



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 08:57 PM UTC

PDB ID : 3LYC / pdb_00003lyc
Title : Crystal structure of Putative pectinase (YP_001304412.1) from Parabacteroides distasonis ATCC 8503 at 2.30 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-02-26
Resolution : 2.30 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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

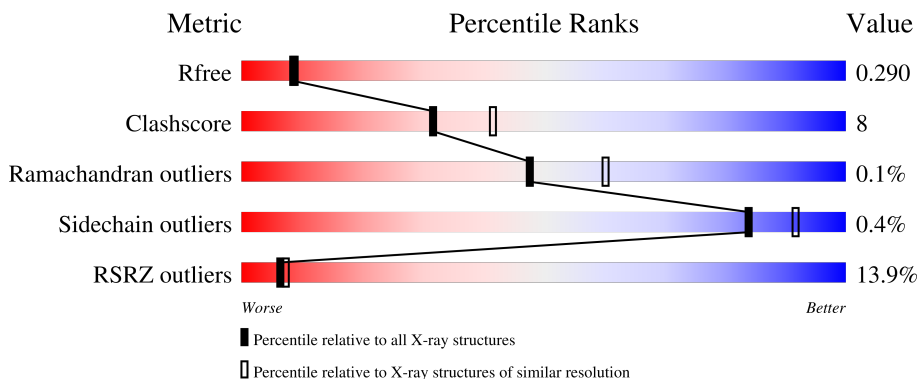
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	241	 5% 86% 13%
1	B	241	 14% 81% 17%
1	C	241	 6% 87% 12%
1	D	241	 23% 85% 14%
1	E	241	 5% 86% 14%

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Mol	Chain	Length	Quality of chain
1	F	241	<p>13% 88% 11%</p>
1	G	241	<p>10% 86% 14%</p>
1	H	241	<p>22% 84% 16%</p>
1	I	241	<p>5% 87% 13%</p>
1	J	241	<p>18% 84% 14%</p>
1	K	241	<p>6% 89% 11%</p>
1	L	241	<p>32% 80% 17%</p>
1	M	241	<p>5% 83% 17%</p>
1	N	241	<p>12% 87% 12%</p>
1	O	241	<p>4% 85% 15%</p>
1	P	241	<p>36% 80% 16%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 29713 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 Putative pectinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	241	Total 1831	C 1142	N 307	O 371	S 6	Se 5	0	7	0
1	B	237	Total 1785	C 1122	N 293	O 361	S 4	Se 5	0	3	0
1	C	241	Total 1831	C 1148	N 305	O 368	S 4	Se 6	0	8	0
1	D	240	Total 1780	C 1116	N 299	O 356	S 4	Se 5	0	4	0
1	E	241	Total 1836	C 1147	N 310	O 369	S 5	Se 5	0	5	0
1	F	239	Total 1782	C 1117	N 294	O 362	S 4	Se 5	0	4	0
1	G	241	Total 1811	C 1134	N 303	O 365	S 4	Se 5	0	5	0
1	H	241	Total 1822	C 1143	N 297	O 373	S 4	Se 5	0	6	0
1	I	241	Total 1811	C 1134	N 297	O 369	S 6	Se 5	0	5	0
1	J	238	Total 1809	C 1134	N 302	O 364	S 4	Se 5	0	7	0
1	K	241	Total 1816	C 1132	N 305	O 369	S 4	Se 6	0	5	0
1	L	235	Total 1746	C 1096	N 287	O 354	S 4	Se 5	0	6	0
1	M	241	Total 1862	C 1169	N 309	O 373	S 6	Se 5	0	10	0
1	N	238	Total 1824	C 1141	N 306	O 368	S 4	Se 5	0	7	0
1	O	240	Total 1836	C 1149	N 306	O 372	S 4	Se 5	0	7	0
1	P	232	Total 1681	C 1053	N 276	O 343	S 4	Se 5	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A6LGH6
B	0	GLY	-	expression tag	UNP A6LGH6
C	0	GLY	-	expression tag	UNP A6LGH6
D	0	GLY	-	expression tag	UNP A6LGH6
E	0	GLY	-	expression tag	UNP A6LGH6
F	0	GLY	-	expression tag	UNP A6LGH6
G	0	GLY	-	expression tag	UNP A6LGH6
H	0	GLY	-	expression tag	UNP A6LGH6
I	0	GLY	-	expression tag	UNP A6LGH6
J	0	GLY	-	expression tag	UNP A6LGH6
K	0	GLY	-	expression tag	UNP A6LGH6
L	0	GLY	-	expression tag	UNP A6LGH6
M	0	GLY	-	expression tag	UNP A6LGH6
N	0	GLY	-	expression tag	UNP A6LGH6
O	0	GLY	-	expression tag	UNP A6LGH6
P	0	GLY	-	expression tag	UNP A6LGH6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	90	Total O 90 90	0	0
2	B	38	Total O 38 38	0	0
2	C	50	Total O 50 50	0	0
2	D	21	Total O 21 21	0	0
2	E	97	Total O 97 97	0	0
2	F	46	Total O 46 46	0	0
2	G	64	Total O 64 64	0	0
2	H	24	Total O 24 24	0	0
2	I	84	Total O 84 84	0	0
2	J	50	Total O 50 50	0	0
2	K	55	Total O 55 55	0	0

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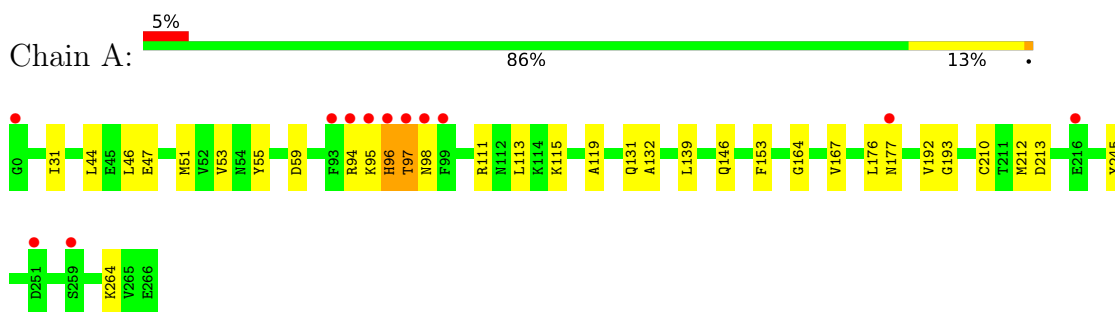
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	L	17	Total O 17 17	0	0
2	M	88	Total O 88 88	0	0
2	N	39	Total O 39 39	0	0
2	O	63	Total O 63 63	0	0
2	P	24	Total O 24 24	0	0

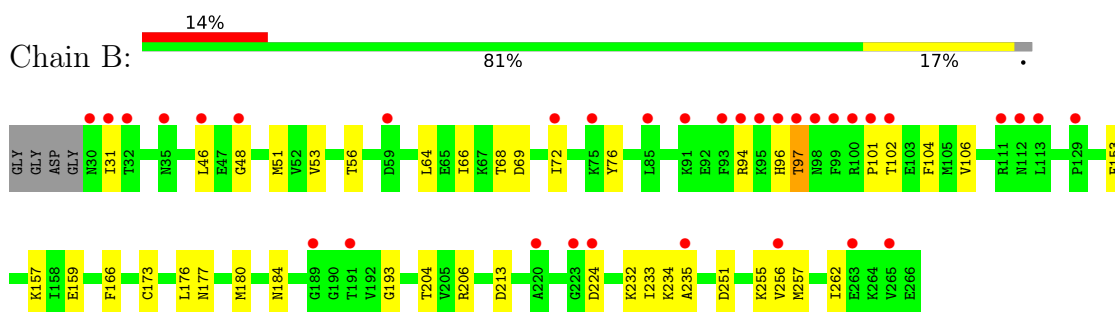
3 Residue-property plots [i](#)

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.

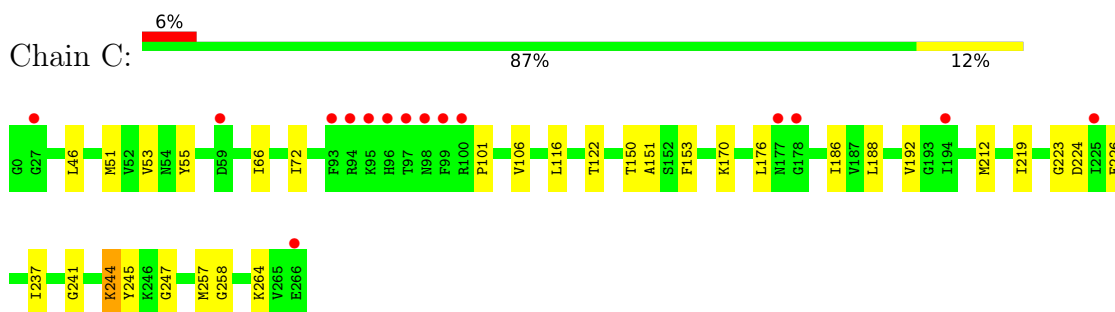
- Molecule 1: Putative pectinase



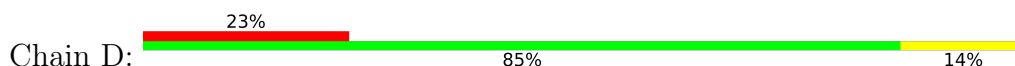
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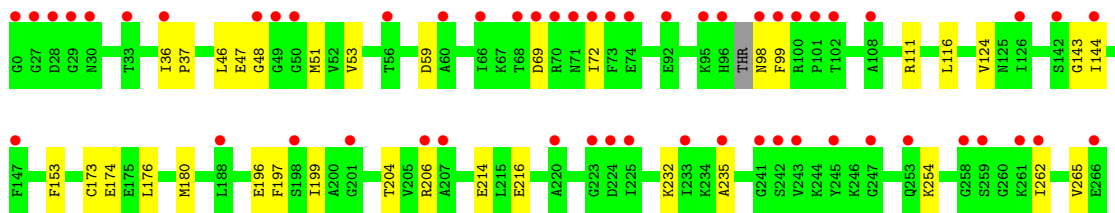


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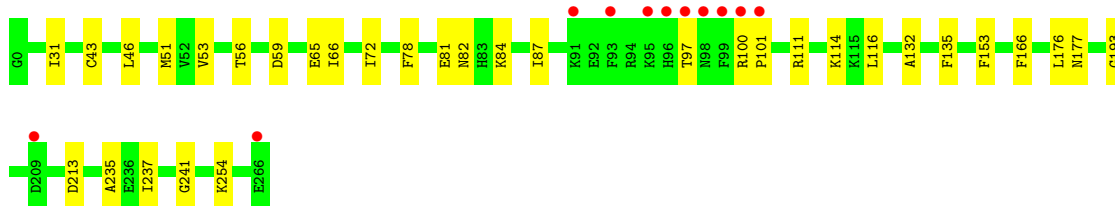
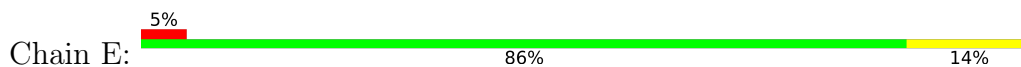


- Molecule 1: Putative pectinase

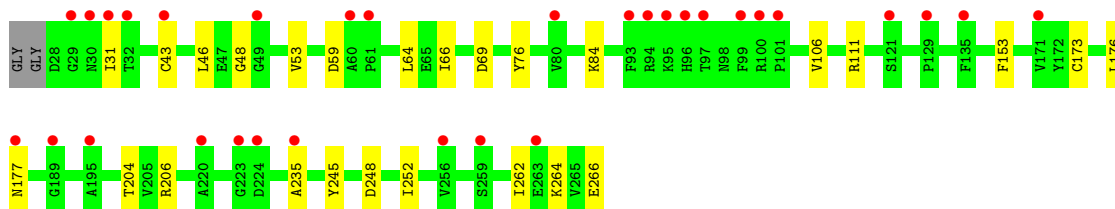
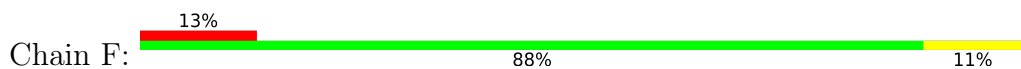




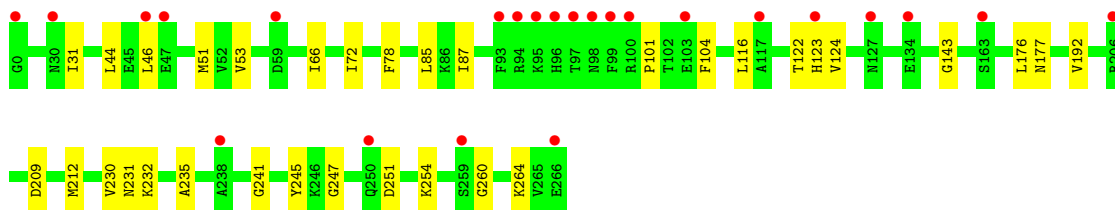
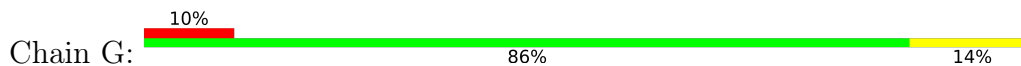
- Molecule 1: Putative pectinase



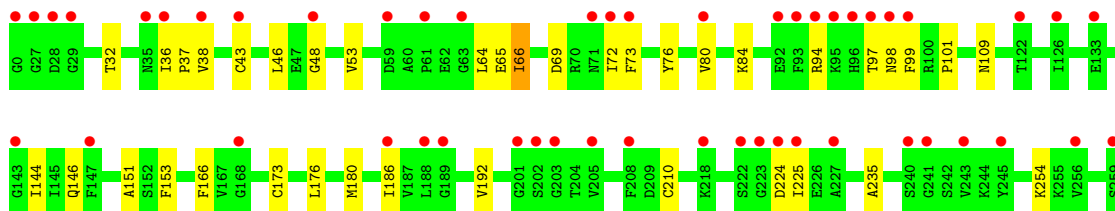
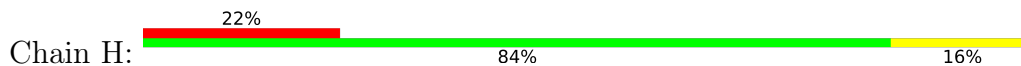
- Molecule 1: Putative pectinase

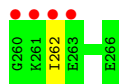


- Molecule 1: Putative pectinase

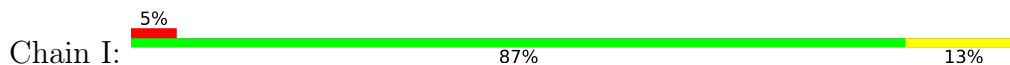


- Molecule 1: Putative pectinase

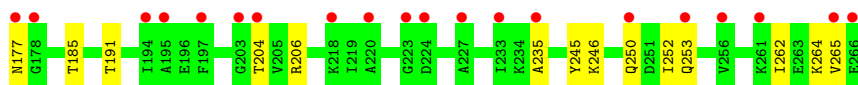
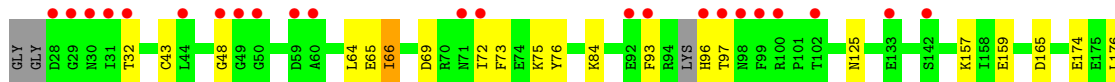
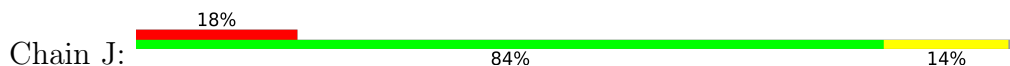




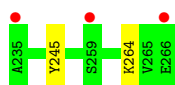
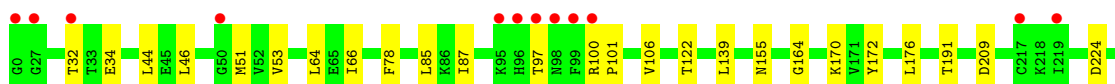
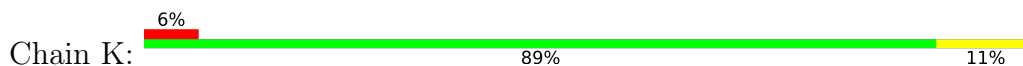
- Molecule 1: Putative pectinase



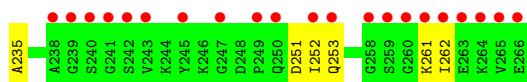
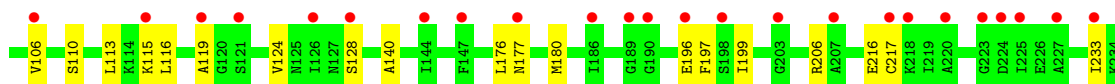
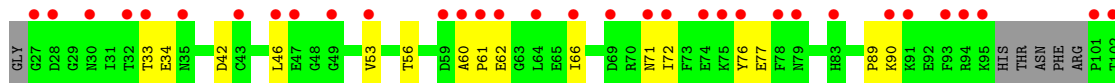
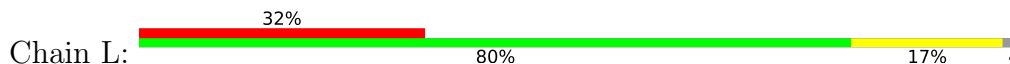
- Molecule 1: Putative pectinase



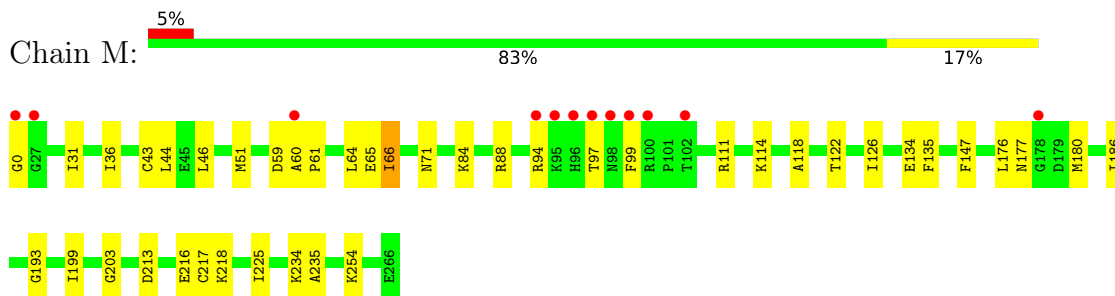
- Molecule 1: Putative pectinase



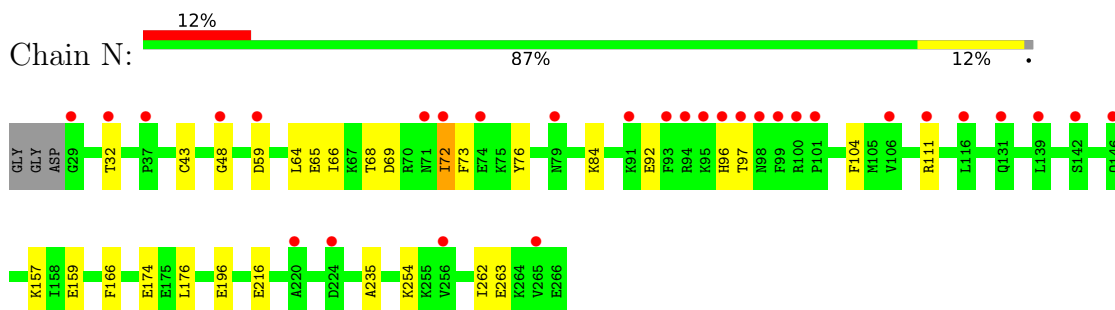
- Molecule 1: Putative pectinase



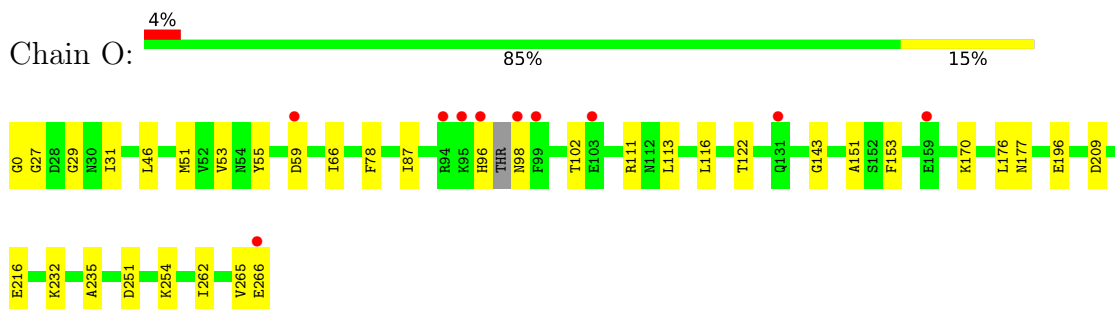
- Molecule 1: Putative pectinase



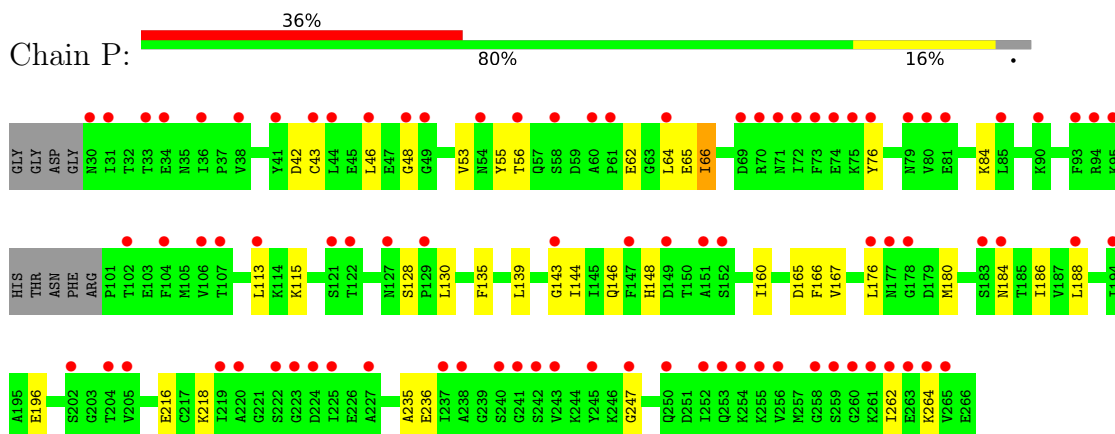
- Molecule 1: Putative pectinase



- Molecule 1: Putative pectinase



- Molecule 1: Putative pectinase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.12Å 104.61Å 393.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.51 – 2.30 49.51 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.5 (49.51-2.30) 97.5 (49.51-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.5.0102, PHENIX	Depositor
R, R_{free}	0.244 , 0.280 0.253 , 0.290	Depositor DCC
R_{free} test set	9370 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtrriage
Anisotropy	0.333	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	29713	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 62.92 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0466e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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	0.81	0/1872	0.67	0/2510
1	B	0.75	0/1815	0.66	1/2435 (0.0%)
1	C	0.75	0/1876	0.66	0/2515
1	D	0.67	0/1812	0.63	0/2431
1	E	0.83	0/1873	0.68	0/2511
1	F	0.69	0/1815	0.65	0/2439
1	G	0.76	0/1847	0.67	0/2477
1	H	0.69	0/1862	0.65	0/2500
1	I	0.81	0/1847	0.67	0/2479
1	J	0.69	0/1848	0.65	0/2479
1	K	0.73	0/1851	0.67	0/2483
1	L	0.70	0/1783	0.63	0/2393
1	M	0.82	0/1915	0.66	0/2565
1	N	0.76	0/1868	0.64	0/2508
1	O	0.76	0/1879	0.67	0/2515
1	P	0.64	0/1702	0.64	0/2291
All	All	0.75	0/29465	0.66	1/39531 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	THR	CB-CA-C	-5.37	110.41	116.63

There are no chirality outliers.

There are no planarity outliers.

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	1831	0	1786	38	0
1	B	1785	0	1730	32	0
1	C	1831	0	1791	25	0
1	D	1780	0	1711	25	0
1	E	1836	0	1792	28	0
1	F	1782	0	1703	18	0
1	G	1811	0	1757	24	0
1	H	1822	0	1744	29	0
1	I	1811	0	1749	33	0
1	J	1809	0	1751	28	0
1	K	1816	0	1768	33	0
1	L	1746	0	1678	28	0
1	M	1862	0	1833	40	0
1	N	1824	0	1768	31	0
1	O	1836	0	1799	33	0
1	P	1681	0	1573	29	0
2	A	90	0	0	2	0
2	B	38	0	0	1	0
2	C	50	0	0	0	0
2	D	21	0	0	1	0
2	E	97	0	0	1	0
2	F	46	0	0	0	0
2	G	64	0	0	1	0
2	H	24	0	0	0	0
2	I	84	0	0	0	0
2	J	50	0	0	2	0
2	K	55	0	0	0	0
2	L	17	0	0	0	0
2	M	88	0	0	1	0
2	N	39	0	0	1	0
2	O	63	0	0	1	0
2	P	24	0	0	0	0
All	All	29713	0	27933	458	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 8.

The worst 5 of 458 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:K:46:LEU:HD23	1:K:51:MSE:CE	1.88	1.04
1:I:46:LEU:CD2	1:I:51:MSE:HE1	1.89	1.02
1:C:46:LEU:HD22	1:C:51:MSE:HE1	1.43	1.00
1:O:46:LEU:HB3	1:O:51:MSE:HE1	1.44	1.00
1:N:72:ILE:HD11	1:N:104:PHE:CZ	2.00	0.97

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	246/241 (102%)	236 (96%)	8 (3%)	2 (1%)	16	20
1	B	238/241 (99%)	224 (94%)	14 (6%)	0	100	100
1	C	247/241 (102%)	232 (94%)	15 (6%)	0	100	100
1	D	240/241 (100%)	231 (96%)	9 (4%)	0	100	100
1	E	244/241 (101%)	236 (97%)	8 (3%)	0	100	100
1	F	241/241 (100%)	231 (96%)	10 (4%)	0	100	100
1	G	244/241 (101%)	232 (95%)	12 (5%)	0	100	100
1	H	245/241 (102%)	234 (96%)	11 (4%)	0	100	100
1	I	244/241 (101%)	234 (96%)	10 (4%)	0	100	100
1	J	241/241 (100%)	231 (96%)	10 (4%)	0	100	100
1	K	244/241 (101%)	237 (97%)	7 (3%)	0	100	100
1	L	237/241 (98%)	223 (94%)	14 (6%)	0	100	100
1	M	249/241 (103%)	237 (95%)	12 (5%)	0	100	100
1	N	243/241 (101%)	231 (95%)	12 (5%)	0	100	100
1	O	243/241 (101%)	233 (96%)	10 (4%)	0	100	100
1	P	229/241 (95%)	216 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3875/3856 (100%)	3698 (95%)	175 (4%)	2 (0%)	48 60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	HIS
1	A	97	THR

5.3.2 Protein sidechains [i](#)

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	194/190 (102%)	194 (100%)	0	100 100
1	B	186/190 (98%)	186 (100%)	0	100 100
1	C	193/190 (102%)	191 (99%)	2 (1%)	68 82
1	D	181/190 (95%)	180 (99%)	1 (1%)	78 89
1	E	194/190 (102%)	194 (100%)	0	100 100
1	F	184/190 (97%)	184 (100%)	0	100 100
1	G	188/190 (99%)	188 (100%)	0	100 100
1	H	188/190 (99%)	186 (99%)	2 (1%)	65 81
1	I	190/190 (100%)	190 (100%)	0	100 100
1	J	190/190 (100%)	188 (99%)	2 (1%)	65 81
1	K	192/190 (101%)	192 (100%)	0	100 100
1	L	180/190 (95%)	180 (100%)	0	100 100
1	M	200/190 (105%)	199 (100%)	1 (0%)	81 90
1	N	194/190 (102%)	191 (98%)	3 (2%)	57 75
1	O	195/190 (103%)	195 (100%)	0	100 100
1	P	167/190 (88%)	166 (99%)	1 (1%)	78 89
All	All	3016/3040 (99%)	3004 (100%)	12 (0%)	84 92

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	66	ILE
1	N	72	ILE
1	P	66	ILE
1	N	174	GLU
1	H	66	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	82	ASN
1	M	146	GLN
1	P	127	ASN
1	N	169	HIS
1	E	82	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

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	236/241 (97%)	0.63	12 (5%) 33 35	15, 32, 44, 64	7 (2%)
1	B	232/241 (96%)	1.32	34 (14%) 6 6	21, 41, 53, 72	3 (1%)
1	C	236/241 (97%)	0.79	15 (6%) 25 27	17, 32, 44, 63	7 (2%)
1	D	235/241 (97%)	1.61	55 (23%) 2 2	22, 42, 52, 69	4 (1%)
1	E	236/241 (97%)	0.62	11 (4%) 36 38	14, 32, 44, 64	5 (2%)
1	F	234/241 (97%)	1.31	31 (13%) 7 8	22, 42, 54, 68	4 (1%)
1	G	236/241 (97%)	1.06	24 (10%) 12 13	17, 33, 44, 63	5 (2%)
1	H	236/241 (97%)	1.59	54 (22%) 2 2	24, 42, 55, 65	6 (2%)
1	I	236/241 (97%)	0.63	11 (4%) 36 38	18, 32, 44, 64	5 (2%)
1	J	233/241 (96%)	1.36	43 (18%) 3 4	21, 42, 52, 64	7 (3%)
1	K	236/241 (97%)	0.77	15 (6%) 25 27	20, 33, 44, 60	4 (1%)
1	L	230/241 (95%)	1.80	78 (33%) 1 1	23, 42, 50, 62	6 (2%)
1	M	236/241 (97%)	0.73	12 (5%) 33 35	17, 32, 44, 62	10 (4%)
1	N	233/241 (96%)	1.32	30 (12%) 7 8	22, 41, 51, 64	7 (3%)
1	O	235/241 (97%)	0.67	10 (4%) 40 41	19, 33, 44, 60	7 (2%)
1	P	227/241 (94%)	1.90	87 (38%) 1 0	25, 42, 49, 60	1 (0%)
All	All	3747/3856 (97%)	1.13	522 (13%) 6 7	14, 37, 50, 72	88 (2%)

The worst 5 of 522 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	98	ASN	8.3
1	D	0	GLY	6.4
1	N	96[A]	HIS	6.4
1	D	99	PHE	6.3
1	A	96	HIS	6.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.