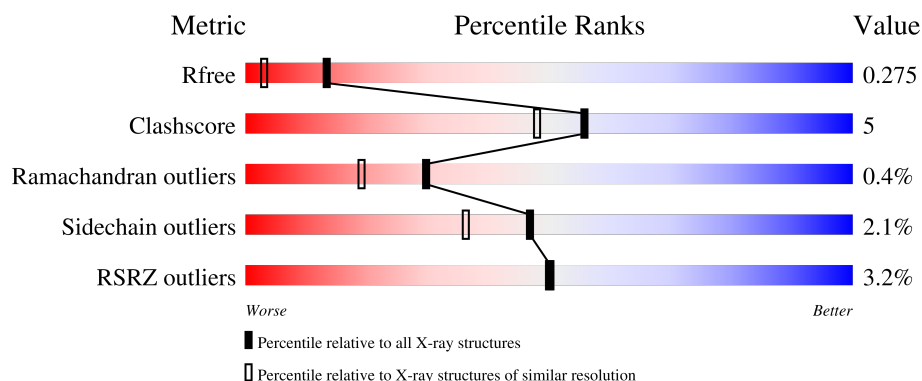
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 $\leq 5\%$. 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	590	
2	B	5	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4905 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 Oligopeptide-binding protein oppA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	3	0
			4374	2775	722	863	14			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A2RJ53
A	579	GLY	-	expression tag	UNP A2RJ53
A	580	SER	-	expression tag	UNP A2RJ53
A	581	ILE	-	expression tag	UNP A2RJ53
A	582	GLU	-	expression tag	UNP A2RJ53
A	583	GLY	-	expression tag	UNP A2RJ53
A	584	ARG	-	expression tag	UNP A2RJ53
A	585	HIS	-	expression tag	UNP A2RJ53
A	586	HIS	-	expression tag	UNP A2RJ53
A	587	HIS	-	expression tag	UNP A2RJ53
A	588	HIS	-	expression tag	UNP A2RJ53
A	589	HIS	-	expression tag	UNP A2RJ53
A	590	HIS	-	expression tag	UNP A2RJ53

- Molecule 2 is a protein called Neuropeptide S.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	0	0	0
			34	21	6	7			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	491	Total	O	0	0
			491	491		

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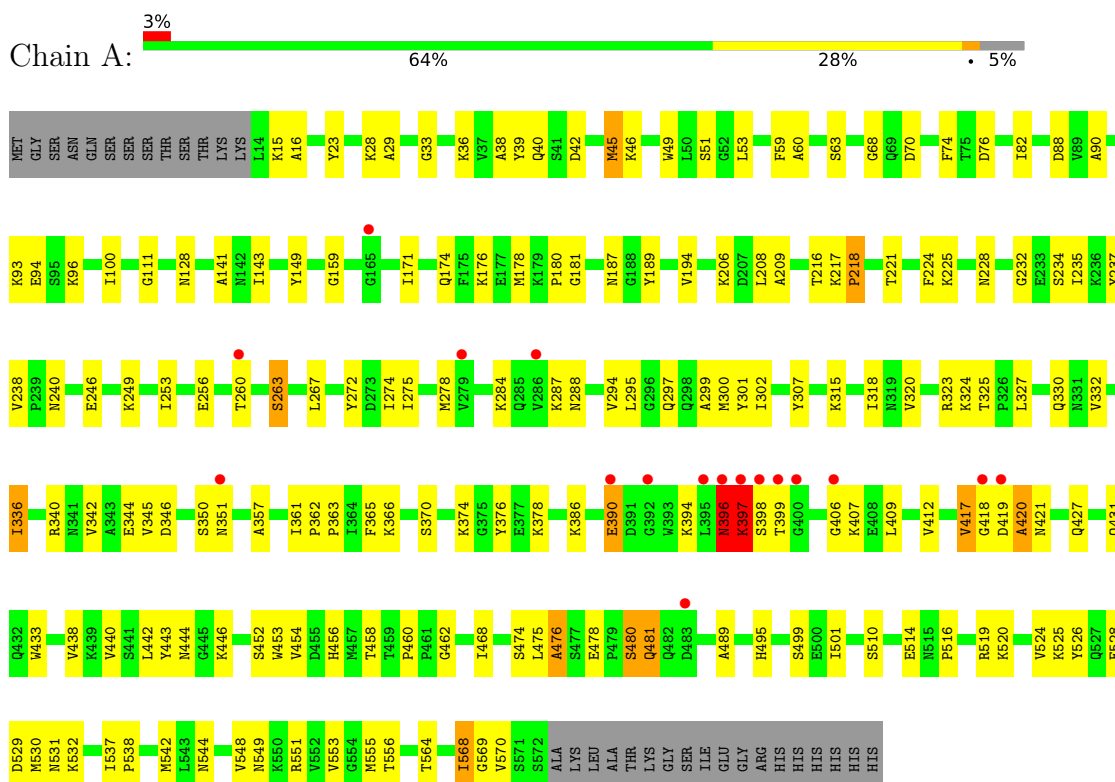
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	6	Total	O	0	0
			6	6		

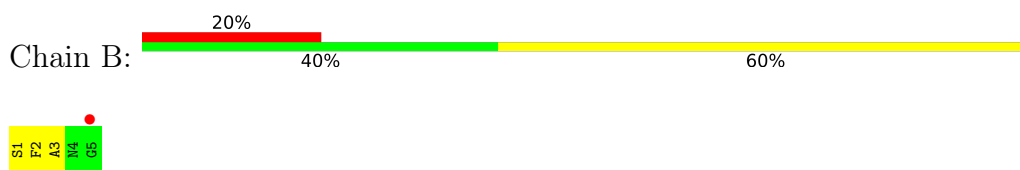
3 Residue-property plots

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: Oligopeptide-binding protein oppA



• Molecule 2: Neuropeptide S



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.62Å 123.13Å 59.28Å 90.00° 102.31° 90.00°	Depositor
Resolution (Å)	32.77 – 1.80 32.77 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.1 (32.77-1.80) 97.1 (32.77-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 1.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.194 , 0.248 (Not available) , 0.275	Depositor DCC
R_{free} test set	2518 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4905	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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

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	1.97	127/4475 (2.8%)	1.12	13/6062 (0.2%)
2	B	2.23	1/34 (2.9%)	1.05	0/44
All	All	1.98	128/4509 (2.8%)	1.12	13/6106 (0.2%)

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

All (128) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	362	PRO	C-O	-9.60	1.16	1.25
1	A	460	PRO	CA-C	9.23	1.56	1.51
1	A	189	TYR	C-O	-8.39	1.13	1.24
1	A	297	GLN	C-O	-8.31	1.13	1.23
1	A	519	ARG	C-O	-8.16	1.14	1.24
1	A	396	ASN	C-N	-8.12	1.22	1.33
1	A	548	VAL	C-O	-7.93	1.15	1.24
1	A	440	VAL	C-O	-7.93	1.15	1.24
1	A	51	SER	C-O	-7.84	1.15	1.24
1	A	570	VAL	C-O	-7.79	1.16	1.24
1	A	460	PRO	C-O	-7.71	1.18	1.25
1	A	332	VAL	C-O	-7.67	1.15	1.24
1	A	70	ASP	C-O	-7.64	1.13	1.23
1	A	253	ILE	C-O	-7.63	1.16	1.24
1	A	378	LYS	C-O	-7.54	1.15	1.24
1	A	235	ILE	C-O	-7.49	1.16	1.24
1	A	374	LYS	C-O	-7.21	1.15	1.24
1	A	171	ILE	C-O	-7.20	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	568	ILE	C-O	-7.08	1.16	1.24
1	A	361	ILE	C-O	-6.94	1.16	1.24
1	A	272	TYR	C-O	-6.92	1.15	1.23
1	A	274	ILE	C-O	-6.74	1.17	1.24
1	A	538	PRO	C-O	-6.69	1.16	1.23
1	A	194	VAL	C-O	-6.62	1.16	1.24
1	A	412	VAL	C-O	-6.60	1.16	1.24
1	A	340	ARG	C-O	-6.57	1.15	1.23
1	A	225	LYS	C-O	-6.52	1.15	1.24
1	A	330	GLN	C-O	-6.51	1.16	1.24
1	A	302	ILE	C-O	-6.49	1.17	1.24
1	A	427	GLN	C-O	-6.49	1.16	1.24
1	A	39	TYR	C-O	-6.45	1.16	1.24
1	A	468	ILE	C-O	-6.38	1.17	1.24
1	A	553	VAL	C-O	-6.37	1.17	1.24
1	A	240	ASN	C-O	-6.31	1.16	1.24
1	A	63	SER	C-O	-6.29	1.16	1.24
1	A	495	HIS	C-O	-6.23	1.15	1.23
1	A	29	ALA	C-O	-6.22	1.16	1.23
1	A	325	THR	C-O	-6.18	1.16	1.24
1	A	489	ALA	C-O	-6.18	1.16	1.24
1	A	174	GLN	C-O	-6.18	1.16	1.24
1	A	60	ALA	C-O	-6.09	1.17	1.24
1	A	569	GLY	C-O	-6.08	1.15	1.23
1	A	218	PRO	C-O	-6.03	1.16	1.23
1	A	228	ASN	C-O	-6.03	1.16	1.23
1	A	555	MET	C-O	-6.02	1.16	1.23
1	A	38	ALA	CA-CB	-6.01	1.41	1.54
1	A	36	LYS	C-O	-6.00	1.17	1.24
1	A	294	VAL	C-O	-5.96	1.17	1.24
1	A	442	LEU	C-O	-5.95	1.16	1.23
1	A	556	THR	C-O	-5.95	1.16	1.23
1	A	299	ALA	CA-CB	-5.91	1.43	1.53
1	A	520	LYS	C-O	-5.91	1.17	1.24
1	A	564	THR	C-O	-5.89	1.17	1.24
1	A	46	LYS	C-O	-5.88	1.17	1.24
1	A	345	VAL	C-O	-5.87	1.17	1.24
1	A	446	LYS	C-O	-5.87	1.16	1.23
1	A	516	PRO	C-O	-5.86	1.16	1.24
1	A	528	GLU	C-O	-5.84	1.17	1.24
1	A	454	VAL	C-O	-5.83	1.17	1.24
1	A	456	HIS	C-O	-5.81	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	VAL	C-O	-5.81	1.17	1.24
1	A	327	LEU	C-O	-5.81	1.16	1.24
1	A	476	ALA	C-O	-5.79	1.16	1.23
1	A	90	ALA	C-O	-5.78	1.16	1.23
1	A	307	TYR	C-O	-5.76	1.16	1.24
1	A	544	ASN	C-O	-5.75	1.16	1.23
1	A	365	PHE	C-O	-5.73	1.17	1.23
1	A	221	THR	C-O	-5.72	1.16	1.24
1	A	33	GLY	C-O	-5.68	1.17	1.23
1	A	249	LYS	C-O	-5.68	1.17	1.24
1	A	481	GLN	C-O	-5.67	1.16	1.24
1	A	29	ALA	CA-CB	-5.66	1.43	1.53
1	A	180	PRO	C-O	-5.66	1.16	1.24
1	A	357	ALA	CA-CB	-5.64	1.44	1.53
1	A	74	PHE	C-O	-5.62	1.16	1.23
1	A	458	THR	C-O	-5.62	1.16	1.24
1	A	324	LYS	C-O	-5.60	1.17	1.24
1	A	452	SER	C-O	-5.59	1.17	1.24
1	A	159	GLY	C-O	-5.58	1.17	1.23
2	B	3	ALA	C-O	-5.57	1.17	1.23
1	A	82	ILE	C-O	-5.56	1.17	1.23
1	A	318	ILE	C-O	-5.55	1.17	1.23
1	A	462	GLY	C-O	-5.55	1.17	1.24
1	A	88	ASP	C-O	-5.52	1.17	1.23
1	A	478	GLU	C-O	-5.52	1.18	1.24
1	A	275	ILE	C-O	-5.49	1.18	1.24
1	A	238	VAL	C-O	-5.47	1.18	1.24
1	A	23	TYR	C-O	-5.45	1.17	1.23
1	A	529	ASP	C-O	-5.44	1.17	1.24
1	A	510	SER	C-O	-5.41	1.16	1.23
1	A	208	LEU	C-O	-5.39	1.18	1.24
1	A	315	LYS	C-O	-5.39	1.17	1.24
1	A	537	ILE	CA-C	5.37	1.57	1.52
1	A	370	SER	C-O	-5.36	1.16	1.23
1	A	537	ILE	C-O	-5.36	1.18	1.23
1	A	499	SER	C-O	-5.36	1.17	1.24
1	A	525	LYS	C-O	-5.35	1.18	1.24
1	A	59	PHE	C-O	-5.33	1.17	1.24
1	A	287	LYS	C-O	-5.33	1.17	1.24
1	A	68	GLY	C-O	-5.29	1.18	1.24
1	A	480	SER	C-O	-5.29	1.17	1.23
1	A	531	ASN	C-O	-5.28	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	GLU	C-O	-5.26	1.17	1.23
1	A	453	TRP	C-O	-5.22	1.18	1.24
1	A	76	ASP	C-O	-5.21	1.18	1.23
1	A	323	ARG	C-O	-5.17	1.17	1.24
1	A	128	ASN	C-O	-5.17	1.18	1.24
1	A	143	ILE	C-O	-5.15	1.18	1.24
1	A	16	ALA	C-O	-5.15	1.18	1.24
1	A	530	MET	C-O	-5.13	1.18	1.24
1	A	524	VAL	C-O	-5.12	1.18	1.24
1	A	346	ASP	C-O	-5.11	1.18	1.24
1	A	336	ILE	C-O	-5.10	1.17	1.24
1	A	267	LEU	C-O	-5.09	1.17	1.24
1	A	263	SER	C-O	-5.08	1.18	1.24
1	A	295	LEU	C-O	-5.05	1.17	1.23
1	A	40	GLN	C-O	-5.05	1.18	1.24
1	A	342	VAL	C-O	-5.04	1.18	1.24
1	A	181	GLY	C-O	-5.03	1.18	1.24
1	A	431	GLN	C-O	-5.03	1.18	1.24
1	A	443	TYR	C-O	-5.03	1.18	1.24
1	A	301	TYR	C-O	-5.03	1.17	1.23
1	A	149	TYR	C-O	-5.03	1.18	1.24
1	A	344	GLU	C-O	-5.03	1.18	1.24
1	A	234	SER	C-O	-5.01	1.17	1.23
1	A	111	GLY	C-O	-5.01	1.17	1.24
1	A	501	ILE	C-O	-5.01	1.18	1.24
1	A	362	PRO	CA-C	5.01	1.54	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	397	LYS	CA-C-N	-12.29	104.43	120.65
1	A	397	LYS	C-N-CA	-12.29	104.43	120.65
1	A	399	THR	N-CA-C	8.79	121.82	111.71
1	A	234	SER	N-CA-C	6.75	119.32	109.07
1	A	300	MET	CB-CA-C	-6.52	102.34	112.12
1	A	149	TYR	N-CA-C	-6.18	104.62	111.36
1	A	417	VAL	CB-CA-C	-6.08	103.41	111.13
1	A	263	SER	N-CA-C	6.07	118.42	111.02
1	A	460	PRO	CA-C-O	-5.90	116.65	120.90
1	A	406	GLY	N-CA-C	5.44	122.59	115.36
1	A	187	ASN	N-CA-C	5.38	117.90	111.71
1	A	514	GLU	CB-CG-CD	5.20	121.44	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	ASN	N-CA-C	5.07	118.59	111.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	396	ASN	Mainchain

5.2 Too-close contacts [i](#)

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	4374	0	4272	41	0
2	B	34	0	30	4	0
3	A	491	0	0	1	0
3	B	6	0	0	0	0
All	All	4905	0	4302	41	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 5.

All (41) 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:417:VAL:HG12	1:A:418:GLY:N	1.92	0.85
1:A:417:VAL:CG1	1:A:418:GLY:N	2.48	0.76
1:A:386:LYS:NZ	1:A:390:GLU:OE1	2.28	0.66
1:A:476:ALA:H	2:B:2:PHE:HD1	1.47	0.63
1:A:481:GLN:HG3	1:A:526:TYR:CE2	2.37	0.59
1:A:396:ASN:O	1:A:397:LYS:C	2.43	0.59
1:A:363:PRO:O	1:A:366:LYS:HD3	2.02	0.59
1:A:419:ASP:OD1	1:A:419:ASP:C	2.46	0.59
1:A:350:SER:O	1:A:351:ASN:HB2	2.02	0.57
1:A:396:ASN:O	1:A:398:SER:N	2.36	0.57
1:A:93:LYS:HG3	1:A:94:GLU:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ALA:O	1:A:176:LYS:HE2	2.06	0.55
1:A:336:ILE:HG23	1:A:433:TRP:NE1	2.22	0.55
1:A:42:ASP:OD2	1:A:260:THR:HG23	2.08	0.54
1:A:288:ASN:OD1	1:A:288:ASN:N	2.36	0.53
1:A:216:THR:C	1:A:217:LYS:HG2	2.35	0.52
1:A:396:ASN:HD22	1:A:396:ASN:C	2.18	0.52
1:A:480:SER:O	2:B:2:PHE:CE2	2.64	0.51
1:A:480:SER:O	2:B:2:PHE:HE2	1.94	0.50
1:A:419:ASP:O	1:A:420:ALA:C	2.56	0.49
1:A:409:LEU:HD23	1:A:438:VAL:HG22	1.96	0.47
1:A:376:TYR:CD2	1:A:376:TYR:N	2.82	0.47
1:A:263:SER:HB3	1:A:278:MET:HE3	1.98	0.46
1:A:217:LYS:HB3	1:A:217:LYS:HE3	1.63	0.46
1:A:363:PRO:HD2	3:A:1068:HOH:O	2.17	0.45
1:A:475:LEU:HA	2:B:2:PHE:CD1	2.53	0.44
1:A:394:LYS:HA	1:A:394:LYS:HD2	1.75	0.44
1:A:396:ASN:C	1:A:396:ASN:ND2	2.75	0.44
1:A:49:TRP:CD1	1:A:218:PRO:HG3	2.53	0.43
1:A:397:LYS:O	1:A:398:SER:C	2.55	0.43
1:A:542[A]:MET:HE2	1:A:542[A]:MET:HB3	1.85	0.43
1:A:100:ILE:N	1:A:100:ILE:HD12	2.34	0.43
1:A:15:LYS:HB3	1:A:15:LYS:HE3	1.78	0.42
1:A:419:ASP:OD1	1:A:420:ALA:N	2.52	0.42
1:A:53:LEU:HD13	1:A:209:ALA:HB2	2.01	0.42
1:A:419:ASP:O	1:A:421:ASN:N	2.53	0.42
1:A:96:LYS:HA	1:A:178:MET:SD	2.60	0.42
1:A:568:ILE:HG21	1:A:568:ILE:HD13	1.73	0.41
1:A:224:PHE:HB3	1:A:237:TYR:HB3	2.03	0.41
1:A:45:MET:O	1:A:232:GLY:HA2	2.21	0.41
1:A:549:ASN:OD1	1:A:551:ARG:HG2	2.21	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	560/590 (95%)	542 (97%)	16 (3%)	2 (0%)	30	19
2	B	3/5 (60%)	3 (100%)	0	0	100	100
All	All	563/595 (95%)	545 (97%)	16 (3%)	2 (0%)	30	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	397	LYS
1	A	420	ALA

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	473/496 (95%)	464 (98%)	9 (2%)	50	41
2	B	3/3 (100%)	2 (67%)	1 (33%)	0	0
All	All	476/499 (95%)	466 (98%)	10 (2%)	47	36

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	45	MET
1	A	206	LYS
1	A	246	GLU
1	A	284	LYS
1	A	390	GLU
1	A	407	LYS
1	A	474	SER
1	A	532	LYS
2	B	1	SER

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	18	ASN
1	A	69	GLN
1	A	142	ASN
1	A	174	GLN
1	A	276	ASN
1	A	396	ASN
1	A	427	GLN
1	A	481	GLN
1	A	527	GLN
1	A	544	ASN
2	B	4	ASN

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](#)

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 [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	559/590 (94%)	0.32	17 (3%) 52 52	7, 18, 30, 39	3 (0%)
2	B	5/5 (100%)	1.43	1 (20%) 3 2	24, 27, 29, 30	0
All	All	564/595 (94%)	0.33	18 (3%) 50 50	7, 18, 30, 39	3 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	GLY	4.2
1	A	398	SER	4.2
1	A	419	ASP	3.3
1	A	397	LYS	3.3
1	A	400	GLY	3.3
1	A	392	GLY	3.2
1	A	399	THR	2.9
1	A	406	GLY	2.8
1	A	165	GLY	2.6
2	B	5	GLY	2.5
1	A	395	LEU	2.4
1	A	390	GLU	2.4
1	A	396	ASN	2.3
1	A	279	VAL	2.3
1	A	286	VAL	2.3
1	A	483	ASP	2.2
1	A	260	THR	2.1
1	A	351	ASN	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.