



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:11 PM UTC

PDB ID : 4CYS / pdb_00004cys
Title : G6 mutant of PAS, arylsulfatase from Pseudomonas Aeruginosa, in complex with Phenylphosphonic acid
Authors : Miton, C.M.; Jonas, S.; Mohammed, M.F.; Fischer, G.; Loo, B.v.; Kintses, B.; Hyvonen, M.; Tokuriki, N.; Hollfelder, F.
Deposited on : 2014-04-14
Resolution : 1.88 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

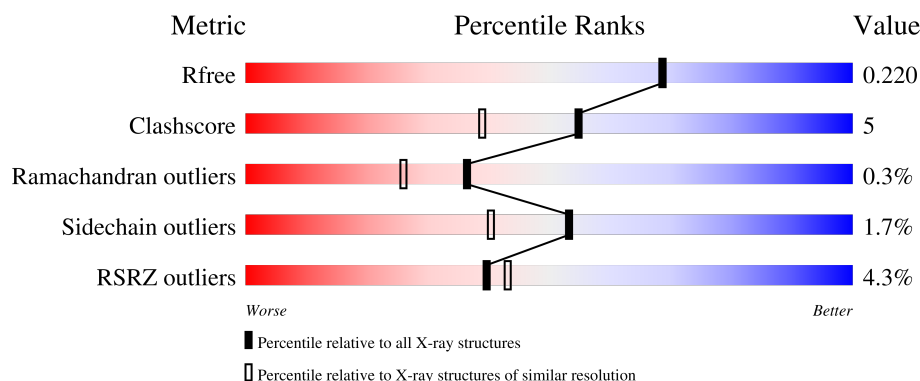
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	536	4% 89% 10%
1	B	536	4% 89% 10%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9391 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 ARYLSULFATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	2	0
			4219	2687	744	780	8			
1	B	534	Total	C	N	O	S	0	3	0
			4231	2693	742	788	8			

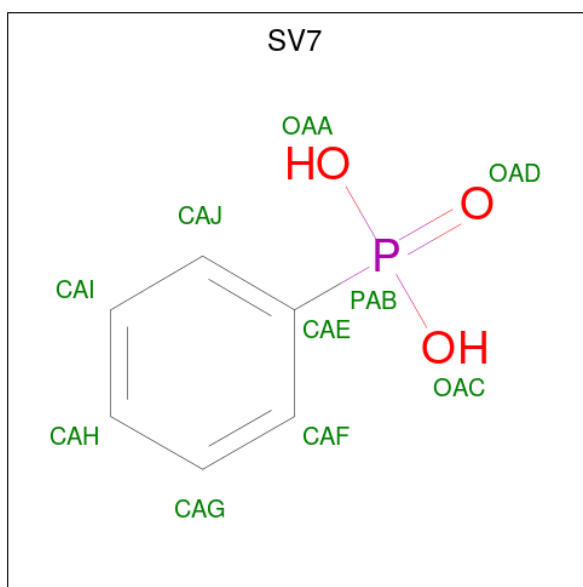
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	ALA	THR	engineered mutation	UNP P51691
A	72	VAL	MET	engineered mutation	UNP P51691
A	337	ASP	GLY	engineered mutation	UNP P51691
A	352	SER	ARG	engineered mutation	UNP P51691
A	461	GLY	GLU	engineered mutation	UNP P51691
A	523	ASP	GLU	engineered mutation	UNP P51691
B	50	ALA	THR	engineered mutation	UNP P51691
B	72	VAL	MET	engineered mutation	UNP P51691
B	337	ASP	GLY	engineered mutation	UNP P51691
B	352	SER	ARG	engineered mutation	UNP P51691
B	461	GLY	GLU	engineered mutation	UNP P51691
B	523	ASP	GLU	engineered mutation	UNP P51691

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

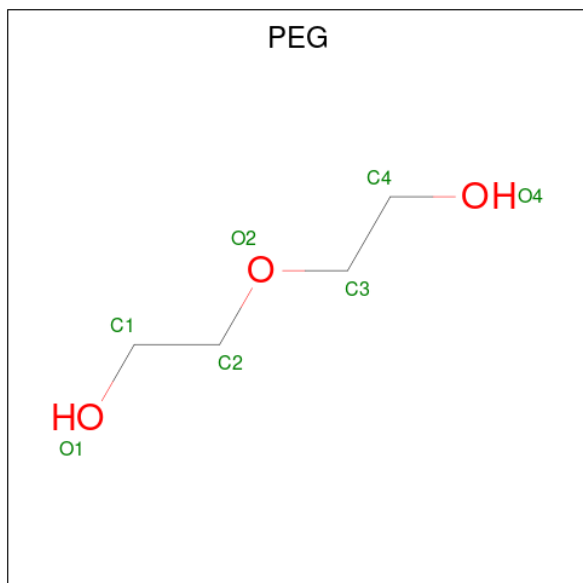
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is phenylphosphonic acid (CCD ID: SV7) (formula: C₆H₇O₃P).



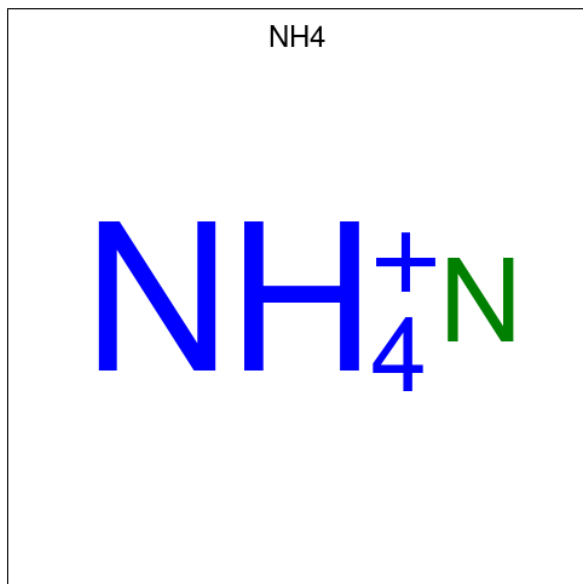
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			10	6	3	1		
3	A	1	Total	C	O	P	0	0
			10	6	3	1		
3	B	1	Total	C	O	P	0	0
			10	6	3	1		
3	B	1	Total	C	O	P	0	0
			10	6	3	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0

- Molecule 5 is AMMONIUM ION (CCD ID: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total N 1 1	0	0
5	B	1	Total N 1 1	0	0

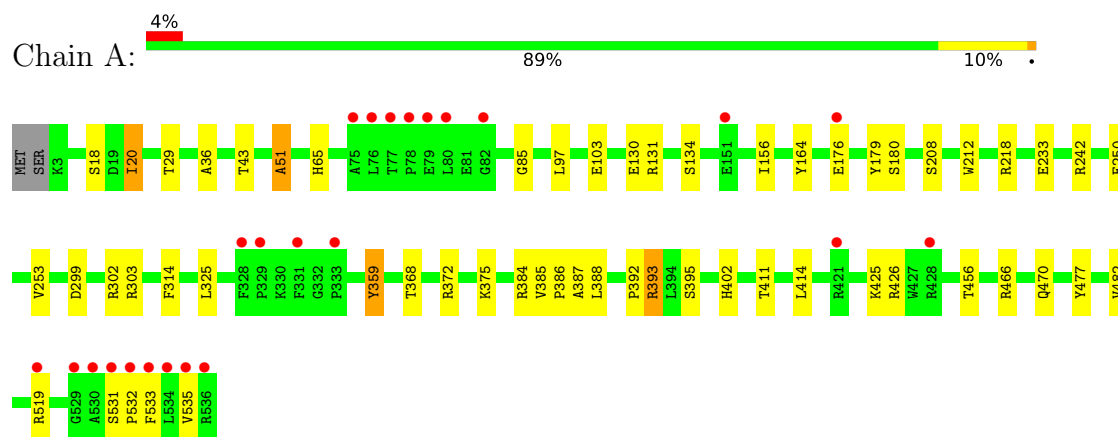
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	455	Total O 455 455	0	0
6	B	421	Total O 421 421	0	0

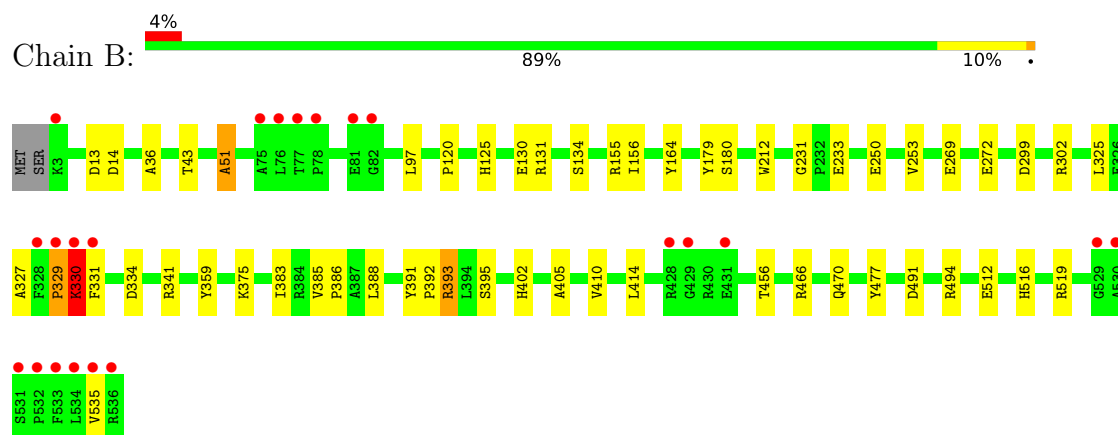
3 Residue-property plots [i](#)

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 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: ARYLSULFATASE



• Molecule 1: ARYLSULFATASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.97Å 66.70Å 89.64Å 90.00° 94.04° 90.00°	Depositor
Resolution (Å)	93.25 – 1.88 93.25 – 1.88	Depositor EDS
% Data completeness (in resolution range)	98.1 (93.25-1.88) 98.1 (93.25-1.88)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.177 , 0.215 0.187 , 0.220	Depositor DCC
R_{free} test set	3863 reflections (4.38%)	wwPDB-VP
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.6	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	0.94	EDS
Total number of atoms	9391	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: DDZ, NH4, CA, PEG, SV7

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	1.16	4/4329 (0.1%)	1.03	1/5889 (0.0%)
1	B	1.20	4/4341 (0.1%)	1.05	2/5907 (0.0%)
All	All	1.18	8/8670 (0.1%)	1.04	3/11796 (0.0%)

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	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	383	ILE	N-CA	6.29	1.52	1.46
1	A	368	THR	C-O	5.91	1.31	1.24
1	A	359	TYR	C-O	5.66	1.31	1.24
1	B	410	VAL	C-O	-5.44	1.18	1.24
1	B	410	VAL	N-CA	-5.40	1.40	1.46
1	A	18	SER	N-CA	5.31	1.52	1.46
1	B	405	ALA	C-O	5.18	1.30	1.23
1	A	208	SER	C-O	-5.16	1.17	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	372	ARG	N-CA-C	5.66	117.91	109.59
1	B	231	GLY	CA-C-N	5.20	124.89	119.64
1	B	231	GLY	C-N-CA	5.20	124.89	119.64

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	330	LYS	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	4219	0	4080	33	1
1	B	4231	0	4082	48	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	20	0	10	2	0
3	B	20	0	10	3	0
4	A	14	0	20	2	0
4	B	7	0	10	0	0
5	A	1	0	0	0	0
5	B	1	0	0	1	0
6	A	455	0	0	4	0
6	B	421	0	0	5	0
All	All	9391	0	8212	80	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 5.

All (80) 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:330:LYS:O	1:B:535:VAL:HG12	1.36	1.20
1:B:327:ALA:O	1:B:329:PRO:HD2	1.59	1.02
1:A:299:ASP:HB3	6:A:2295:HOH:O	1.61	0.98
1:B:330:LYS:O	1:B:535:VAL:CG1	2.15	0.95
3:B:1540:SV7:OAA	5:B:1542:NH4:N	2.01	0.94
1:B:250:GLU:HG2	1:B:253[A]:VAL:HG23	1.50	0.93
1:B:125:HIS:HD2	6:B:2117:HOH:O	1.50	0.92
1:B:327:ALA:O	1:B:329:PRO:CD	2.16	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:ALA:C	1:B:329:PRO:HD3	2.01	0.86
1:B:341:ARG:NH2	6:B:2141:HOH:O	2.18	0.74
1:B:327:ALA:C	1:B:329:PRO:CD	2.59	0.74
1:B:393:ARG:NH2	6:B:2329:HOH:O	2.13	0.74
1:B:329:PRO:HA	1:B:330:LYS:HB2	1.69	0.74
1:B:330:LYS:HB3	1:B:331:PHE:HA	1.68	0.73
1:A:392:PRO:O	1:B:393:ARG:NH1	2.22	0.72
1:A:250:GLU:CG	1:A:253[A]:VAL:HG23	2.20	0.71
1:B:250:GLU:HG2	1:B:253[A]:VAL:CG2	2.19	0.71
1:A:393:ARG:NH1	1:B:392:PRO:O	2.23	0.68
1:B:330:LYS:HB3	1:B:331:PHE:CA	2.23	0.68
1:B:299[A]:ASP:OD1	1:B:302:ARG:NH2	2.30	0.65
1:B:329:PRO:HA	1:B:330:LYS:CB	2.26	0.64
1:B:269:GLU:HG3	1:B:272:GLU:OE1	1.98	0.62
1:B:391:TYR:CZ	1:B:393:ARG:HG2	2.35	0.62
1:A:97:LEU:HD21	1:A:414:LEU:HD12	1.83	0.61
1:B:250:GLU:CD	1:B:253[A]:VAL:CG2	2.74	0.60
1:B:97:LEU:HD21	1:B:414:LEU:HD12	1.84	0.59
1:A:299:ASP:OD1	1:A:302:ARG:NH2	2.37	0.58
1:A:250:GLU:CG	1:A:253[A]:VAL:CG2	2.82	0.58
1:A:20:ILE:HD12	1:A:29:THR:HG21	1.86	0.58
1:B:250:GLU:CG	1:B:253[A]:VAL:HG23	2.29	0.56
1:B:375:LYS:NZ	3:B:1539:SV7:OAD	2.38	0.55
1:B:250:GLU:O	1:B:253[B]:VAL:HG22	2.06	0.54
1:A:156:ILE:HD13	1:A:325:LEU:HD13	1.92	0.52
1:B:43:THR:OG1	1:B:402:HIS:CD2	2.63	0.51
1:A:303:ARG:NH1	6:A:2295:HOH:O	2.44	0.51
1:A:393:ARG:NH1	6:A:2362:HOH:O	2.41	0.51
1:B:250:GLU:CG	1:B:253[A]:VAL:CG2	2.87	0.51
1:A:43:THR:OG1	1:A:402:HIS:CD2	2.65	0.50
1:A:43:THR:OG1	1:A:402:HIS:HD2	1.94	0.50
1:A:532:PRO:HB2	1:A:533:PHE:CD1	2.47	0.50
1:B:43:THR:OG1	1:B:402:HIS:HD2	1.95	0.49
1:B:130:GLU:HG3	1:B:131:ARG:HG3	1.94	0.49
1:B:385:VAL:HB	1:B:386:PRO:HD2	1.94	0.49
1:B:156:ILE:HD13	1:B:325:LEU:HD13	1.94	0.48
1:B:516:HIS:ND1	6:B:2411:HOH:O	2.17	0.48
1:B:519:ARG:HB2	1:B:519:ARG:CZ	2.42	0.48
1:B:51:DDZ:OG1	3:B:1539:SV7:OAC	2.31	0.48
1:A:130:GLU:HG3	1:A:131:ARG:HG3	1.95	0.47
1:A:375:LYS:NZ	3:A:1539:SV7:OAD	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:SER:O	1:A:164:TYR:HA	2.14	0.47
1:B:134:SER:O	1:B:164:TYR:HA	2.15	0.47
1:A:233:GLU:OE1	1:A:233:GLU:HA	2.15	0.46
1:A:51:DDZ:OG1	3:A:1539:SV7:OAC	2.34	0.46
1:B:156:ILE:HD11	1:B:212:TRP:CH2	2.51	0.45
1:A:482:VAL:HG11	4:A:1541:PEG:H31	1.99	0.45
1:A:36:ALA:HB2	1:A:388:LEU:HD22	2.00	0.44
1:A:425:LYS:C	1:A:426:ARG:HG2	2.41	0.44
1:B:327:ALA:O	1:B:329:PRO:HD3	1.97	0.44
1:B:179:TYR:O	1:B:180:SER:C	2.61	0.43
1:A:456:THR:O	1:A:470:GLN:HA	2.19	0.42
1:B:456:THR:O	1:B:470:GLN:HA	2.18	0.42
1:A:156:ILE:CD1	1:A:325:LEU:HD13	2.49	0.42
1:B:155:ARG:HB2	1:B:535:VAL:HG13	2.01	0.42
1:B:36:ALA:HB2	1:B:388:LEU:HD22	2.02	0.42
1:B:330:LYS:HE2	6:B:2294:HOH:O	2.19	0.42
1:A:385:VAL:HB	1:A:386:PRO:HD2	2.01	0.42
1:A:179:TYR:O	1:A:180:SER:C	2.63	0.41
1:A:242:ARG:NH2	4:A:1542:PEG:H42	2.35	0.41
1:A:65:HIS:O	1:A:85:GLY:HA3	2.21	0.41
1:A:384:ARG:HD2	1:A:384:ARG:C	2.45	0.41
1:B:466:ARG:HB2	1:B:477:TYR:HB3	2.03	0.41
1:A:314:PHE:O	1:A:387:ALA:HA	2.21	0.41
1:A:466:ARG:HB2	1:A:477:TYR:HB3	2.03	0.41
1:A:156:ILE:HD11	1:A:212:TRP:CH2	2.55	0.41
1:B:13:ASP:O	1:B:14:ASP:HB2	2.20	0.41
1:B:491:ASP:OD2	1:B:494:ARG:NH2	2.54	0.40
1:B:233:GLU:HA	1:B:233:GLU:OE1	2.21	0.40
1:B:393:ARG:N	1:B:393:ARG:CD	2.85	0.40
1:A:103:GLU:HG3	6:A:2108:HOH:O	2.20	0.40
1:B:156:ILE:CD1	1:B:325:LEU:HD13	2.52	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:A:425:LYS:NZ	1:B:512:GLU:OE2[4_556]	2.00	0.20

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	533/536 (99%)	515 (97%)	17 (3%)	1 (0%)	43	34
1	B	534/536 (100%)	515 (96%)	17 (3%)	2 (0%)	30	18
All	All	1067/1072 (100%)	1030 (96%)	34 (3%)	3 (0%)	36	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	329	PRO
1	B	330	LYS
1	A	531	SER

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	424/428 (99%)	414 (98%)	10 (2%)	43	27
1	B	427/428 (100%)	422 (99%)	5 (1%)	63	53
All	All	851/856 (99%)	836 (98%)	15 (2%)	53	38

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ILE
1	A	176	GLU
1	A	218	ARG

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Mol	Chain	Res	Type
1	A	359	TYR
1	A	393	ARG
1	A	395	SER
1	A	411	THR
1	A	519[A]	ARG
1	A	519[B]	ARG
1	A	535	VAL
1	B	120	PRO
1	B	334	ASP
1	B	359	TYR
1	B	393	ARG
1	B	395	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	402	HIS
1	B	125	HIS
1	B	402	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	$\# Z > 2$
1	DDZ	B	51	2,1	4,6,7	1.79	2 (50%)	3,7,9	3.11	2 (66%)
1	DDZ	A	51	2,1	4,6,7	2.46	2 (50%)	3,7,9	2.70	2 (66%)

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
1	DDZ	B	51	2,1	-	0/2/6/8	-
1	DDZ	A	51	2,1	-	0/2/6/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	51	DDZ	OG2-CB	3.75	1.48	1.40
1	A	51	DDZ	OG1-CB	3.17	1.47	1.40
1	B	51	DDZ	OG2-CB	2.93	1.46	1.40
1	B	51	DDZ	OG1-CB	2.06	1.44	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	51	DDZ	OG2-CB-OG1	4.67	119.31	111.26
1	A	51	DDZ	OG2-CB-OG1	4.01	118.17	111.26
1	B	51	DDZ	O-C-CA	-2.44	118.49	124.77
1	A	51	DDZ	O-C-CA	-2.20	119.12	124.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	51	DDZ	1	0
1	A	51	DDZ	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 2 are monoatomic and 2 are modelled with single atom - leaving 7 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$
3	SV7	A	1539	-	10,10,10	2.43	3 (30%)	14,14,14	1.75	2 (14%)
3	SV7	B	1540	-	10,10,10	3.52	2 (20%)	14,14,14	1.86	5 (35%)
3	SV7	A	1540	5	10,10,10	2.75	2 (20%)	14,14,14	1.90	6 (42%)
4	PEG	A	1542	-	6,6,6	0.42	0	5,5,5	0.41	0
4	PEG	B	1541	-	6,6,6	0.42	0	5,5,5	0.42	0
4	PEG	A	1541	-	6,6,6	0.62	0	5,5,5	0.57	0
3	SV7	B	1539	-	10,10,10	1.86	3 (30%)	14,14,14	1.42	1 (7%)

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	SV7	A	1539	-	-	0/6/6/6	0/1/1/1
3	SV7	B	1540	-	-	0/6/6/6	0/1/1/1
3	SV7	A	1540	5	-	0/6/6/6	0/1/1/1
4	PEG	A	1542	-	-	2/4/4/4	-
4	PEG	B	1541	-	-	1/4/4/4	-
4	PEG	A	1541	-	-	2/4/4/4	-
3	SV7	B	1539	-	-	0/6/6/6	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1540	SV7	PAB-OAA	8.11	1.74	1.54
3	B	1540	SV7	PAB-CAE	7.01	1.93	1.79
3	A	1540	SV7	PAB-OAA	6.52	1.70	1.54
3	A	1540	SV7	PAB-CAE	5.08	1.89	1.79
3	A	1539	SV7	PAB-OAC	-4.89	1.42	1.54
3	A	1539	SV7	PAB-OAD	-3.81	1.43	1.49
3	B	1539	SV7	PAB-OAC	-3.79	1.45	1.54
3	A	1539	SV7	PAB-CAE	3.70	1.87	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1539	SV7	PAB-OAD	-3.24	1.44	1.49
3	B	1539	SV7	PAB-CAE	2.38	1.84	1.79

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1539	SV7	OAC-PAB-CAE	4.11	116.05	106.78
3	A	1540	SV7	OAA-PAB-OAD	-4.05	101.29	112.49
3	A	1539	SV7	OAA-PAB-OAD	-3.82	101.92	112.49
3	B	1540	SV7	OAA-PAB-OAD	-3.56	102.64	112.49
3	A	1539	SV7	OAC-PAB-CAE	3.22	114.03	106.78
3	B	1540	SV7	OAA-PAB-CAE	-2.66	100.80	106.78
3	B	1540	SV7	OAC-PAB-CAE	2.60	112.64	106.78
3	A	1540	SV7	OAC-PAB-CAE	2.48	112.37	106.78
3	A	1540	SV7	CAJ-CAE-CAF	2.26	121.83	119.23
3	A	1540	SV7	CAH-CAI-CAJ	-2.19	117.53	120.24
3	B	1540	SV7	OAD-PAB-CAE	2.17	114.55	109.67
3	B	1540	SV7	CAJ-CAE-CAF	2.15	121.70	119.23
3	A	1540	SV7	OAA-PAB-CAE	-2.06	102.14	106.78
3	A	1540	SV7	OAD-PAB-CAE	2.01	114.20	109.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1542	PEG	O2-C3-C4-O4
4	A	1541	PEG	O1-C1-C2-O2
4	A	1541	PEG	C4-C3-O2-C2
4	A	1542	PEG	C4-C3-O2-C2
4	B	1541	PEG	C1-C2-O2-C3

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1539	SV7	2	0
3	B	1540	SV7	1	0
4	A	1542	PEG	1	0
4	A	1541	PEG	1	0
3	B	1539	SV7	2	0

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

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	533/536 (99%)	0.00	24 (4%)	38 41	6, 14, 38, 77	7 (1%)
1	B	533/536 (99%)	-0.01	22 (4%)	41 45	6, 14, 39, 76	8 (1%)
All	All	1066/1072 (99%)	-0.01	46 (4%)	40 43	6, 14, 39, 77	15 (1%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	535	VAL	7.3
1	A	534	LEU	6.8
1	B	331	PHE	5.5
1	B	533	PHE	5.3
1	B	532	PRO	4.6
1	A	533	PHE	4.6
1	B	329	PRO	4.4
1	B	330	LYS	4.1
1	A	530	ALA	4.0
1	B	534	LEU	4.0
1	A	78	PRO	4.0
1	A	77	THR	4.0
1	A	536	ARG	3.9
1	A	532	PRO	3.7
1	B	328	PHE	3.7
1	B	77	THR	3.5
1	B	535	VAL	3.5
1	A	331	PHE	3.3
1	B	76	LEU	3.3
1	B	530	ALA	3.2
1	B	81	GLU	3.2
1	A	531	SER	3.1
1	A	329	PRO	3.1
1	B	428	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	428	ARG	2.8
1	A	328	PHE	2.7
1	A	76	LEU	2.6
1	A	176	GLU	2.6
1	A	519[A]	ARG	2.5
1	B	431	GLU	2.5
1	A	75	ALA	2.5
1	B	536	ARG	2.4
1	A	333	PRO	2.4
1	A	79	GLU	2.3
1	A	80	LEU	2.3
1	A	82	GLY	2.2
1	B	78	PRO	2.2
1	B	3	LYS	2.2
1	A	421	ARG	2.2
1	A	529	GLY	2.2
1	B	531	SER	2.1
1	B	82	GLY	2.1
1	B	429	GLY	2.1
1	A	151	GLU	2.0
1	B	529	GLY	2.0
1	B	75	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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($\text{\AA}^2$)	Q<0.9
1	DDZ	A	51	7/8	0.98	0.04	8,9,9,9	0
1	DDZ	B	51	7/8	0.98	0.04	9,10,10,10	0

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($\text{\AA}^2$)	Q<0.9
3	SV7	B	1540	10/10	0.78	0.16	21,26,42,46	0
4	PEG	A	1542	7/7	0.78	0.16	39,41,42,43	0
3	SV7	A	1540	10/10	0.81	0.14	21,26,42,42	0
4	PEG	B	1541	7/7	0.84	0.15	38,40,41,42	0
4	PEG	A	1541	7/7	0.88	0.12	32,36,38,38	0
3	SV7	A	1539	10/10	0.95	0.11	24,29,35,36	0
3	SV7	B	1539	10/10	0.95	0.10	26,31,34,35	0
5	NH4	A	1543	1/1	0.96	0.10	15,15,15,15	0
5	NH4	B	1542	1/1	0.97	0.10	15,15,15,15	0
2	CA	B	1538	1/1	0.99	0.06	16,16,16,16	0
2	CA	A	1538	1/1	0.99	0.06	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.