



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:36 AM UTC

PDB ID : 3L4G / pdb_00003l4g
Title : Crystal structure of Homo Sapiens cytoplasmic Phenylalanyl-tRNA synthetase
Authors : Finarov, I.; Moor, N.; Kessler, N.; Klipcan, L.; Safro, M.G.
Deposited on : 2009-12-20
Resolution : 3.30 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

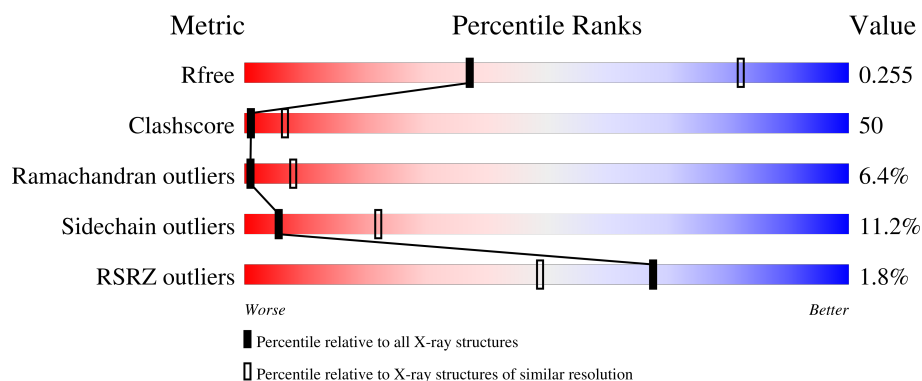
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	508	
1	C	508	
1	E	508	
1	G	508	
1	I	508	

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Mol	Chain	Length	Quality of chain
1	K	508	
1	M	508	
1	O	508	
2	B	589	
2	D	589	
2	F	589	
2	H	589	
2	J	589	
2	L	589	
2	N	589	
2	P	589	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PHE	A	509	-	-	X	-
3	PHE	K	509	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 59395 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 Phenylalanyl-tRNA synthetase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2589	1661	453	464	11			
1	C	508	Total	C	N	O	S	0	0	0
			4058	2571	724	747	16			
1	E	309	Total	C	N	O	S	0	0	0
			2517	1618	439	449	11			
1	G	309	Total	C	N	O	S	0	0	0
			2521	1620	440	450	11			
1	I	313	Total	C	N	O	S	0	0	0
			2551	1639	445	456	11			
1	K	349	Total	C	N	O	S	0	0	0
			2746	1755	482	498	11			
1	M	321	Total	C	N	O	S	0	0	0
			2582	1652	456	463	11			
1	O	309	Total	C	N	O	S	0	0	0
			2527	1623	443	450	11			

- Molecule 2 is a protein called Phenylalanyl-tRNA synthetase beta chain.

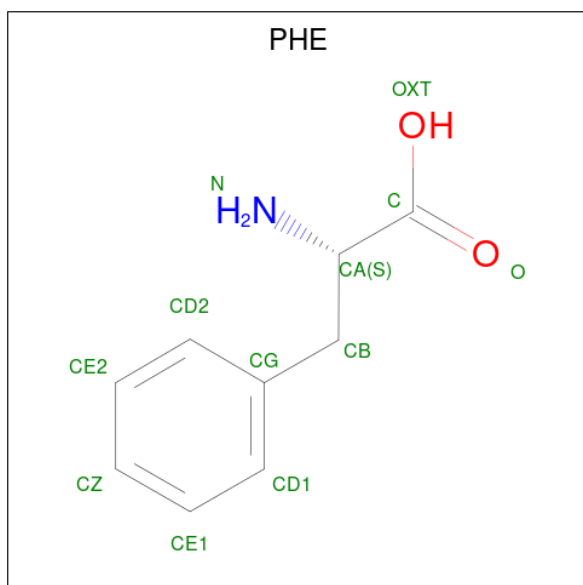
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	D	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	F	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	H	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	J	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	L	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			

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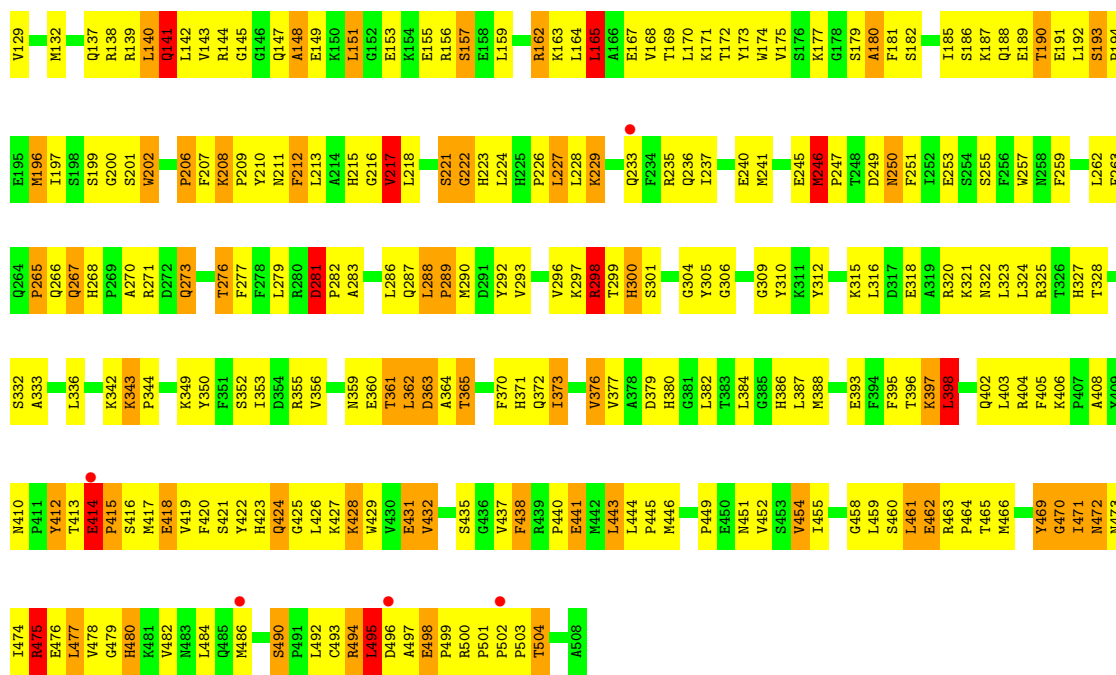
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			
2	P	589	Total	C	N	O	S	0	0	0
			4651	2981	781	866	23			

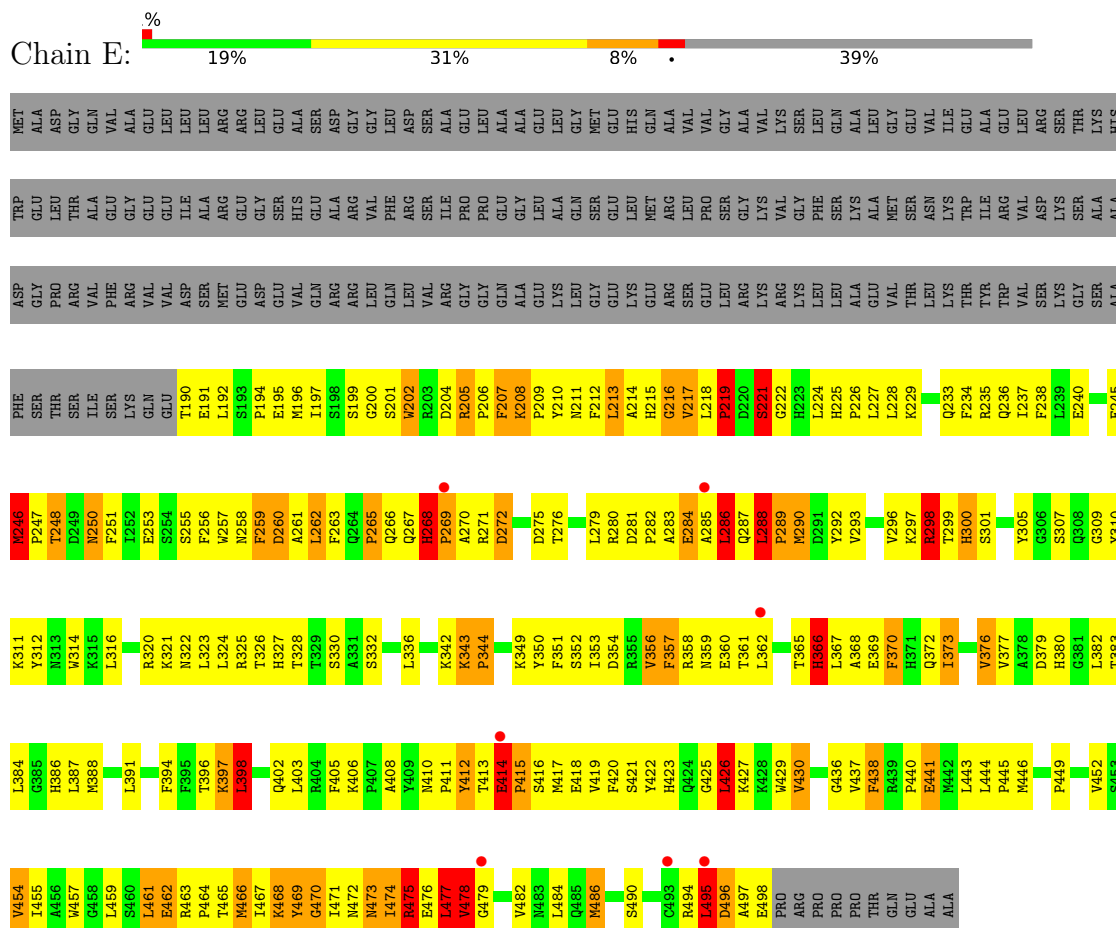
- Molecule 3 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



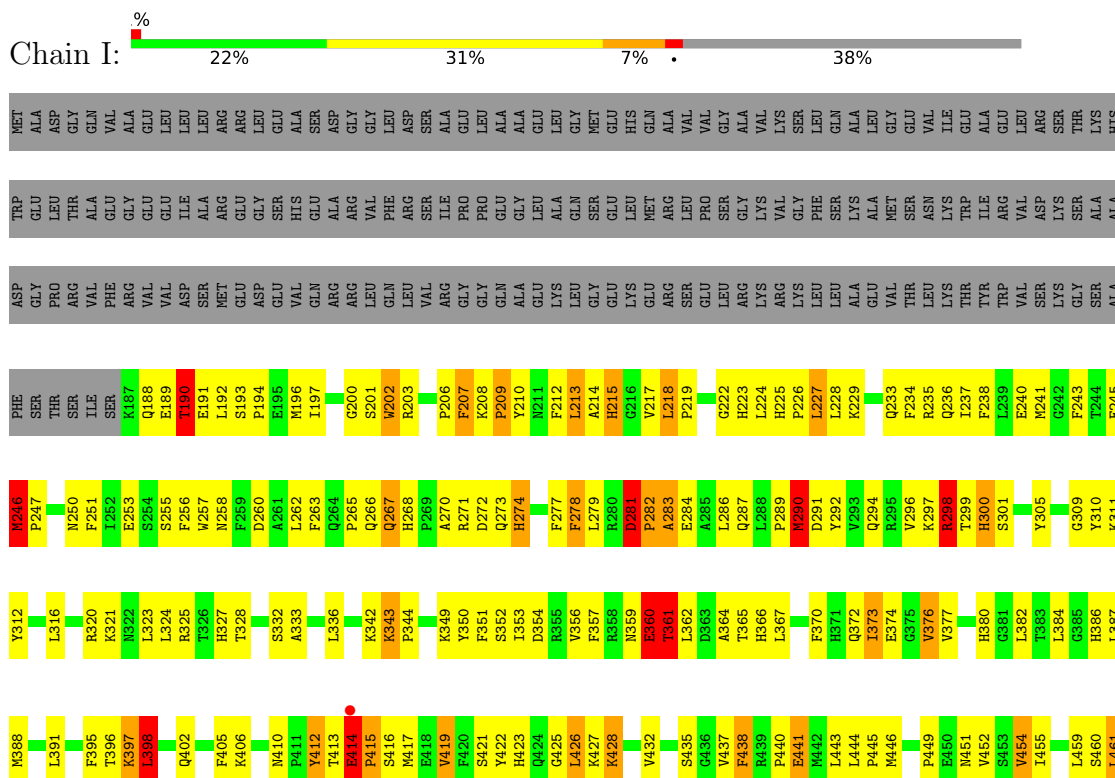
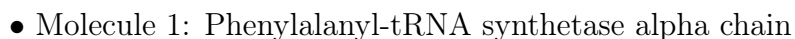
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	9	1	2		
3	C	1	Total	C	N	O	0	0
			12	9	1	2		
3	E	1	Total	C	N	O	0	0
			12	9	1	2		
3	G	1	Total	C	N	O	0	0
			12	9	1	2		
3	I	1	Total	C	N	O	0	0
			12	9	1	2		
3	K	1	Total	C	N	O	0	0
			12	9	1	2		
3	M	1	Total	C	N	O	0	0
			12	9	1	2		
3	O	1	Total	C	N	O	0	0
			12	9	1	2		



• Molecule 1: Phenylalanyl-tRNA synthetase alpha chain

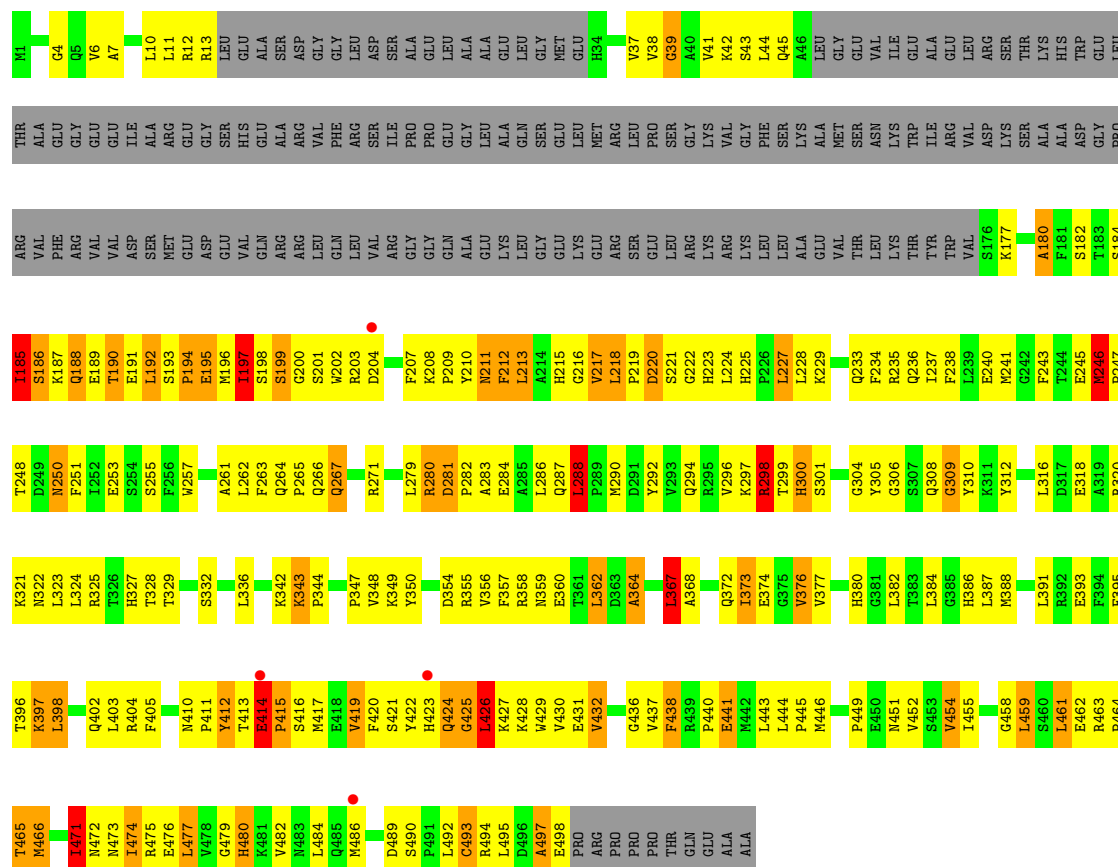
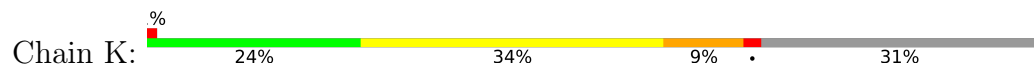


• Molecule 1: Phenylalanyl-tRNA synthetase alpha chain

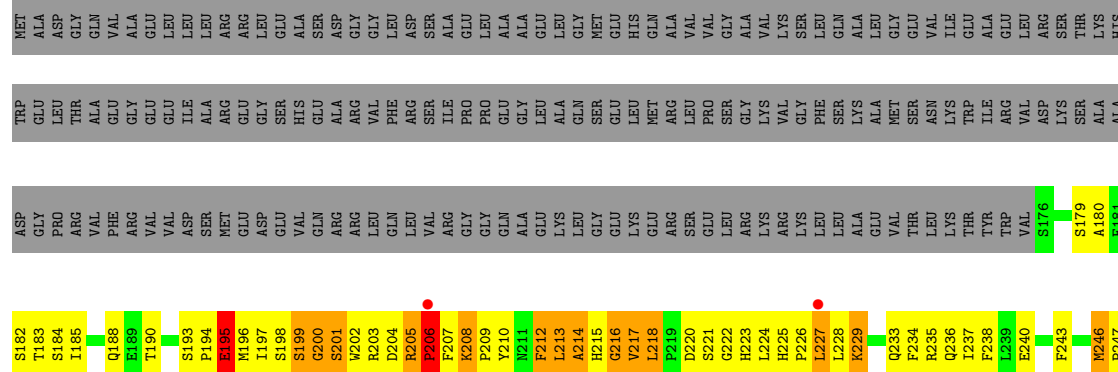


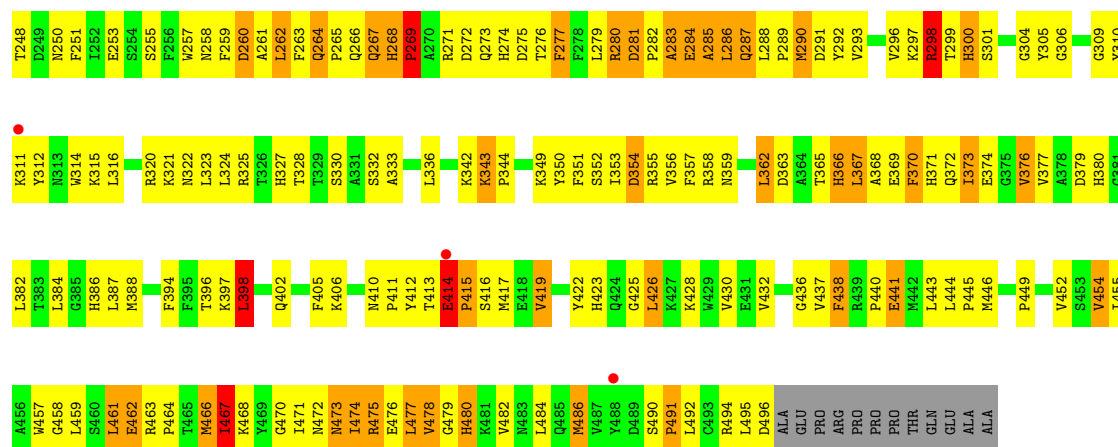


• Molecule 1: Phenylalanyl-tRNA synthetase alpha chain

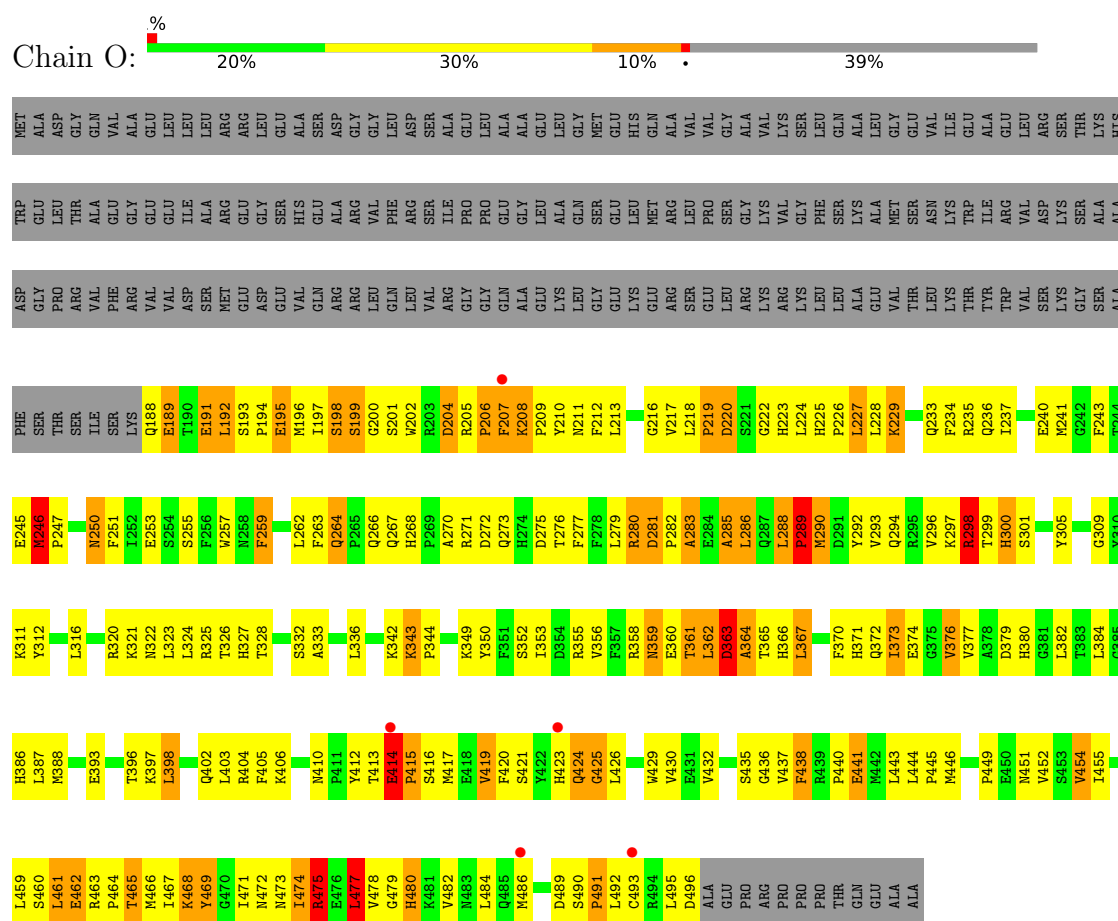


• Molecule 1: Phenylalanyl-tRNA synthetase alpha chain

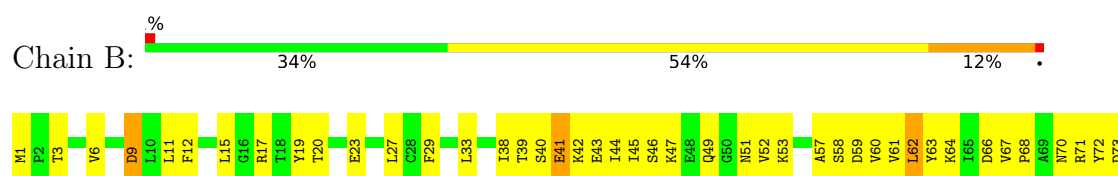


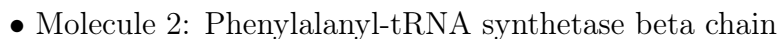


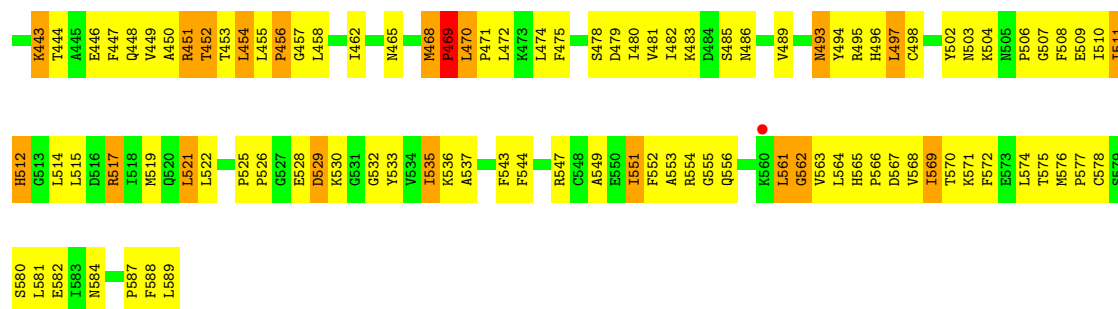
• Molecule 1: Phenylalanyl-tRNA synthetase alpha chain



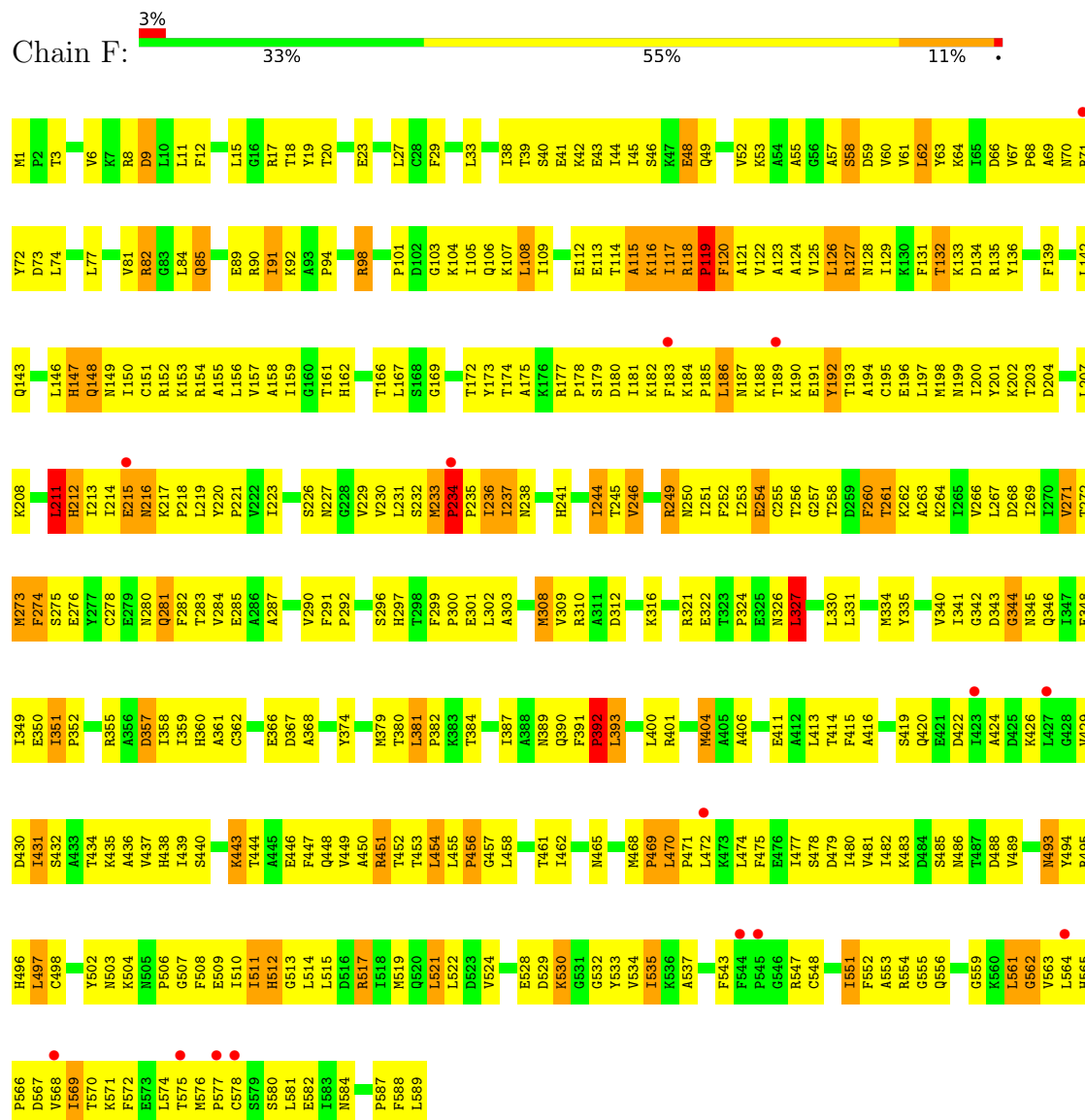
• Molecule 2: Phenylalanyl-tRNA synthetase beta chain





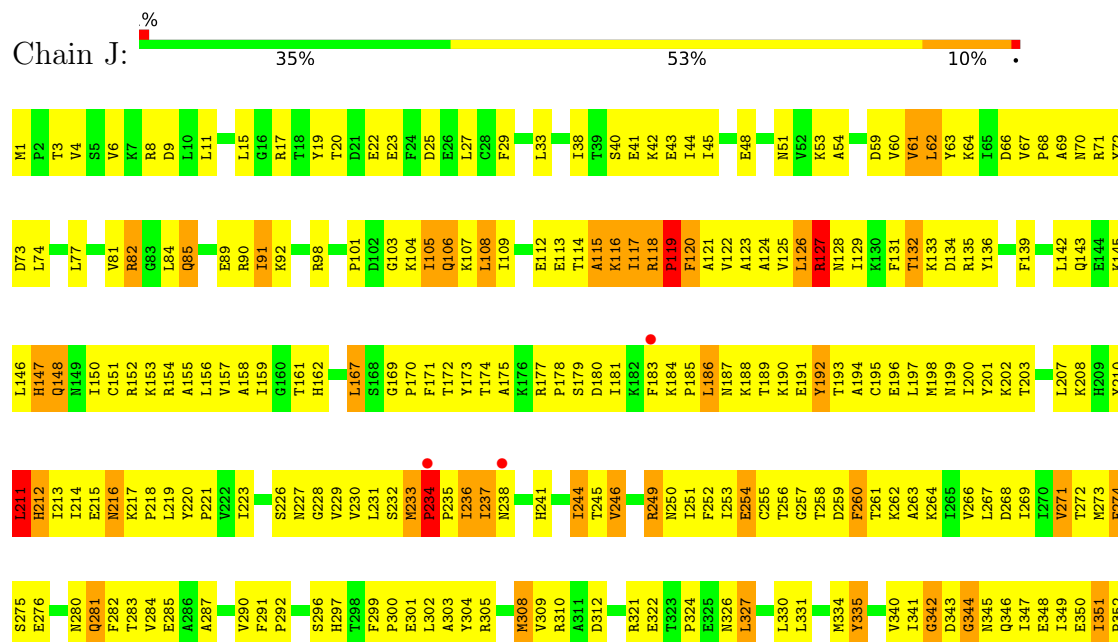
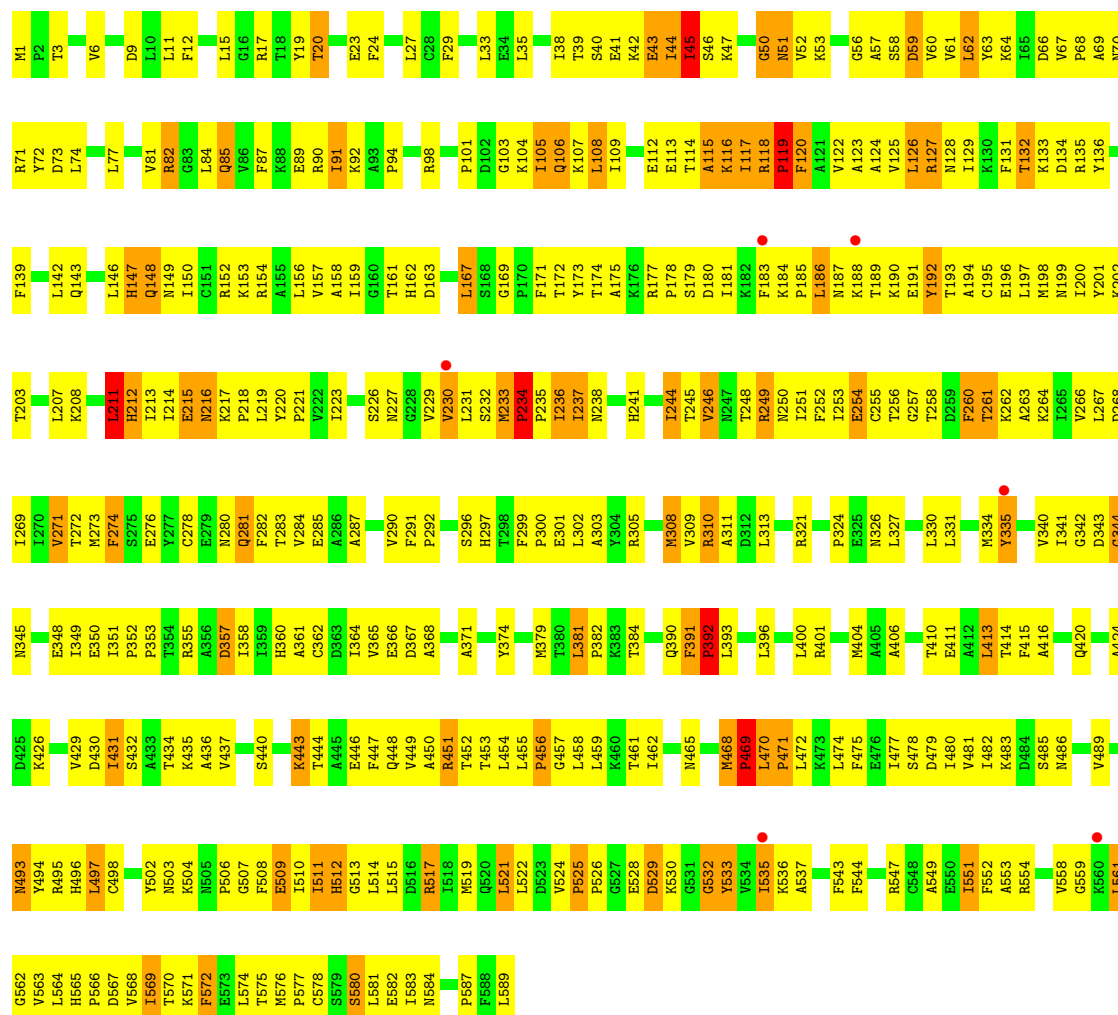


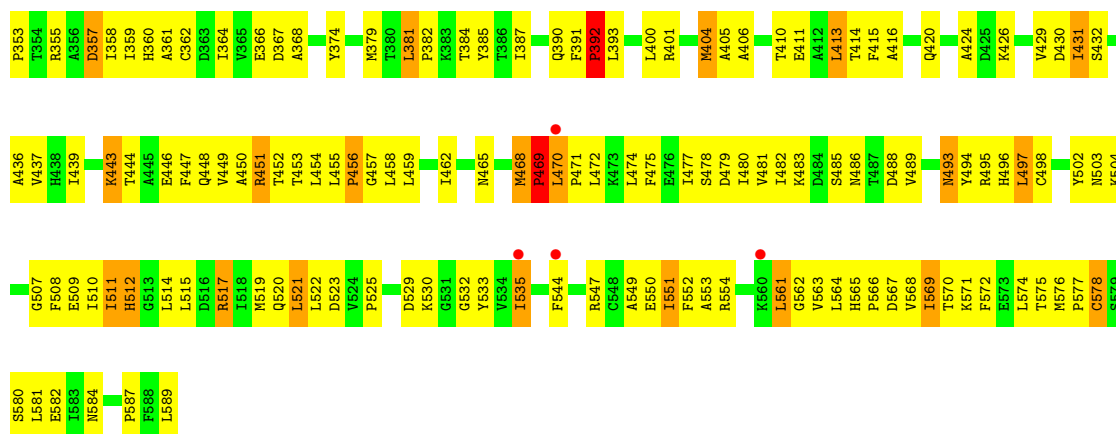
• Molecule 2: Phenylalanyl-tRNA synthetase beta chain



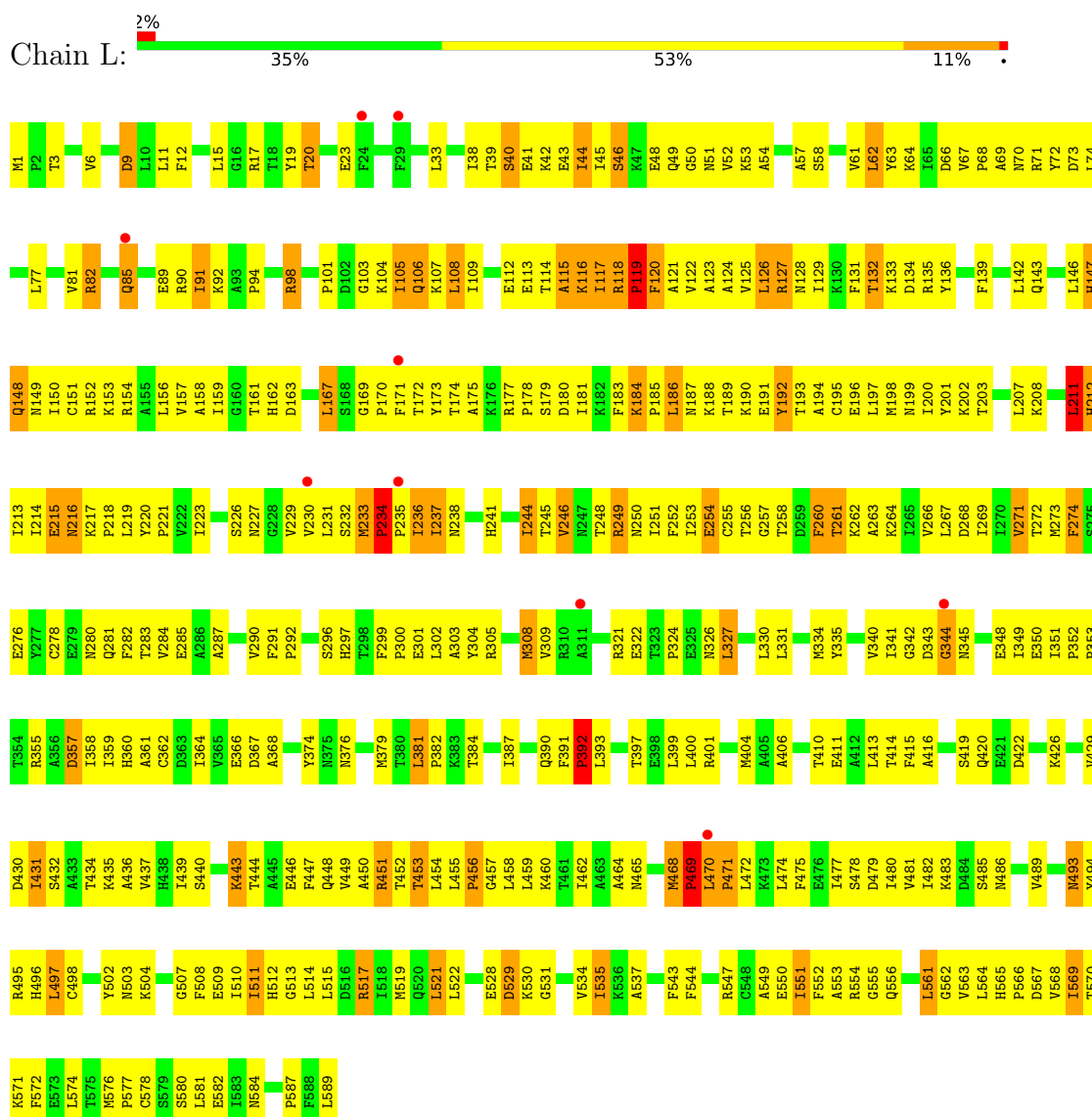
• Molecule 2: Phenylalanyl-tRNA synthetase beta chain



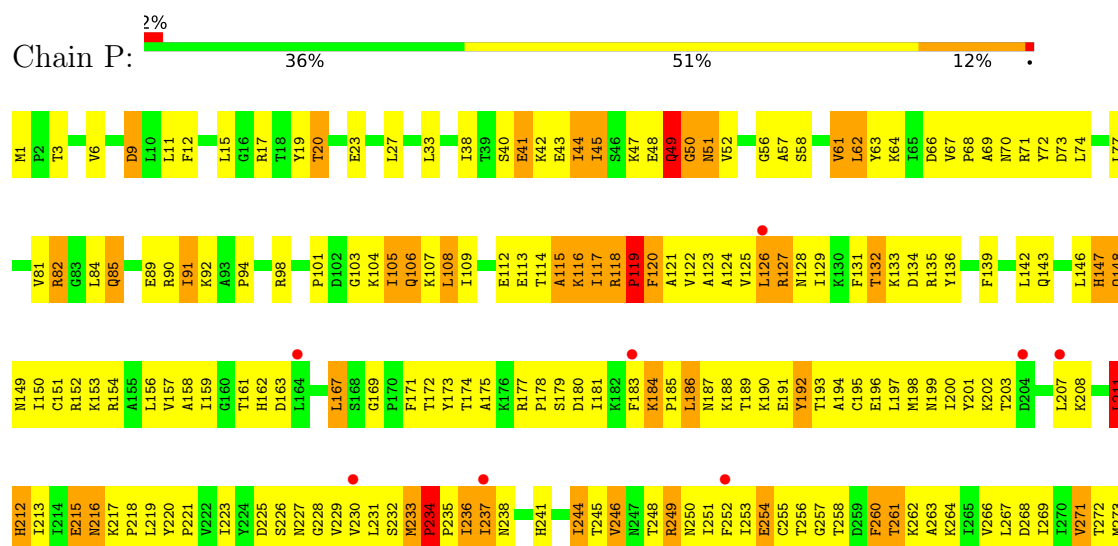


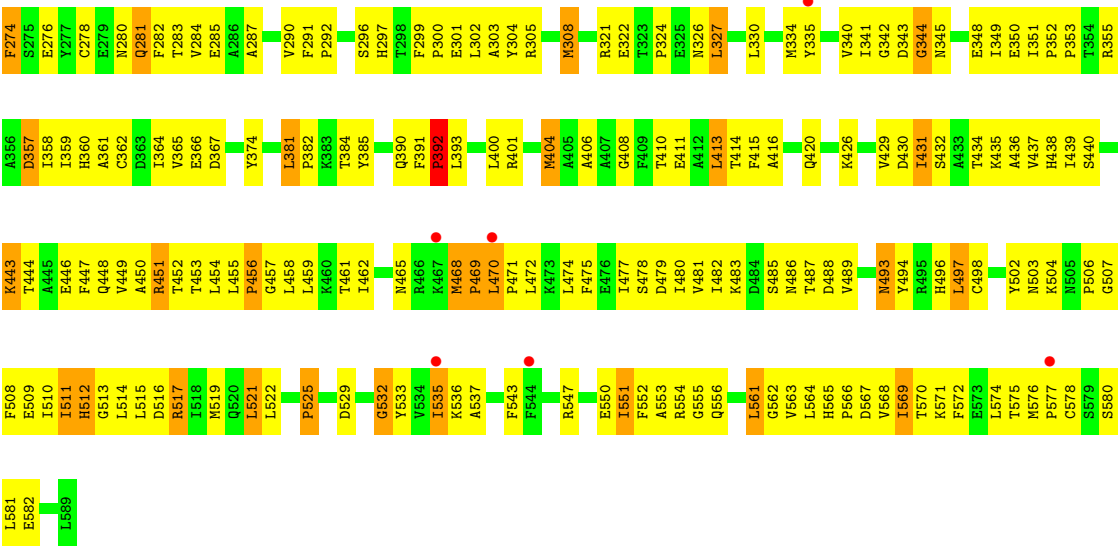


● Molecule 2: Phenylalanyl-tRNA synthetase beta chain



● Molecule 2: Phenylalanyl-tRNA synthetase beta chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	363.34Å 213.88Å 212.96Å 90.00° 125.20° 90.00°	Depositor
Resolution (Å)	30.00 – 3.30 30.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	96.0 (30.00-3.30) 96.8 (30.00-3.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 3.31Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.242 , 0.287 0.251 , 0.255	Depositor DCC
R_{free} test set	9780 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	94.6	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 98.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.009 for -h+k-l,-l,-k 0.002 for -h-k-l,l,k 0.000 for 1/2*h+1/2*k+2*1,1/2*h+1/2*k,-1/2*h+1/2*k-l 0.000 for -1/2*h-3/2*k-l,-1/2*h+1/2*k-l,1/2*h+1/2*k 0.000 for -1/2*h+3/2*k-l,1/2*h+1/2*k+l,1/2*h-1/2*k 0.000 for 1/2*h-1/2*k+2*1,-1/2*h+1/2*k,-1/2*h-1/2*k-l 0.000 for -1/2*h+1/2*k+l,1/2*h-1/2*k+l,1/2*h+1/2*k 0.000 for -1/2*h-1/2*k+l,-1/2*h-1/2*k-l,1/2*h-1/2*k 0.000 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h-1/2*k-l 0.000 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h+1/2*k-l 0.019 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	59395	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

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.

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.61	0/2664	1.09	19/3609 (0.5%)
1	C	0.53	0/4154	1.11	40/5611 (0.7%)
1	E	0.57	0/2591	1.10	24/3511 (0.7%)
1	G	0.55	0/2595	1.09	21/3516 (0.6%)
1	I	0.59	0/2626	1.10	21/3558 (0.6%)
1	K	0.55	0/2819	1.11	27/3818 (0.7%)
1	M	0.51	0/2656	1.04	15/3592 (0.4%)
1	O	0.50	0/2601	0.99	12/3523 (0.3%)
2	B	0.56	0/4742	1.07	31/6420 (0.5%)
2	D	0.50	0/4742	1.03	22/6420 (0.3%)
2	F	0.56	1/4742 (0.0%)	1.06	28/6420 (0.4%)
2	H	0.50	3/4742 (0.1%)	1.03	21/6420 (0.3%)
2	J	0.54	0/4742	1.06	25/6420 (0.4%)
2	L	0.48	0/4742	1.03	22/6420 (0.3%)
2	N	0.52	4/4742 (0.1%)	1.03	24/6420 (0.4%)
2	P	0.45	0/4742	1.02	23/6420 (0.4%)
All	All	0.53	8/60642 (0.0%)	1.06	375/82098 (0.5%)

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
2	N	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	311	ALA	N-CA	-6.18	1.38	1.46
2	N	310	ARG	CA-C	-5.91	1.45	1.52
2	N	310	ARG	C-N	-5.85	1.25	1.33
2	H	311	ALA	N-CA	5.83	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	273	MET	SD-CE	5.78	1.94	1.79

The worst 5 of 375 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	233	MET	CA-C-N	12.24	132.99	120.38
2	J	233	MET	C-N-CA	12.24	132.99	120.38
2	N	233	MET	CA-C-N	11.90	132.64	120.38
2	N	233	MET	C-N-CA	11.90	132.64	120.38
2	D	233	MET	CA-C-N	11.89	132.63	120.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	N	533	TYR	Sidechain

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	2589	0	2537	279	0
1	C	4058	0	4030	474	0
1	E	2517	0	2462	300	0
1	G	2521	0	2465	315	0
1	I	2551	0	2496	248	0
1	K	2746	0	2632	295	0
1	M	2582	0	2506	334	0
1	O	2527	0	2476	293	0
2	B	4651	0	4751	491	0
2	D	4651	0	4751	477	0
2	F	4651	0	4751	520	0
2	H	4651	0	4751	467	0
2	J	4651	0	4751	477	0
2	L	4651	0	4751	473	0
2	N	4651	0	4751	508	0
2	P	4651	0	4751	472	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	12	0	8	7	0
3	C	12	0	8	2	0
3	E	12	0	8	1	0
3	G	12	0	8	3	0
3	I	12	0	8	2	0
3	K	12	0	8	7	0
3	M	12	0	8	4	0
3	O	12	0	8	4	0
All	All	59395	0	59676	5959	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.

The worst 5 of 5959 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)
2:N:49:GLN:HE21	2:N:52:VAL:HG11	1.06	1.13
2:N:381:LEU:HD23	2:N:382:PRO:HD2	1.30	1.12
2:J:381:LEU:HD23	2:J:382:PRO:HD2	1.26	1.11
2:N:117:ILE:HG23	2:N:217:LYS:HD2	1.33	1.11
1:O:188:GLN:HB2	1:O:206:PRO:HG2	1.33	1.10

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	316/508 (62%)	246 (78%)	42 (13%)	28 (9%)	0 4
1	C	506/508 (100%)	382 (76%)	84 (17%)	40 (8%)	1 5
1	E	307/508 (60%)	233 (76%)	42 (14%)	32 (10%)	0 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	307/508 (60%)	241 (78%)	34 (11%)	32 (10%)	0	2
1	I	311/508 (61%)	254 (82%)	38 (12%)	19 (6%)	1	9
1	K	343/508 (68%)	257 (75%)	58 (17%)	28 (8%)	0	5
1	M	319/508 (63%)	233 (73%)	46 (14%)	40 (12%)	0	1
1	O	307/508 (60%)	243 (79%)	36 (12%)	28 (9%)	0	3
2	B	587/589 (100%)	484 (82%)	77 (13%)	26 (4%)	2	13
2	D	587/589 (100%)	480 (82%)	77 (13%)	30 (5%)	1	11
2	F	587/589 (100%)	485 (83%)	78 (13%)	24 (4%)	2	15
2	H	587/589 (100%)	478 (81%)	74 (13%)	35 (6%)	1	9
2	J	587/589 (100%)	482 (82%)	78 (13%)	27 (5%)	2	13
2	L	587/589 (100%)	478 (81%)	82 (14%)	27 (5%)	2	13
2	N	587/589 (100%)	479 (82%)	75 (13%)	33 (6%)	1	9
2	P	587/589 (100%)	474 (81%)	84 (14%)	29 (5%)	1	12
All	All	7412/8776 (84%)	5929 (80%)	1005 (14%)	478 (6%)	1	8

5 of 478 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	GLY
1	A	203	ARG
1	A	206	PRO
1	A	215	HIS
1	A	265	PRO

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	281/434 (65%)	252 (90%)	29 (10%)	7	25
1	C	434/434 (100%)	383 (88%)	51 (12%)	5	20
1	E	272/434 (63%)	234 (86%)	38 (14%)	3	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	273/434 (63%)	243 (89%)	30 (11%)	6	23
1	I	276/434 (64%)	248 (90%)	28 (10%)	7	26
1	K	284/434 (65%)	245 (86%)	39 (14%)	3	16
1	M	276/434 (64%)	242 (88%)	34 (12%)	4	19
1	O	274/434 (63%)	239 (87%)	35 (13%)	4	18
2	B	513/513 (100%)	454 (88%)	59 (12%)	5	21
2	D	513/513 (100%)	459 (90%)	54 (10%)	6	25
2	F	513/513 (100%)	461 (90%)	52 (10%)	7	26
2	H	513/513 (100%)	458 (89%)	55 (11%)	6	24
2	J	513/513 (100%)	460 (90%)	53 (10%)	7	25
2	L	513/513 (100%)	459 (90%)	54 (10%)	6	25
2	N	513/513 (100%)	455 (89%)	58 (11%)	5	21
2	P	513/513 (100%)	458 (89%)	55 (11%)	6	24
All	All	6474/7576 (86%)	5750 (89%)	724 (11%)	6	22

5 of 724 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	288	LEU
1	M	477	LEU
1	K	432	VAL
1	K	286	LEU
2	L	327	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 261 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	258	ASN
1	O	372	GLN
2	P	584	ASN
1	G	211	ASN
2	F	493	ASN

5.3.3 RNA ⓘ

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](#)

8 ligands 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	$\# Z > 2$
3	PHE	G	509	-	11,12,12	0.67	0	11,15,15	0.27	0
3	PHE	E	509	-	11,12,12	0.85	0	11,15,15	0.25	0
3	PHE	C	509	-	11,12,12	0.76	0	11,15,15	0.41	0
3	PHE	K	509	-	11,12,12	0.73	0	11,15,15	0.34	0
3	PHE	M	509	-	11,12,12	0.70	0	11,15,15	0.34	0
3	PHE	O	509	-	11,12,12	0.88	0	11,15,15	0.27	0
3	PHE	A	509	-	11,12,12	0.97	0	11,15,15	0.43	0
3	PHE	I	509	-	11,12,12	0.66	0	11,15,15	0.24	0

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	PHE	G	509	-	-	2/8/8/8	0/1/1/1
3	PHE	E	509	-	-	4/8/8/8	0/1/1/1
3	PHE	C	509	-	-	0/8/8/8	0/1/1/1
3	PHE	K	509	-	-	1/8/8/8	0/1/1/1
3	PHE	M	509	-	-	4/8/8/8	0/1/1/1
3	PHE	O	509	-	-	4/8/8/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PHE	A	509	-	-	0/8/8/8	0/1/1/1
3	PHE	I	509	-	-	4/8/8/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	509	PHE	O-C-CA-N
3	I	509	PHE	N-CA-CB-CG
3	O	509	PHE	N-CA-CB-CG
3	O	509	PHE	C-CA-CB-CG
3	E	509	PHE	OXT-C-CA-N

There are no ring outliers.

8 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	509	PHE	3	0
3	E	509	PHE	1	0
3	C	509	PHE	2	0
3	K	509	PHE	7	0
3	M	509	PHE	4	0
3	O	509	PHE	4	0
3	A	509	PHE	7	0
3	I	509	PHE	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	318/508 (62%)	-0.19	5 (1%)	70 52	47, 84, 168, 200	0
1	C	508/508 (100%)	-0.14	6 (1%)	76 58	50, 107, 181, 201	0
1	E	309/508 (60%)	0.02	7 (2%)	61 42	47, 103, 181, 201	0
1	G	309/508 (60%)	-0.04	4 (1%)	75 56	54, 103, 179, 200	0
1	I	313/508 (61%)	-0.24	4 (1%)	75 56	42, 91, 164, 192	0
1	K	349/508 (68%)	-0.15	4 (1%)	78 60	48, 101, 178, 201	0
1	M	321/508 (63%)	0.21	5 (1%)	70 52	51, 133, 189, 201	0
1	O	309/508 (60%)	-0.06	5 (1%)	70 52	65, 112, 183, 201	0
2	B	589/589 (100%)	-0.12	7 (1%)	76 58	47, 93, 154, 201	0
2	D	589/589 (100%)	0.15	7 (1%)	76 58	56, 129, 199, 201	0
2	F	589/589 (100%)	0.14	15 (2%)	58 39	51, 104, 175, 201	0
2	H	589/589 (100%)	0.16	6 (1%)	79 63	63, 131, 188, 201	0
2	J	589/589 (100%)	-0.04	7 (1%)	76 58	57, 99, 158, 201	0
2	L	589/589 (100%)	0.13	9 (1%)	72 53	61, 139, 201, 201	0
2	N	589/589 (100%)	0.44	31 (5%)	32 22	58, 134, 192, 201	0
2	P	589/589 (100%)	0.28	14 (2%)	59 40	73, 153, 201, 201	0
All	All	7448/8776 (84%)	0.06	136 (1%)	67 49	42, 114, 190, 201	0

The worst 5 of 136 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	486	MET	4.0
2	N	535	ILE	3.9
1	M	227	LEU	3.8
2	H	335	TYR	3.7
2	N	577	PRO	3.6

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	PHE	A	509	12/12	0.91	0.17	90,92,129,130	0
3	PHE	M	509	12/12	0.91	0.16	96,99,201,201	0
3	PHE	C	509	12/12	0.92	0.15	81,83,172,174	0
3	PHE	G	509	12/12	0.93	0.14	81,86,201,201	0
3	PHE	O	509	12/12	0.93	0.10	82,84,201,201	0
3	PHE	K	509	12/12	0.95	0.11	82,83,189,189	0
3	PHE	E	509	12/12	0.95	0.15	68,71,201,201	0
3	PHE	I	509	12/12	0.95	0.12	64,69,201,201	0

6.5 Other polymers [i](#)

There are no such residues in this entry.