



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:52 AM EDT

PDB ID : 5XQ3 / pdb_00005xq3
Title : Crystal structure of a PL 26 exo-rhamnogalacturonan lyase from *Penicillium chrysogenum*
Authors : Kunishige, Y.; Iwai, M.; Tada, T.; Nishimura, S.; Sakamoto, T.
Deposited on : 2017-06-06
Resolution : 2.85 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

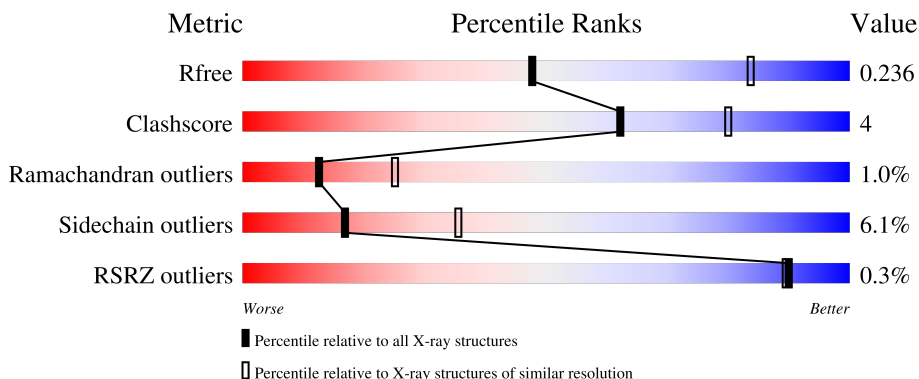
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	908	 85% 13% ..
2	B	906	 81% 14% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14033 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 Perglx protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	901	Total	C	N	O	S	Se	0	1	0
			7040	4490	1181	1363	3	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	928	LEU	-	expression tag	UNP A0A0C6EFY4
A	929	GLU	-	expression tag	UNP A0A0C6EFY4

- Molecule 2 is a protein called Perglx protein.

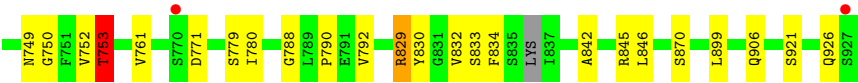
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	881	Total	C	N	O	S	Se	0	2	0
			6889	4403	1157	1323	3	3			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	61	Total	O	0	0
			61	61		
4	B	41	Total	O	0	0
			41	41		



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	167.47Å 167.47Å 172.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	120.09 – 2.85 120.09 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.8 (120.09-2.85) 97.8 (120.09-2.85)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.171 , 0.237 0.175 , 0.236	Depositor DCC
R_{free} test set	1956 reflections (3.39%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k 0.009 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14033	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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: CA

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	0.88	1/7244 (0.0%)	1.01	8/9890 (0.1%)
2	B	0.89	1/7094 (0.0%)	1.03	13/9688 (0.1%)
All	All	0.89	2/14338 (0.0%)	1.02	21/19578 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	100	ILE	C-O	-5.25	1.18	1.24
1	A	277	PRO	C-O	-5.23	1.19	1.24

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	661	LEU	N-CA-C	-7.17	100.60	110.35
2	B	56	ARG	CA-C-N	6.83	126.34	119.24
2	B	56	ARG	C-N-CA	6.83	126.34	119.24
1	A	696	TRP	N-CA-C	6.55	124.75	110.80
2	B	296	GLY	N-CA-C	6.19	118.60	111.36
1	A	731	GLU	N-CA-C	-6.12	100.02	109.76
2	B	574	TRP	N-CA-C	-5.96	102.66	110.53
1	A	507	GLU	CA-C-N	5.48	124.94	119.24
1	A	507	GLU	C-N-CA	5.48	124.94	119.24
2	B	466	ASP	CB-CA-C	-5.45	103.62	111.91
1	A	756	GLY	N-CA-C	5.45	122.25	112.77
2	B	305	ILE	N-CA-CB	-5.36	106.31	112.21
1	A	771	ASP	CA-C-N	-5.34	114.74	120.03
1	A	771	ASP	C-N-CA	-5.34	114.74	120.03
2	B	753	THR	N-CA-C	-5.30	102.07	109.96
2	B	278	LEU	N-CA-C	5.15	121.78	110.80
2	B	834	PHE	N-CA-C	5.08	116.48	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	338	THR	N-CA-C	-5.05	103.81	110.33
2	B	57	PRO	N-CA-C	5.03	121.93	113.78
2	B	731	GLU	N-CA-C	-5.02	105.70	111.07
2	B	753	THR	N-CA-CB	5.01	117.42	109.51

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	7040	0	6589	55	0
2	B	6889	0	6418	57	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	61	0	0	1	0
4	B	41	0	0	0	0
All	All	14033	0	13007	110	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 4.

All (110) 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:586:SER:OG	1:A:617:THR:HG21	1.73	0.88
1:A:564:MSE:HE1	1:A:576:TYR:HB3	1.58	0.83
1:A:754:GLY:O	1:A:755:SER:OG	1.98	0.81
1:A:74:LEU:HA	4:A:1122:HOH:O	1.86	0.74
1:A:564:MSE:HE3	1:A:574:TRP:HB2	1.72	0.71
2:B:340:LEU:HD23	2:B:343:ILE:HD12	1.75	0.68
1:A:515:GLN:NE2	1:A:519:GLU:OE2	2.26	0.68
1:A:580:GLY:O	1:A:635:HIS:HD2	1.78	0.66
1:A:588:LEU:HD12	1:A:902:ASN:HB3	1.78	0.65
2:B:382:GLY:O	2:B:498:MSE:HE1	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:564:MSE:HE1	2:B:576:TYR:HB3	1.82	0.61
2:B:842:ALA:O	2:B:845:ARG:HD3	2.02	0.60
1:A:456:ILE:HG23	1:A:457:THR:HG23	1.83	0.60
1:A:754:GLY:HA2	1:A:779:SER:HB3	1.86	0.58
2:B:554:TRP:HE1	2:B:564:MSE:HE2	1.69	0.58
2:B:750:GLY:O	2:B:753:THR:HG23	2.03	0.57
2:B:282[B]:GLU:HG2	2:B:284:TYR:CZ	2.39	0.57
2:B:212:THR:HG22	2:B:215:ARG:O	2.05	0.57
2:B:158:ILE:HD11	2:B:242:PHE:CE2	2.41	0.56
2:B:363:LYS:HB2	2:B:374:ILE:HD11	1.89	0.55
1:A:752:VAL:HG13	1:A:780:ILE:HD11	1.88	0.55
2:B:595:TRP:CE2	2:B:610:ALA:HB1	2.42	0.55
1:A:587:GLU:OE2	1:A:648:ARG:NH1	2.40	0.54
1:A:595:TRP:CE2	1:A:610:ALA:HB1	2.43	0.53
2:B:564:MSE:HE3	2:B:574:TRP:HB2	1.91	0.53
2:B:734:LYS:O	2:B:738:THR:OG1	2.26	0.53
1:A:817:TYR:O	1:A:862:ARG:NH2	2.37	0.52
2:B:575:ARG:HB3	2:B:578:VAL:HG22	1.90	0.52
1:A:708:LEU:HG	1:A:755:SER:HA	1.92	0.52
2:B:31:VAL:HG13	2:B:504:LEU:HG	1.91	0.52
2:B:578:VAL:HG23	2:B:578:VAL:O	2.10	0.52
2:B:752:VAL:HG21	2:B:830:TYR:CZ	2.44	0.52
2:B:788:GLY:O	2:B:792:VAL:HG23	2.10	0.52
2:B:458:TYR:O	2:B:634:ARG:NH2	2.42	0.51
2:B:749:ASN:HB2	2:B:753:THR:HG22	1.92	0.51
1:A:707:GLY:HA2	1:A:755:SER:HB3	1.93	0.51
2:B:288:ILE:HD13	2:B:349:TYR:CE1	2.46	0.51
1:A:307:GLY:O	2:B:578:VAL:HG21	2.11	0.50
1:A:139:LEU:HD21	1:A:209:VAL:HG22	1.94	0.50
1:A:652:PRO:HG3	1:A:675:LEU:HD13	1.94	0.50
2:B:568:ASP:HB2	2:B:575:ARG:HG2	1.95	0.49
2:B:633:THR:HG21	2:B:640:TRP:HA	1.95	0.49
1:A:478:TYR:CD1	1:A:498:MSE:HG3	2.48	0.49
2:B:169:ILE:HD13	2:B:393:GLY:O	2.13	0.48
1:A:253:VAL:HB	1:A:477:VAL:HB	1.95	0.48
1:A:754:GLY:HA2	1:A:779:SER:CB	2.43	0.48
2:B:829:ARG:HD2	2:B:830:TYR:CE2	2.48	0.48
1:A:173:GLY:HA2	1:A:273:ARG:O	2.14	0.48
2:B:227:THR:OG1	2:B:228:ASP:N	2.45	0.48
2:B:33:TRP:CE3	2:B:504:LEU:HD13	2.49	0.48
2:B:288:ILE:HD13	2:B:349:TYR:CD1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:790:PRO:HG3	2:B:846:LEU:HD21	1.96	0.48
1:A:310:ARG:HG3	1:A:335:ARG:HG2	1.96	0.47
2:B:288:ILE:CD1	2:B:349:TYR:CE1	2.97	0.47
2:B:845:ARG:NH1	2:B:906:GLN:OE1	2.47	0.47
1:A:396:VAL:HG23	1:A:479:LEU:HD23	1.96	0.47
2:B:217:LEU:HD11	2:B:241:ARG:HB3	1.96	0.47
1:A:752:VAL:HG21	1:A:830:TYR:CZ	2.50	0.47
1:A:225:THR:HG22	1:A:234:PRO:HB3	1.97	0.46
1:A:351:LEU:HD12	1:A:361:LEU:HD13	1.98	0.46
1:A:59:GLU:HA	1:A:111:LEU:HD22	1.98	0.46
2:B:177:LEU:HD22	2:B:236:LEU:HD23	1.98	0.46
1:A:661:LEU:O	1:A:662:SER:CB	2.64	0.45
2:B:45:THR:HA	2:B:92:HIS:O	2.16	0.45
2:B:638:GLN:HB2	2:B:641:SER:HB3	1.97	0.45
2:B:284:TYR:CD1	2:B:326:LEU:HD12	2.51	0.45
2:B:299:ASN:OD1	2:B:488:SER:OG	2.32	0.45
1:A:157:ILE:HA	1:A:204:ILE:HD11	1.97	0.45
2:B:592:LEU:HD13	2:B:654:TYR:CD1	2.51	0.45
1:A:340:LEU:HD23	1:A:343:ILE:HD12	1.98	0.45
1:A:575:ARG:HD3	2:B:307:GLY:O	2.17	0.45
1:A:753:THR:O	1:A:754:GLY:C	2.56	0.44
2:B:64:LEU:HD22	2:B:74:LEU:HD13	1.99	0.44
1:A:754:GLY:O	1:A:755:SER:CB	2.65	0.44
1:A:268:THR:O	1:A:428:PRO:HA	2.18	0.44
2:B:382:GLY:HA3	2:B:401:PHE:CG	2.53	0.44
2:B:64:LEU:HD11	2:B:104:TYR:HB3	1.98	0.44
2:B:82:TRP:CE2	2:B:88:LYS:HG3	2.53	0.44
1:A:535:GLU:OE1	1:A:600:ARG:NH2	2.51	0.43
1:A:564:MSE:HE3	1:A:574:TRP:CB	2.45	0.43
1:A:527:ALA:O	1:A:528:SER:C	2.60	0.43
2:B:899:LEU:C	2:B:899:LEU:HD12	2.44	0.43
2:B:501:PRO:O	2:B:503:VAL:HG23	2.19	0.43
1:A:535:GLU:CD	1:A:600:ARG:HH22	2.27	0.42
1:A:752:VAL:HG21	1:A:830:TYR:CE2	2.54	0.42
1:A:896:ALA:CB	1:A:899:LEU:HG	2.49	0.42
2:B:162:LYS:HA	2:B:167:LYS:O	2.19	0.42
1:A:289:ARG:HA	1:A:298:PHE:O	2.20	0.42
1:A:305:ILE:HD13	1:A:305:ILE:HA	1.77	0.42
2:B:484:GLN:O	2:B:485:THR:C	2.62	0.42
1:A:664:GLY:O	1:A:665:ASP:C	2.63	0.41
2:B:54:LYS:HG2	2:B:55:TYR:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:599:LEU:CD1	2:B:661:LEU:HD11	2.50	0.41
2:B:650:SER:O	2:B:651:GLN:C	2.62	0.41
1:A:600:ARG:HD3	1:A:912:ILE:HG23	2.02	0.41
2:B:396:VAL:HG12	2:B:479:LEU:HD23	2.01	0.41
1:A:221:ARG:HH22	1:A:670:GLU:CD	2.27	0.41
2:B:139:LEU:HD21	2:B:209:VAL:CG2	2.51	0.41
2:B:391[B]:GLN:HA	2:B:391[B]:GLN:OE1	2.20	0.41
1:A:31:VAL:HG12	1:A:104:TYR:HB2	2.03	0.41
1:A:638:GLN:HB2	1:A:641:SER:HB3	2.02	0.41
1:A:731:GLU:O	1:A:732:GLU:CB	2.69	0.41
2:B:682:TYR:HB3	2:B:704:VAL:HG11	2.02	0.41
2:B:771:ASP:O	2:B:771:ASP:CG	2.64	0.41
1:A:473:ARG:HG3	1:A:474:THR:N	2.36	0.40
1:A:896:ALA:O	1:A:897:ALA:CB	2.69	0.40
1:A:470:GLY:HA2	1:A:625:ILE:HG12	2.03	0.40
1:A:215:ARG:HB3	1:A:245:TYR:CD2	2.56	0.40
1:A:262:ASP:O	1:A:264:ASN:N	2.55	0.40
2:B:829:ARG:HD2	2:B:830:TYR:CD2	2.56	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	896/908 (99%)	832 (93%)	58 (6%)	6 (1%)	18	35
2	B	875/906 (97%)	810 (93%)	53 (6%)	12 (1%)	9	19
All	All	1771/1814 (98%)	1642 (93%)	111 (6%)	18 (1%)	12	25

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263	GLU
1	A	732	GLU
1	A	755	SER
2	B	193	SER
1	A	897	ALA
2	B	137	ASP
2	B	525	GLY
2	B	833	SER
1	A	466	ASP
1	A	651	GLN
2	B	277	PRO
2	B	694	ASP
2	B	579	GLY
2	B	651	GLN
2	B	870	SER
2	B	926	GLN
2	B	524	PRO
2	B	832	VAL

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	722/744 (97%)	678 (94%)	44 (6%)	17	35
2	B	697/742 (94%)	653 (94%)	44 (6%)	16	34
All	All	1419/1486 (96%)	1331 (94%)	88 (6%)	17	34

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	VAL
1	A	44	VAL
1	A	58	GLN
1	A	65	THR
1	A	67	ASP
1	A	118	SER

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Mol	Chain	Res	Type
1	A	128	SER
1	A	132	VAL
1	A	148	VAL
1	A	157	ILE
1	A	183	VAL
1	A	186	ASN
1	A	193	SER
1	A	209	VAL
1	A	211	GLN
1	A	213	SER
1	A	215	ARG
1	A	223	ASN
1	A	230	THR
1	A	256	SER
1	A	305	ILE
1	A	306	THR
1	A	329	THR
1	A	337	SER
1	A	345	THR
1	A	378	THR
1	A	381	GLU
1	A	394	LEU
1	A	411	ILE
1	A	458	TYR
1	A	473	ARG
1	A	493	SER
1	A	523	LEU
1	A	550	GLU
1	A	564	MSE
1	A	614	THR
1	A	622	VAL
1	A	655	ARG
1	A	696	TRP
1	A	765	LEU
1	A	779	SER
1	A	802	ASP
1	A	837	ILE
1	A	865	LYS
2	B	31	VAL
2	B	39	THR
2	B	65	THR
2	B	79	THR

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Mol	Chain	Res	Type
2	B	109	SER
2	B	133	THR
2	B	157	ILE
2	B	161	ILE
2	B	175	LEU
2	B	189	ASN
2	B	192	ASN
2	B	212	THR
2	B	230	THR
2	B	239	VAL
2	B	240	VAL
2	B	250	THR
2	B	252	LYS
2	B	257	ILE
2	B	258	VAL
2	B	270	LEU
2	B	282[A]	GLU
2	B	282[B]	GLU
2	B	305	ILE
2	B	310	ARG
2	B	361	LEU
2	B	372	VAL
2	B	391[A]	GLN
2	B	391[B]	GLN
2	B	412	SER
2	B	504	LEU
2	B	523	LEU
2	B	553	ARG
2	B	587	GLU
2	B	599	LEU
2	B	620	VAL
2	B	642	ASP
2	B	648	ARG
2	B	738	THR
2	B	753	THR
2	B	761	VAL
2	B	779	SER
2	B	780	ILE
2	B	829	ARG
2	B	921	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	A	58	GLN
1	A	75	GLN
1	A	98	ASN
1	A	189	ASN
1	A	203	ASN
1	A	303	GLN
1	A	324	GLN
1	A	369	GLN
1	A	635	HIS
1	A	810	GLN
2	B	178	GLN
2	B	203	ASN
2	B	205	ASN
2	B	247	ASN
2	B	369	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 [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	898/908 (98%)	-0.49	2 (0%)	91 91	41, 59, 85, 108	1 (0%)
2	B	878/906 (96%)	-0.40	4 (0%)	87 85	32, 61, 87, 119	2 (0%)
All	All	1776/1814 (97%)	-0.45	6 (0%)	90 89	32, 60, 87, 119	3 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	THR	3.2
2	B	65	THR	2.8
2	B	770	SER	2.3
2	B	927	SER	2.2
2	B	228	ASP	2.2
1	A	127	ASN	2.0

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($\text{\AA}^2$)	Q<0.9
3	CA	B	1001	1/1	0.99	0.03	37,37,37,37	0
3	CA	A	1001	1/1	1.00	0.04	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.